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version 5.1.9  - 2006 Biocceleration Ltd.  v model  22:48:41; Search time 14.8101 Seconds (without alignments)  84.457 Million cell updates/sec  1.5  1.5  1.5  1.5  1.5  1.5  1.5  1.	edicted by chance to have one of the result being praise of the result being praise of the distribution.  ES	antifreeze protein hypothetical protein ribosomal protein probable MASH-2 pr achaete scute prot homeotic protein H genomic screen hom paired type homeob homeotic protein H zing-finger protein homeotic protein H zing-finger protein protein Kinase C-b gene NKx6.1 protein probable homeobox probable homeobox probable homeobox probable homeobox basic helix-loop-h engrailed homeodom homeotic protein e zing-finger protein e zing-finger protein basic helix-loop-h phosophatidylinosit zing finger protei basic helix-loop-h phosphatidylinosit zing finger protei transcription fact myg-associated zin polyomavirus enhan
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C;Species: Homo sapiens (man)
C;Date: 16-U1-1999 #sequence_revision 16-Jul-1999 #text_change 02-Sep-2000
C;Accession: JC5954
R;Tanaka, M.; Tanaka, T.; Harata, M.; Suzuki, T.; Mitsui, Y.
Biochem. Biophys. Res. Commun. 243, 531-537, 1998
A;Title: Triplet repeat-containing ribosomal protein L14 gene in immortalized human endc
A;Reference number: JC5954; MUID:98153799; PMID:9480843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-220 <TAN>
A;Cross-references: UNIPARC:UPI000004E622; DDBJ:D87735; NID:g1620021; PIDN:BAA13443.1; E
C;Superfamily: rat ribosomal protein L14
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Cispecies: Rattus norvegicus (Norway rat)
Cibate: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
CiAccession: 811563
RiJohnson, J.E.; Birren, S.J.; Anderson, D.J.
Rature 346, 858-861, 1990
AlyTitle: Two rat homologues of Drosophila achaete-scute specifically expressed in neurol A;Reference number: 811562; MUID:90363294; PMID:2392153
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A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-233 <JOH>
A;Cross-references: UNIPROT:P19359; UNIPARC:UPI0000047567; EMBL:X53725; NID:g56630; PIDIC;Keywords: DNA binding
23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
                       C;Accession: T12547
R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, submitted to the Protein Sequence Database, June 1999
A;Reference number: Z17528
                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:Q9Y4M1; UNIPARC:UPI0000071DDD; EMBL:AL080235 A;Experimental source: adult uterus; clone DKFZp586E1621 C;Genetics:
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84.6%; Pred. No. 15;
ive 0; Mismatches
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Best Local Similarity 84.0
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Best Local Similarity 84.6
Matches 11; Conservative
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                                                                                                                                             A, Accession: T12547
A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-150 <OTT>
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A;Molecule type: DNA
A;Rosiouse: 1-63,'V',65-91 <GAU>
A;Cross-references: UNIPARC:UP10000001382; EMBL:X53718; NID:g64213; PIDN:CAA37754.1; PID
C;Genetics:
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A; Residues: 1-91 - GGUJ-
A; Cross-references: UNIPROT: P07835; UNIPARC: UPI0000125B4B; GB: M10148; NID: g213579; PIDN:
R; Gauthier, S.; Wu, Y.; Davies, P.L.
R; Gauthier, S.; Wu, Y.; Bavies, P.L.
R; Gauthier, S.; Wu, Y.; Davies, P.L.
A; Title: Mucleotide seguence of a variant antifreeze protein gene.
A; Reference number: S12604; MUID: 90384854; PMID: 2402466
                                                                                                                                                antifreeze protein 4 precursor - winter flounder (Species: Pseudopleuronectes americanus (Winter flounder)
C;Species: Pseudopleuronectes americanus (Winter flounder)
C;Accession: A01193
R;Lin, Y.; Gross, J.K.
Proc. Natl. Acad. Sci. U.S.A. 78, 2825-2829, 1981
A;Title: Molecular cloning and characterization of winter flounder antifreeze cDNA.
A;Reference number: A03193; MUID:81247379; PMID:6265915
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C;Date: 05-0ct-1988 #sequence_revision 05-0ct-1988 #text_change 09-Jul-2004
C;Accession: A2592; 812604
J; Biol. Chem. 259, 14960-14965, 1984
A;Title: Winter flounder antifreeze proteins: a multigene family.
A;Reference number: A22592; MUID:85084993; PMID:6548752
A;Accession: A22592.
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C;Keywords: antifreeze; tandem repeat
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-91/Product: antifreeze protein IIA7 #status predicted <MAT>
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C;Superfamily: antifreeze protein
C;Kywords: antifreeze protein
F;1-21/Domain: signal sequence #status predicted <SIG>F;22-85/Product: antifreeze protein 4 #status predicted <MAT>
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hypothetical protein DKFZp586E1621.1 - human (fragment)
C;Species: Homo sapiens (man)
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Pred. No. 7;
0; Mismatches 2
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           ALIGNMENTS
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Best Local Similarity 84.6%;
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A; Residues: 1-85 <LIN>
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R;Yokoyama, M.; Nishi, Y.; Yoshii, J.; Okubo, K.; Matsubara, K.
DNA Res. 3, 311-320, 1996
A;Title: Identification and cloning of neuroblastoma-specific and nerve tissue-specific A;Reference number: JC5272; MUID:97191543; PMID:9039501
A;Contents: neuroblastma cell
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A;Residues: 1-314 <YOK>
A;Cross-references: UNIPROT:Q99453; UNIPARC:UPI0000131D16; DDBJ:D82344; NID:g1841337; P:CCOSSS-references: UNIPROT:Q99453; UNIPARC:UPI0000131D16; DDBJ:D82344; NID:g1841337; P:C;Comment: This protein is a transcriptional repressor involved in regulating gene expr.C;Reywords: DNA binding; homeobox; nucleus; transcription regulation
F;99,-155/Domain: homeobox homology <HOX>
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C;Species: Mus musculus (house mouse)
C;Date: 13-dan-1995 #sequence revision 13-Jan-1995 #text_change 05-Oct-2004
C;Accession: 516318; 540403; $57443
R;Izpisua-Belmonte, J.C.; Falkenstein, H.; Dolle, P.; Renucci, A.; Duboule, D.
R;RDO J. 10, 2279-2289, 1991
A;Title: Murine genes related to the Drosophila AbdB homeotic gene are sequentially exp
A;Reference number: $16317; MUID:91293104; PMID:1676674
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A; Residues: 1-32 < IZEP.
A; Residues: 1-32 < IZEP.
A; Cross-references: UNIPROT: P23813; UNIPARC: UP10000029F10; EMBL: X60761; NID: 951420; PIDI
R; Gerard, M.; Duboule, D.; Zakany, J.
B; Gerard, M.; Duboule, D.; Zakany, J.
B; Gerard, M.; Duboule, D.; Zakany, J.
A; Title: Structure and activity of regulatory elements involved in the activation of the
A; Reference number: $40403; MUID: 94074553; PMID: 7902810
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A;Cross-references: UNIPARC:UPI0000026A38; EMBL:X60395; NID:g871427; PIDN:CAA42943.1; P
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A; Cross-treferences: UNIPARC: UPI0000029F10; EMBL: X71422; NID: 9397508; PIDN: CAA50553.1;
R; Takada, S.; Cook, M.; Kramlauf, R.; McMahon, A.P.
R; Takada, S.; Cook, M.; Kramlauf, R.; McMahon, A.P.
R; Description: Genomic sequence of mouse Hox-4.6.
A; Reference number: S57443
A; Accession: S57443
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C;Species: Homo sapiens (man)
C;Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 05-Oct-2004
                                                                                                                                                                Gaps
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C;Keywords: DNA binding; homeobox; nucleus; transcription regulation F;204-260/Domain: homeobox homology <HOX>
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0; Mismatches
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A;Status: nucleic acid sequence not shown
                                                                                   Query Match
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Matches 11; Conservative
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Matches 11, Conservative
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                                                                                                                                                                                                                                                                                    셤
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                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 31-May-1996 #text_change 09-Jul-2004
C;Accession: A4829
R;Ball, D.W.; Azzoli, C.G.; Baylin, S.B.; Chi, D.; Dou, S.; Donis-Keller, H.; Cumaraswam Proc. Natl. Acad. Sci. U.S.A. 90, 5648-5652, 1993
A;Title: Identification of a human achaete-scute homolog highly expressed in neuroendocx A;Reference number: A48279; MUID:93296195; PMID:8390674
A;Reference number: A48279
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Reference trype: mRNA
A;Residues: 1-238 cRES.
A;Cross-references: UNIPROT:P50553; UNIPARC:UPI0000047566; GB:L08424; NID:g306459; PID:g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homeotic protein Hox D8 - mouse

NyAlternate names: homeotic protein Hox 4.3

C;Species: Mus musculus (house mouse)

C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004

C;Accession: A43562

R;Izpisua-Belmonte, J.C.; Dolle, P.; Renucci, A.; Zappavigna, V.; Falkenstein, H.; Dubou Development 110, 733-745, 1990

A;Title: Primary structure and embryonic expression pattern of the mouse Hox-4.3 homeobc A;Reference number: A43562; MUID:91209232; PMID:1982431

A;Accession: A43562

A;Status: preliminary; not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H.; Potter, S.S.
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A;Residues: 1-289 <1ZP>
A;Cross-references: UNIPROT:P23463; UNIPARC:UP10000177DA6
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A;Molecule type: mRNA
A;Residues: 1-305 <RES>
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84.6%; Pred. No. 15;
cive 0; Mismatches
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0; Mismatches
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Best Local Similarity 84.6
Matches 11; Conservative
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                                                                                                                           scute protein - human
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A;Cross-references: UNIPARC:UPI000016A2D0; EMBL:U48250; NID:g1199656; PIDN:AAC72247.1; P
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Plant J. 7, 927-938, 1995
A;Title: Alternative RNA products from a rice homeobox gene.
A;Reference number: Z15126; MUID:95322999; PMID:7599652
A;Accession: T03875
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-374 <TAM>
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C;Comment: For alternative splice forms, see PIR:T03874.
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C;Species: Mesocricetus auratus (golden hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
C;Accession: 148188
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Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-Oct-2004
                                                                                                  C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
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A;Title: Pancreatic beta cells express a diverse set of homeobox genes. A;Reference number: I48185; MUD:95083670; PMID:7991607
A;Accession: I48188
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R,Kurcda, S.; Tokunaga, C.; Kiyohara, Y.; Konishi, H.; Kikkawa,
submitred to the EMBL Data Library, February 1996
A;Reference number: H01212
A;Accession: G02409
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                                                        protein kinase C-binding protein RACK17 - human (fragment)
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A;Molecule type: mRNA
A;Residues: 1-334 <KUR>
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A;Molecule type: mRNA
A;Residues: 1-364 <RES>
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Best Local Similarity 84.6%; Pred. No. 21;
Matches 11; Conservative 0; Mismatches
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A,Gene: H45
A,Introns: 174/3; 215/1; 277/3; 321/3; 367/2
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Best Local Similarity 84.6
Matches 11; Conservative
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B47236
zinc-finger protein Pur-1 - golden hamster
zinc-finger protein Pur-1 - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 05-Apr-1995
C;Accession: B47236
R;Kennedy, G.C.; Rutter, W.J.
R;Kennedy, G.C.; Rutter, W.J.
A;Kennedy, G.C.; Rutter, W.J.
A;Kennedy, G.C.; Rutter, W.J.
A;Kennedy, G.C.; Rutter, W.J.
A;Keference number: A47236; MUID:93087555; PMID:1454839
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Cippedies: Procession: 1992 mar.)
Cippedies: 20-Mar.1992 mar.
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C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;46-102/Domain: homeobox homology <HOX>
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A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
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A;Cross-references: UNIPARC:UPI000017C615
A;Experimental source: insulinoma cell line T
A;Nore: sequence extracted from NCBI backbone (NCBIP:119832)
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84.6%; Pred. No. 20;
tive 0; Mismatches
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84.6%; Pred. No. 20;
:ive 0; Mismatches
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                                  A,Gene: Hoxd-11
A,Introns: 246/1
C,Keywords: DNA binding; homeobox; nucleu:
F,252-308/Domain: homeobox homology <HOX>
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homeotic protein EVX2 - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 AASAAAAAAAA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                        93 AAAAAAAAAAA 105
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Matches 11; Conserv
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Best Local Similarity
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Best Local Similarity
Matches 11; Conserv
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
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Gaps

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C;Species: Homo sapiens (man)
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 31-Dec-2004
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C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;313-369/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 44; DE
84.6%; Pred. No. 23;
ive 0; Mismatches
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A;Residues: 311-401 <JO2>
A;Cross-references: UNIPARC:UP1000017A2B0
                                                                                  84.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84.6%;
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                                                                                                                                                                                                                                                                        269 AAAAAAAAAAAA 281
                                                                                                                                                                                             1 AAXAAAAAAAAA 13
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                                                                                                                          11; Conservative
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homeotic protein HB9 - human
                                           Query Match
Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable homeobox protein OSH45, splice form OSH44 (similarity) - rice N; Contains: probable homeobox protein OSH45, splice form OSH42 C; Species: Oryza sativa (rice) C; Species: Oryza sativ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ajintrons: 174/3; 215/1; 277/3; 321/3; 367/2
C;Keywords: alternative initiators; alternative splicing; DNA binding; homeobox; nucleus
Fi.1375/Product: probable homeobox protein OSH45, splice form OSH44 #status predicted <M
F;197-367/Product: probable homeobox protein OSH45, splice form OSH42 #status predicted
F;291-357/Domain: homeobox homology <HOX>
C; Keywords: alternative initiators; alternative splicing; DNA binding; homeobox; nucleus F;291-352/Domain: homeobox homology <HOX>
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basic helix-loop-helix transcription repressor H - fruit fly (Drosophila virilis)
C;Species: Drosophila virilis
C;Species: Drosophila virilis
C;Accession: A4443

R;Wainwright, S.M.; Ish-Horowicz, D.
Mol. Cell. Biol. 12, 2475-2483, 1992
A;Title: Point wutations in the Drosophila hairy gene demonstrate in vivo requirements
A;Reference number: A44443; MUID:92269819; PMID:1588951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: UNIPARC:UPI00016DEBB; EMBL:D49704; NID:g1805615; PIDN:BAA08554.1; A; Experimental source: cv. Nipponbare; splice form OSH42 C; Comment: For an alternative splice form, see PIR:T03875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:P93424; UNIPARC:UP100000AA5D5; EMBL:D49704; NID:g1805615;
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A;Note: sequence extracted from NCBI backbone (NCBIN:102964, NCBIP:102966)
                                                                                                                                                                                             Gaps
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                                                                                                                  Length 374;
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                                                                                                                  5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Accession: T03876
A,Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                              s; Score 44; DB
Pred. No. 21;
0; Mismatches
                                                                                                                  DB
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A,Cross-references: FlyBase:FBgn0013115
                                                                                                          100.0%;
84.6%; F
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Conservative
                                                                       Query Match
Best Local Similarity
Local 11; Conservative
                                                                                                                                                                                                                                                                                                                                           64 AAAAAAAAAAA 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-375 < TAM1>
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nes 11; Conserv
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A; Residues: 1-378 < WAI>
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Gaps

DB 2; Length 401;

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C;Species: Mus musculus (house mouse)
C;Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004
C;Accession: A49423; S13009; A26629; A24778
R;Logan, C.; Hanks, M.C.; Noble-Topham, S.; Nallainathan, D.; Provart, N.J.; Joyner, A. Dev. Genet. 13, 345-358, 1992
A;Title: Cloning and sequence comparison of the mouse, human, and chicken engrailed gen A;Reference number: A48423; MUID:93185339; PMID:1363401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Holland, P.W.H.; Williams, N.A.
PEBS Lett. 277, 250-252, 1990
A;Title: Conservation of engrailed-like homeobox sequences during vertebrate evolution.
A;Reference number: $13009; MUID:91099509; PMID:1980115
A;Accession: $13009
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A; Title: En-1 and En-2, two mouse genes with sequence homology to the Drosophila engrain A; Reference number: A91620; MUID:88112776; PMID:2892757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: A26629
A;Molecule type: DNA; mRNA
A;Residues: 278-401 < 407×
A;Across-references: 278-401 < 407×
A;Cross-references: UNIPARC:UPI00016CA7C; GB:Y00201; GB:M11987; NID:g49587; PIDN:CAA68
R;Joyner, A.L.; Kornberg, T.; Coleman, K.G.; Cox, D.R.; Martin, G.R.
A;Title: Expression during embryogenesis of a mouse gene with sequence homology to the A;Reference number: A24778; MUID:86079501; PMID:2416459
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                                                                                Gaps
                                                                                    ö
        Length 378;
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A;Experimental source: CD-1, embryo
A;Note: sequence extracted from NCBI backbone (NCBIP:126620)
                                                                                                                                                                                                                                                                                                                                                                                                                                   engrailed homeodomain-containing protein En-1 - mouse
DB 2;
    Score 44; DE
Pred. No. 22;
0; Mismatches
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A;Residues: 321-380 440L.
A;Cross-references: UNIPARC:UP1000017A2AF
R;JOyner, A.L.; Martin, G.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N;Alternate names: homeotic protein En-1
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Gaps

; 0

Indels

Length 443;

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 143-158,'P',160-218 <STE2>
A;Cross-references: UNIPARC:UPI0000071C8C; EMBL:X71137; NID:g468793; PIDN:CAA50467.1; PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: A43915
R;Dush, M.K.; Martin, G.R.
Bev. Biol. 151, 273-287, 1992
A;Title: Analysis of mouse Evx genes: Evx-1 displays graded expression in the primitive
A;Reference number: A43915; MUID:92249649; PMID:1349539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA; mRNA
A;Mosidues: 1-475 - 5UUS.
A;Rosidues: 1-475 - 5UUS.
A;Cross-references: UNIPROT: P49749; UNIPARC: UPI0000020BC6; GB:S34322; NID:G249137; PIDN:
A;Note: sequence extracted from NCBI backbone (NCBIN:100478, NCBIN:100480,
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C;Species: Mas musculus (house mouse)
C;Accession: A47236
R;Kennedy, G.C.; Rutter, W.J.
A;Title: Pur-1, a zino-finger protein that binds to purine-rich sequences, transactivate A;Reference number: A47236; MUD: 93087555; PMID: 1454839
A;Accession: A47236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homeotic protein even-skipped homolog Evx-2 - mouse
N;Atternate names: mesoderamal cell dorsoventral fates determinator Evx-2
C;Species: Mus musculus (house mouse)
C;Dete: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Keywords: DNA binding; homeobox; nucleus; transcription regulation
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A;Experimental source: islet cell line beta TC3
A;Note: sequence extracted from NCBI backbone (NCBIP:119831)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 44; DB 2; Best Local Similarity 84.6%; Pred. No. 26; Matches 11; Conservative 0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                 ; Score 44; DB 1;
Pred. No. 24;
0; Mismatches 2
                                                                                                                                                                                                            A;Map position: Xq26-Xq27
C;Superfamily: human SOX3 protein; HMG box homology
F;136-211/Domain: HMG box homology <HMG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 44; DB
84.6%; Pred. No. 26;
live 0; Mismatches
                                                                                                                                                          A;Gene: GDB:SOX3; SOX-3; SOXB
A;Cross-references: GDB:250376; OMIM:313430
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F;192-248/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                           100.0%;
84.6%; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AASAAAAAAAAA 371
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Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: A43915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   359
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                                                                                                                                  C;Genetics
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A;Accession: 138242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:082037; UNIPARC:UPI00000A12C8; EMBL:Y10810; NID:93336904; PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 20
T14911
bZIP DNA-binding protein - parsley
C;Species: Petroselinum crispum (parsley)
C;Species: Petroselinum crispum (parsley)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 31-Dec-2004
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 31-Dec-2004
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 31-Dec-2004
R;Kircher, S.; Ledger, S.; Hayashi, H.; Weisshaar, B.; Schafer, E.; Frohnmeyer, H.
Mol. Gen. Genet. 257, 595-605, 1998
Mol. Gen. Cenet. 257, 595-605, 1998
MyTitle: CRPR4a, a novel plant bZIP protein of the CPRF family: comparative analysis of A;Reference number: Z18261; MUID:98265918; PMID:9604882
A;Accession: T14911
                                        R;Harrison, K.A.; Druey, K.M.; Deguchi, Y.; Tuscano, J.M.; Kehrl, J.H.
J. Biol. Chem. 269, 19968-19975, 1994
A;Title: A novel human homeobox gene distantly related to proboscipedia is expressed in
A;Reference number: A53662; MUID:94327547; PMID:7914194
                                                                                                                                                                                                                                                                                A,Cross-references: UNIPARC:UPI000017A29E, GB:U07663
A,Note: the nucleotide sequence and conceptual translation as given are self-consistent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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A;Note: CPR44b
C;Superfamily: BZIP G-box-binding protein; fos/jun DNA-binding domain homology
C;Keywords: DNA binding; leucine zipper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NyAlternate names: SRY (sex determining region Y)-box 3
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
Cipacession: I38239; I38242; S67816
Ristevanovic, M.; Lovell-Badge, R.; Collignon, J.; Goodfellow, P.N.
Hum. Mol. Genet. 2, 2013-2018, 1993
Airtle: SOX3 is an X-linked gene related to SRY.
Airtle: SOX3 is an X-linked gene related to SRY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 1q41-1q42.1
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;244-300/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
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84.6%; Pred. No. 23;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GDB:136411; OMIM:142994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 AAAAAAAAAAA 133
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Best Local Similarity 84.0.
The 11; Conservative
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A;Cross-references: UNIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                          A; Residues: 1-403 <HAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-420 <KIR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
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                                                                                                                                                                                                                                 A; Molecule type: DNA
                                                                                                                                                                A; Accession: A53662
                     C; Accession: A53662
                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: GDB:HLXB9
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2; Indels

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DB

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Indels

Length 477;

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Biochemistry 31, 4102-4110, 1992
Affille: Isolation of a novel cDNA encoding a zinc-finger protein that binds to two sit A;Title: Isolation of a novel cDNA encoding a zinc-finger protein that binds to two sit A;Reference number: A42170; MUID:92232709; PMID:1567856
A;Accession: A42170
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-494 <PYR>
                                                                                                                                                                                                                   A,Cross-references: UNIPROT:P56270; UNIPARC:UP1000017C427; GB:J05371
A;Note: it is uncertain whether Met-18 is the initiator or whether translation is initi
B,Sossone, S.A.; Asselin, C.; Patel, A.J.; Marcu, K.B.
Proc. Natl. Acad. Sci. U.S.A. 89, 7452-7456, 1992
A,Title: MAZ, a zinc finger protein, binds to c-MYC and C2 gene sequences regulating tr
A;Reference number: A46153; MUID:92366479; PMID:1502157
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A, Status: preliminary
A, Molecule type: DNA
A, Molecule type: DNA
A, Molecule type: DNA
A, Residues: 1-495 < HAR>
A, Residues: 1-495 < HAR>
A, Cross-references: UNIPROT:P31361; UNIPARC; UPI0000029AAF; EMBL: M88299; NID:g200444; PI
C, Superfamily: transcription factor Brn-1; homeobox homology: POU domain homology
C, Superfamily: transcription factor Brn-1; homeobox; nucleus; transcription regulation
F;27-49/Region: alanime-rich
F;101-112/Region: alanime-rich
F;102-118/Region: alanime-rich
F;186-201/Region: histidine/proline-rich
F;236-247/Region: histidine/proline-rich
F;236-247/Region: histidine/proline-rich
F;316-383/Domain: POU domain homeobox homology <POU>F;402-458/Domain: homeobox homology <HOX>
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Proc. Natl. Acad. Szl. U.5A. 89, 3280-3284, 1992
A;Title: Structure and evolution of four POU domain genes expressed in mouse brain.
A;Reference number: S31223; MUID:92228768; PMID:1565620
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NyAlternate names: class III POU domain protein brain-1
C;Species: Wus musculus (house mouse)
C;Bate: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S31223
                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mENA
A;Residues: 18-417, 'L' 419-494 <BOS>
A;Cross-references: UNIPARC:UPI000012ECF8; GB:M94046
A;Experimental source: HeLa cells
A;Note: sequence extracted from NCBI backbone (NCBIN:110666, NCBIP:110667)
C;Keywords: DNA binding; zinc finger
F;113-125/Region: alanine-rich
F;174-183/Region: alanine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 44; DE ilarity 84.6%; Pred. No. 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 44; DF
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0; Mismatches
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Best Local Similarity 84.00,
Local 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;207-230/Region: zinc finger
F;296-318/Region: zinc finger
F;324-346/Region: zinc finger
F;354-368/Region: zinc finger
F;373-405/Region: zinc finger
F;409-430/Region: zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 AAAAAAAAAAA 125
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F;452-468/Region: alanine-rich
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les 11; Conserv
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T09084
phosphatidylinositol 3-kinase - Chlamydomonas reinhardtii (fragment)
C;Species: Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Decies: Chlamydomonas reinhardtii
C;Decies: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Speciession: T09084
R;Molendijk, A.J; Irvine, R.F.
Plant Mol. Biol. 37, 53-66, 1998
A;Title: Inositide signalling in Chlamydomonas: Characterization of a phosphatidylinosit
A;Recence number: Z16411; MUID:98281574; PMID:9620264
A;Reterence number: Z16411; MUID:98281574; PMID:9620264
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T09084
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: 14-90 cMOL>
A;Residues: 1-490 cMOL>
A;Residues: 1-490 cMOL>
A;Experimental source: strain cw-15
C;Genetics:
A;Introns: 265/3; 331/3; 455/1; 481/3
                                                                                                                                                                                                      Dasic helix-loop-helix protein, DEC2 - human C; Species: Homo sapiens (man)
S; Fujimoto, K.; Shen, M.; Noshiro, M.; Matsubara, K.; Shingu, S.; Honda, K.; Yoshida, E. Biochem. Biophys. Res. Commun. 280, 164-171, 2001
A; Title: Molecular cloning and characterization of DEC2, a new member of basic helix-loc A; Reference number: JC7583, MUID:21092582; PMID:11162494
A; Rocession: JC7583
A; Molecula type: mRNA
A; Residues: J-482 < FUJA
A; Cross-references: UNIPROT:09C0J9; UNIPARC:UPI000052B52; DDBJ:AB044088
C; Comment: This protein, a novel member of the DEC subfamily of basic helix-loop-helix E
A; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       zinc finger protein MAZ - human (fragment)
N;Alternate names: MYC-associated zinc finger protein MAZ; zinc finger protein ZF87 C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004
C;Accession: A42170; A46153
R;Pyrc, J.J.; Moberg, K.H.; Hall, D.J.
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C;Keywords: transcription factor
F;1-173/Region: highly conserved #status predicted
F;130-173/Domain: Orange #status predicted <ORA>
F;286-411/Region: alanine and glycine-rich #status predicted
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0; Mismatches
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                                                             96 AAAAAAAAAAAA 108
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115 AATAAAAAAAA 127
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Best Local Similarity 84.6
Matches 11; Conservative
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RESULT 28

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C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 09-Jul-2004
C;Accession: A90862; A93354; A03321; A03322; A25682; S03667
R;Poole, S.J.; Kauvar, L.M.; Drees, B.; Kornberg, T.
Cell 40, 37-43, 1985
A;Title: The engrailed locus of Drosophila: structural analysis of an embryonic transcri A;Reference number: A90862; MUID:85099327; PMID:3917855
                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-525 <POO.
A;Cross-references: UNIPROT: P02836; UNIPARC: UPI000012CA13; GB:M10017; NID:g157363; PIDN:
R;Fjose, A.; McGinnis, W.J.; Gehring, W.J.
Rature all, 284-289; 1985
A;Title: Isolation of a homoco box-containing gene from the engrailed region of Drosophi
A;Reference number: A93354; MUID:90114393; PMID:2481829
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A/Accession: A17-485, E', 487-518, WH' <FJO>
A/Accession: A17-485, E', 487-518, WH' <FJO>
A/Accession: A268-264-264
A/Accession: A268-2689
A/Accession: A268-3589
A/Accession: A268-3589
A/Accession: A268-3589
A/Accession: A268-3589
A/Accession: A268-3589
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A/Accession: A268-3689
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C; Superfamily: engrailed homeotic protein; homeobox homology
C; Kaywords: DNA binding: embryo; homeobox; nucleus; segmentation; transcription regulati
F; 26-53/Region: glutamine-rich
F; 68-87/Region: alanine-rich
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R;Kojima, T.; Ishimaru, S.; Higashijima, S.; Takayama, E.; Akimaru, H.; Sone, M.; Emori, Proc. Natl. Acad. Sci. U.S.A. 88, 4343-4347, 1991
A;Title: Identification of a different-type homeobox gene, BarHI, possibly causing Bar A;Reference number: A39369; MUID:91239564; PMID:1674606
A;Accession: A39369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q23838; UNIPARC:UPI0000075A37; GB:M59962; GB:M59963; NID:g1
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C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 31-Dec-2004
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A,Cross-references: FlyBase:FBgn0012114
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;331-387/Domain: homeobox homology <HOX>
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A;Molecule type: DNA
A;Residues: 1-604 <KOJ>
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Best Local Similarity
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A;Cross-references: UNIPARC:UPI000002B2F9; GB:D14637; NID:g391768; PIDN:BAA03486.1; PID: C;Genetics: PEBP2alphaA
A;Gene: PEBP2alphaA
C;Superfamily: transcription factor CBF alpha 2
C;Keywords: alternative splicing: DNA binding: T-cell: transcrintion factor: transcrinti
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NyAlternate names: PEA2 alpha chain type 1; PEA2 alpha chain type 2; PEBP2 alpha chain type (5,Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
C;Accession: A48233, B48233
R;Ogawa, E.; Maruyama, M.; Kagoshima, H.; Inuzuka, M.; Lu, J.; Satake, M.; Shigesada, K.
Proc. Natl. Acad. Sci. US.A. 90, 6859-6863, 1993
A;Title: PEBP2/PEA2 represents a family of transcription factors homologous to the produ A;Reference number: A48233; MUID:93342088; PMID:8341710
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Keywords: alternative splicing; DNA binding; T-cell; transcription factor; transcripti
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A;Molecule type: mRNA
A;Residues: 1-513 <OGA>
A;Cross-references: UNIPROT:Q08775; UNIPARC:UPI000002B2F8; GB:D14636; NID:g391766; PIDN:A;Accession: B48233
A;Status: preliminary
A;Molecule type: mRNA
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84.6%; Pred. No. 27;
iive 0; Mismatches 2;
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0; Mismatches
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Best Local Similarity 84.6%;
Matches 11; Conservative
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Matches 11; Conserv
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RESULT 30

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box A-binding factor - fruit fly (Drosophila melanogaster)
N;Alternate names: ABF; transcription factor dGATAb
C;Species: Drosophila melanogaster
C;Date: 13-Jan-1995 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C;Accession: S40382
E;Abel, T.; Michelson, A.M.; Maniatis, T.
Development 119, 623-633, 1993
A;Title: A Drosophila GATA family member that binds to Adh regulatory sequences is expri-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-779 <ABE>
A;Cross-references: UNIPROT:P52172; UNIPARC:UPI0000135F5F; EMBL:X76217; NID:g441491; PII
C;Comment: This transcriptional activator is the earliest known marker of the developin
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A;Cross-references: FlyBase:FBgn0003507
S,Superfamily: box A-binding factor; GATA-type zinc finger homology
C;Keywords: DNA binding; nucleus; transcription factor; transcription regulation; zinc
F;316-359/Domain: GATA-type zinc finger homology <GZF>
F;319-343/Region: zinc finger GATA motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                         R,Wimmer, E.A.; Jaeckle, H.; Pfeifle, C.; Cohen, S.M.
Nature 366, 690-694, 1993
A,Title: A Drosophila homologue of human Spl is a head-specific segmentation gene.
A,Reference number: S39356; MUID:94081952; PMID:8259212
A,Recession: S39356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-644 <WIM>A;Residues: UNIPARC:UPIO000124C17; EMBL:Z29361; NID:g441283; PID:g441284
                                                                                                                                                                                                                                                                                                                                                                             C;Species: Drosophila sp.
C;Date: 18-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 07-May-1999
C;Accession: S39356
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C, Superfamily: FtsH/SEC18/CDC48-type ATP-binding domain homology
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84.6%; Pred. No. 37;
tive 0; Mismatches
                                                     100.0%; Score 44; DE 84.6%; Pred. No. 32; ive 0; Mismatches
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Pred. No. 32;
0; Mismatches
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A;Introns: 245/2
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84.6%; I
                                                  Query Match
Best Local Similarity 84.6%;
Matches 11; Conservative
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Best Local Similarity 84.6
Matches 11; Conservative
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Best Local Similarity 84.6
Matches 11; Conservative
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A;Gene: FlyBase:btd
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C)Species: Drosophila ananassae
C)Species: Drosophila ananassae
C)Species: Drosophila ananassae
C)Accession: S13367
R)Tanda, S.: Corces, V.G.
ENBO J. 10, 407-417, 1991
A;Title: Retrotransposon-induced overexpression of a homeobox gene causes defects in eye A;Reference number: S13367, MUID:91122048; PMID:1671353
A;Accession: S13367
A;Status: prellminary
A;Molecule type: DNA
A;Residues: 1-606 < TAN>
A;Residues: UNIPROT:P22544; UNIPARC:UPI000012C97A; EMBL:X56682; NID:97146; PIDN:
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A;Cross-references: UNIPROT:O80983; UNIPARC:UPI000017885F; EMBL:AC004747; NID:g3413696;
A;Cross-references: UNIPROT:O80983; UNIPARC:UPI000017885F; EMBL:AC004747; NID:g3413696;
A;Experimental source: cultivar Columbia
B;Exin, X.; Raul, S.; Rounaley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable YME1 ATP-dependant proteinase [imported] - Arabidopsis thaliana
N;Alternate names: YTA11 protein homolog T19L18.5
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Mar-1999 #text_change 31-Dec-2004
C;Accession: T02610; H84656
E;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, August 1998
A;Description: Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence.
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                                                                                 Gaps
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A;Introns: 307/1; 383/2
C;Keywords: DNA binding: homeobox; nucleus; transcription regulation F;332-388/Domain: homeohox homeofox
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                      Length 604;
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                         Score 44; DB 2;
Pred. No. 31;
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live 0; Mismatches
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A;Status: translated from GB/EMBL/DDBJ
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A, Introns: 40/1; 119/1; 160/3; 319/3
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                                                     84.68;
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234 AAAAAAAAASAA 246
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234 AAAAAAAAASAA 246
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                      Query Match 100.
Best Local Similarity 84.6
Matches 11; Conservative
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Best Local Similarity 84.6
Matches 11; Conservative
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A,Status: preliminary
A,Molecule type: DNA
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A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference umber: A75000, WUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Status: preliminary
A;Status: preliminary
A;Residues: 1-828 <STO>
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R;Burtis, K.C.; Thummel, C.S.; Jones, C.W.; Karim, F.D.; Hogness, D.S.
Cell 61, 85-99, 1990
A;Title: The brosophila 74EF early puff contains E74, a complex ecdysone-inducible gene A;Reference number: A90912; MUID:90199900; PMID:2107982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: UNIPROT: Q9TXU2; UNIPARC: UPI000007CE2B; GB: chr_III; PIDN: AAC68790.1;
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N;Alternate names: ets-related protein E74A
C;Species: Drosophila melanogaster
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 15-Mar-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Species: Caenorhabditis elegans
C.Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
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R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
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Pred. No. 38;
0; Mismatches
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84.6%; Pred. No. 39;
ive 0; Mismatches
                      A;Cross-references: FlyBase:FBgn0025833
A;Introns: 37/3; 448/3; 611/2; 690/3
A;Note: EG:EG0003.2
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84.6%; I
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| AAAAAAAAAAA 370
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Best Local Similarity
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A; Residues: 1-829 <BUR>
                                                                                                                                                                      Query Match
Best Local Similarity
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R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000
A;Reference number: 225022
A;Accession: T49385
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Kossi-references: UNIPROT: Q9P682; UNIPARC: UPI000017B46C; EMBL: AL355927; GSPDB:GN00116;
A;Experimental source: BAC clone B1D1; strain OR74A
RESULT 36
JC7555
C140xf4 protein - human
C; Species: Homo sapiens (man)
C; Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C; Accession: JC7555
R; Rampazzo, A.; Pivotto, F.; Occhi, G.; Tiso, N.; Bortoluzzi, S.; Rowen, L.; Hood, L.; N
Biochem. Biophys. Res. Commun. 278, 766-774, 2000
A; Title: Characterization of C140xf4, a novel intronless human gene containing a polyglu
A; Reference number: JC7555; MUID: 20549026; PMID:11095982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-806 <MUR>
A;Cross-references: UNIPROT:096828; UNIPARC:UP1000007B3C4; EMBL:AL031863; NID:e1331652;
                                                                                                                                                                                                                                                                                                                                                              A;Accession: JC7555
A;Molecule type: DNA
A;Residues: 1-796 < RAM>
A;Residues: 1-796 < RAM>
A;Cross-references: UNIPROT: Q9H1B7; UNIPARC: UPI00000738BA; GB:AJ277365
C;Comment: This protein, a proline-rich nuclear protein, functions as a transcriptional s and undergoes rapid degradation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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c;Species: Drosophila melanogaster
c;Species: Drosophila melanogaster
c;Date: 13-Mag-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
c;Accession: T13690
R;Murphy, L.; Harris, D.; Barrell, B.
submitted to the BMBL Data Library, November 1998
A;Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A;Reference number: Z17699
A;Accession: T13690
A;Accession: T13690
A;Accession: T13690
A;Accession: T18690
A;Accession: T18690
A;Molecule type: DNA
A;Residues: 1-806 AMBRA
A;Residues: 1-806 AMBRA
A;Residues: 1-806 AMBRA
A;Residues: 1-800 AMBRA
A;Residues
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C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
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0; Mismatches
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Matches 11; Conserv
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Matches 11; Conserv
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A,Gene: C14orf4
A,Map position: 14q24.3
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A;Introns: 54/3; 212/3
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Query Match

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Search completed: September 9, 2006, 23:01:51 Job time: 15.8101 secs

mint virus mint virus mint virus rattus norv oryza sativ homo sapien homo sapien ashbya goss homo sapien mus musculu drosophila gallus gall drosophila kluyveromyc petromyzon homo sapien drosophila drosophila drosophila drosophila drosophila drosophila drosophila homo sapien drosophila drosophila drosophila homo sapien drosophila rosophila drosophila drosophila drosophila drosophila drosophila drosophila drosophila drosophila drosophila 05BQD5\_9VIRU 05BQD8\_9VIRU 05BGD9\_9VIRU 05BGD9\_9VIRU 05BGD9\_9VIRU 05BGD4\_HUMAN 06GDA4\_HUMAN 06GDA4\_HUMAN 06GBB5\_9DIPT 06BLB5\_9DIPT 

ALIGNMENTS

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100.08;
                                    100.0%;
84.6%;
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                                                    Local Similarity 84.6
nes 11; Conservative
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71
71 AA;
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                                                                                                                                                                               ANP4 PSEAM
P02734;
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SEQUENCE
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                                                                                                                                                                                                                        Totoki Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A.,
Narusaka M., Shin-i T., Nakagawa M., Sakamoto N., Oishi K., Kohara Y.,
Kobayashi M., Toyoda A., Sakaki Y., Sakurai T., Iida K., Akiyama K.,
Satou M., Toyoda T., Konagaya A., Carninci P., Kawai J.,
Hayashizaki Y., Shinozaki K.,
"Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs.";
Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005840; C:ribosome; IEA.
GO; GO:000823; F:peptidase activity; IEA.
GO; GO:0003735; F:structural constituent of ribosome; IEA.
GO; GO:0006422; P:protein biosynthesis; IEA.
InterPro; IPRO0456; RIBOSOMALP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44; DB 2; Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang A., Gonzalez-Santos J.M., Hu J.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 1
52 AA; 4750 MW; D8B358D27E6813B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-007-2002, integrated into UniprotKB/TrEMBL. 01-007-2002, sequence version 1. 07-FBB-2006, entry version 8. RNA-binding protein (Fragment). Homo sapiens (Human).
                                                                   10-MAY-2005, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF261889; AAM21972.1; -; Genomic_DNA.
Ensembl; ENSG0000163694; Homo sapiens.
NON_TER
                                           52 AA.
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0; Mismatches
                                                                                                                        Name=At2g26140;
Arabidopsis thaliana (Mouse-ear cress).
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                                           PRT;
                                                                               10-MAY-2005, sequence version 1. 07-FEB-2006, entry version 3. FtsH like protease (Fragment).
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                                           PRELIMINARY;
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                         NCBI_TaxID=3702;
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QBNIS3;
                                        QS6ZW8_ARATH
QS6ZW8;
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [MRNA].
MEDLINE=81247379; PubMed=6265915;
Lin Y., Gross J.K.;
"Molecular cloning and characterization of winter flounder antifreeze
                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995, sequence version 2.
07-FBB-2006, entry version 35.
Ice-structuring protein 2A7 precursor (ISP 2A7) (Antifreeze protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-FEB-2006, entry version 32.
Ice-structuring protein 4 precursor (ISP 4) (Antifreeze peptide 4).
Pseudopleuronectes americanus (Winter flounder) (Pleuronectes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes; Pleuronectoidei; Pleuronectidae; Pseudopleuronectes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. (Natl. Acad. Sci. U.S.A. 78:2825-2829(1981).
-!- FUNCTION: Antifreeze proteins lower the blood freezing point.
-!- SIMILARITY: Belongs to the type-I AFP family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 85;
                                                        DB 2; Length 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ice-structuring protein 4. /FTId=PRO 0000001684. 8E62E1D2B44117BC CRC64;
6958 MW; 3A0B336CD1048D99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1988, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986, integrated into UniProtKB/Swiss-Prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 AA.
                                                                                                                                                                                                                                                                                                                                                                                           85 AA
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0; Mismatches
                                                        ; Score 44; DB
Pred. No. 52;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000104; Antifreeze_1.
PRINTS; PR00308; ANTIFREEZEE.
Antifreeze protein; Repeat; Signal.
21GNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; J00930; AAA49467.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-AUG-1987, sequence version 1. 07-FEB-2006, entry version 32.
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                                                                                                                     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Davia V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
Ambesi-Impiombato A., Apweller R., Aturaliya R.N., Bailey T.L.,
Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
Crowe M.L., Choudhary V., Christoffels A., Clutterbuck D.R.,
Crowe M.L., Dalla Gatta G.,
di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninoi P., Hayashizaki Y.;
Hiddh-efficiency Hayashizaki T.;
Methods Enzymol. 303:19-44(1999).
                                         MEDLINE-85054999; PubMed=6548752; Gourlie B., Lin Y., Price J., Devries A.L., Powers D., Huang R.C.C.; "Winter flounder antifreeze proteins: a multigene family."; J. Biol. Chem. 259:14960-14965(1984).
-!- FUNCTION: Antifreeze proteins lower the blood freezing point.
-!- SIMILARITY: Belongs to the type-I AFP family.
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:Al30089M21 product:HBV pX associated protein 8 large isoform
                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                         Removed by a dipeptidylpeptidase
                                                                                                                                                                                                                                                                                                      DB 1; Length 91;
                                                                                                                                                                                                                                  (Probable).
/FIId=PRO 0000001687.
ICe-structuring protein 2A7.
/FIId=PRO 0000001688.
DIFC542FDB65012C CRC64;
                                                                                                                                                                                                                                                                                                                           Indels
Pleuronectoidei; Pleuronectidae; Pseudopleuronectes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-OCT-2005, integrated into UniProtKB/TrEMBL.
11-OCT-2005, sequence version 1.
07-FEB-2006, entry version 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-C57BL/6J; TISSUE-Thymus;
PubMed=16141072; DOI=10.1126/Science.1112014;
                                                                                                                                                                                                                                                                                                                                                                                                                             112 AA
                                                                                                                                                                                                                                                                                                               Pred. No. 63;
0; Mismatches
                                                                                                                                                                                                                                                                                                      Score 44;
                                                                                                                                                                                                              Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                PIR; A22592, A22592.
InterPro; IPR000104; Antifreeze 1.
PRINTS; PR00308; ANTIFREEZEI.
                                                                                                                                                     EMBL; M10148; AAA49465.1; -; mRNA.
                                                                                                                                                                                                  Antifreeze protein; Repeat; Signal
                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                            Q3UUSS MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                84.68;
                                                                                                                                                                                                                                                                                8326 MW;
                                NUCLEOTIDE SEQUENCE [MRNA]
                                                                                                                                                                                                                                                                                                                                                1 AAXAAAAAAAA 13
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                                                                                                                                                                                                                                                                                91 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Hbxap;
                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                  MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                         Q3UUSS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homolog
                                                                                                                                                                                                              SIGNAL
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RA Geocrail-Hemming P., Gingeras T.R., Golobori T., Green R.E.,

RA Kitano H., Kollias G., Katahana S.P., Kruger A., Kalmaris H.,

RA Kitano H., Kollias G., Katahana S.P., Kruger A., Kummeried S.K.,

RA Kitano H., Kollias G., Katahana S.P., Kruger A., Kummeried S.H.,

RA Kitano H., Kollias G., Katahana S.P., Kruger A., Kummeried S.,

RA Milanou H., Matuliam S., Madda Babu W., Madra Du W., Marchouni L.,

RA Milanou B., Mathijam S., Madda Babu W., Madra Du W., Marchouni L.,

RA Milanou B., Mathijam S., Midhisa S., Norga G., Pesolo G.,

RA Petroveky N., Plazas S., Kinhisa S., Norga G., Pesolo G.,

RA Milanou B., Wathijam S., Midhisa S., Norga G., Pesolo G.,

RA Milanou B., Wathijam S., Midhisa S., Norga G., Pesolo G.,

RA Milanou B., Wathijam S., Midhisa S., Norga G., Pesolo G.,

RA Milanou B., Wathijam S., Midhisa S., Norga G., Pesolo G.,

RA Milanou B., Wathijam S., Midhisa S., Norga G., Pesolo G.,

RA Milanou B., Wathijam S., Midhisa S., Norga G., Pesolo G.,

RA Milanou B., Wathijam S., Midhisa S., Norga G., Pesolo G.,

RA Milanou B., Wathijam S., Midhisa S., Norga G., Sessa L., Shang Y.,

RA Milanou G., Matcher S., Sandel N., Sindal B., Midha Y.,

RA Manaladhi H., Zabhrowky S., Zhu S., Zimmer A., Hidd W., Bult C.,

RA Manaladhi H., Zabhrowky S., Zhu S., Zimmer A., Midd W., Bult C.,

RA Manaladhi H., Zabhrowky S., Man B., Zimmer A., Midd W., Bult C.,

RA Manaladhi H., Xabhrowky S., Han B., Lill B.T., Brusic V., Quackenbush J.,

RA Manaladhi H., Matchiki A., Okamura Olo Y., Surahi H., Kawai J.,

RA Milanou S., Kalandi K., Matchiki A., Okamura Olo Y., Surahi H., Kawai J.,

RA Milanou S., Matchiki A., Matchiki A., Okamura Olo Y., Surahi H., Kawai J.,

RA Milanou S., Matchiki A., Matchiki A., Okamura Olo Y., Surahi H., Kawai J.,

RA Milanou S., Matchiki J., Wathiya M., Kana M., Matchiki B.,

RA Milanou S., Matchiki J., Wathiya M., Matchiki B., Matchiki B.,

RA Milanou S., Matchiki J., Matchiki B., Ma

115 AA

PRT;

PRELIMINARY;

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Assaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y., Nu U., Nimura Y., Cheng Z., Magamura Y., Antonio B.A., Kanamori H., Hosokawa S., Masukawa M., Arikawa K., Chidden Y., Hayashi M., Antonio B.A., Kanamori H., Antonio B.A., Kanamori H., Antonio B.A., Kanamori H., Antonio B.A., Kanamori H., Antonio B.A., Kanamori M., Antonio B.A., Kanamori M., Hijshita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M., Ikeno M., Ito S., Ito Y., Ito Y., Iwabuchi A., Kamiya K., Marasawa W., Kategiri S., Kikuta A., Kobayashi M., Rono I., Marasawa W., Kategiri S., Kikuta A., Kobayashi T., Mukai Y., Nakamara T., Mizuno H., Makashima M., Nakama Y., Nakamichi Y., Nakamura M., Nakama Y., Nakamichi Y., Nakamura M., Nakama Y., Nakamichi Y., Sakai K., Shibata M., Shinokawa T., Shomura A., Song J., Takazashi Y., Terasawa K., Tsuji K., Amangata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K., Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.-I., Eun M.-Y., Maran M., Jiang J., Golobori T., Maran M., Maran M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta; Liliopsida; Poales; Poaceae, BEP clade;
                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22337376; PubMed=12447438; DOI=10.1038/nature01184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The genome sequence and structure of rice chromosome 1."; Nature 420:312-316(2002)
                                               25-OCT-2004, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AP003413; BAD45189.1; -; Genomic_DNA
                                                                                                                                 Cell division protein (FtsH)-like.
Name=B1151A10.24-1;
                                                                               25-OCT-2004, sequence version 1.
                                                                                                                                                                                                                                                                                    Ehrhartoideae; Oryzeae; Oryza.
                                                                                                         07-FEB-2006, entry version
                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                      NCBI_TaxID=39947;
ð
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           RA Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Itoh M., Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Itoh M., Itoh M., Itoh M., Itoh M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Raidota T., Chazaki Y., Gojobori P., Kondo H., Kasukawa T., Saito R., A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Raicoth M., Masukawa T., Saito R., Raidota K., Matsuda H., Ashburner M., Batalov S., Casavant T., Raicoth M., Rastellov S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Rashio T., Askai K., Okido T., Furuno M., Anno H., Baldarelli R., Barsh G., Askai K., Okido T., Furuno M., Anno H., Baldarelli R., Barsh G., Asharinci Ch S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchim L., Mashima M., Mazzarelli J., Mombaerts P., A Lyons P., Marchim L., Mashima M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whyshizaki S., Haysshizaki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Haysshizaki Y., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J; IISSUB=Thywnus; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Shibata K., Itoh M., Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., TISOM—X. Nagada N., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagada T., Tashiro H., Itoh M., Sumi N., Ishii K., Hazama M., Nishine T., Tashiro H., Itoh M., Sumi N., Ishii K., Makamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiiwagi K., Pujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watahiiwayi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rikik Nintegrated sequence analysis (RISA) system—384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
Shibata K., Shizaki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
Muramatsu M., Hayashizaki Y.,
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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     MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 AA; 11657 MW; 3F364EA14DDFD076 CRC64;
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Pred. No. 74;
0; Mismatches 2
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MGI; MGI:2682305; HDxap.
SEQUENCE 112 AA; 11657 MW; 3F3641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
84.6%; I
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                  11-0CT-2005, integrated into UnibrotKB/TrEMBL.
11-0CT-2005, sequence version 1.
07-FEB-2006, entry version 5.
Adult male testis cDNA, RIKEN full-length enriched library, clone:4933416E08 product:hypothetical Proline-rich region profile/Alanine-rich region profile containing protein, full insert
                                                                                                                                                                                      ö
                                                                                                                                                     Length 115;
                                                                                                                                                                                      Indels
                                                                                                                   115 AA; 11813 MW; B64A595C9756DEC5 CRC64;
Gramment; wools.
Gramment; wools.
GO; GO:0004222; F:metalloendopeptidase activity; IEA.
GO; GO:0051301; F:metalloendopeptidase activity; IEA.
GO; GO:0051301; P:cell division; IEA.
GO; GO:006508; P:proteolysis; IEA.
Interpro; IPRO0642; Peptidase M41.
                                                                                                                                                                                      5
                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                        117 AA.
                                                                                                                                      100.0%; Score 44; DE
                                                                                                                                                                      Pred. No. 75;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muridae, Murinae, Mus.
                                                                                      Pfam; PF01434; Peptidase M41;
                                                                                                                                                                                                                                                                                                                                          Q3V062_MOUSE PRELIMINARY;
Q3V062;
                                                                                                                                                                                                                          1 AAXAAAAAAAA 13
                                                                                                                                                                                                                                                       85 AASAAAAAAAA 97
                                                                                                                                                                                           11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                          Cell division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sednence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Muroidea;
                                                                                                                          SEQUENCE
                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                              MOUSE
                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                             RESULT 7
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NUCLEOTIDE SEQUENCE

; 0

Gaps

; 0

Indels

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RESULT 6 Q656T8 ORYSA

Best Local Similarity 84.6 Matches 11; Conservative

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RE STRAIN-CS798/651, TISSUR-TEACHER,

RE STRAIN-CS798/651, PROMEDIAGES, DOI-10.10.6/SOO76-6879(99)03004-9,
REDITING-29.205253; PROMEDIAGES, DOI-10.10.10.6/SOO76-6879(99)03004-9,
REDITING-29.205253; PROMEDIAGES, OCCUPANT, STRAIN-CS798/651, TISSUR-TEACHER, No. 10 STR
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Raveair T. Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schmeddon, C., Septe M. S., Steren M. Shimada M., Sakai M., Sasaki M., Sasaki M., Shimada M., Sakai M., Sasaki M., Shimada M., Shim
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PUCLEOTIDE SEQUENCE.

NUCLEOTIDE SETTING A.,

                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                      Mortlock D.P., Sateesh P., Innis J.W.; "Evolution of N-terminal sequences of the vertebrate HOXA13 protein."; Mamm. Genome 11:151-158(2000).
Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Felidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tetraodon nigroviridis (Green puffer).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostei;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
NCBI_TAXID=99883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUL-2005, sequence version 1.
07-FEB-2006, entry version 3.
Chromosome undetermined SCAF7119, whole genome shotgun sequence.
                                                                                                                                   MEDLINE=20122168; PubMed=10656931; DOI=10.1007/s003350010029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Length 131;
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Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
                                                                                                                                                                                                                                                                                                                                 EMBL; AF083095; AAD54640.1; -; Genomic_DNA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005840; C:ribosome; IEA.
GO; GO:000412; P:protein biosynthesis; IEA.
GO; GO:000412; P:protein biosynthesis; IEA.
InterPro; IPRO01859; Ribosomal_P2.
PRINTS; PR00456; RIBOSOMALP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 131
131 AA; 11046 MW; 950562B80E529D4F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 44; DB Pred. No. 83; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 84.6
                                                                                                             NUCLEOTIDE SEQUENCE
                                                        NCBI_TaxID=9685;
                                  Felinae; Felis.
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                                     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
MEDLINE=20122168; PubMed=10656931; DOI=10.1007/s003350010029;
MORTIOCK D.P., Satesh P., Innis J.W.;
Mortlock D.P., Satesh P., Innis J.W.;
Mortlock D.P., Marchial sequences of the vertebrate HOXA13 protein.";
Mamm. Genome 11:151-158(2000).
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Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pelis silvestris catus (Cat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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GO; GO:0005634; C:nucleus; IEA.

GO; GO:0005840; C:rubosome; IEA.

GO; GO:0003745; F:structural constituent of ribosome; IEA.

GO; GO:0006412; P:protein biosynthesis; IEA.

INTERPRO; PR004656; RIBOSOMALP2.

Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 AA; 10975 MW; CCCA1A7B52221394 CRC64;
                                                                                                                                              Hypothetical protein.
SEQUENCE 117 AA; 12609 MW; 61282448B68F9365 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
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01-MAY-2000, integrated into UniProtKB/TrEMBL.
07-FEB-2006, entry version 1.
Transcription factor HOXA13 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 AA.
                                                                                                                                                                                                                      k; Score 44; DB
Pred. No. 76;
0; Mismatches
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0; Mismatches
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07-FEB-2006, entry version 15.
Transcription factor HOXA13 (Fragment).
                                                                                                                     EMBL; AK133410; BAE21643.1; -; mRNA.
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                                                                                                                                                                                                                      100.0%;
84.6%; 1
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Q9TUC9;
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                                                                                                                                                                                                           Query Match
Best Local Similarity 84.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                               1 AAXAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                               AASAAAAAAAA 34
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SEQUENCE
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Matches

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Indels

Gaps

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Matches

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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
                                                       Pubmed=16292255;
Fry B.G., Vidal N., Norman J.A., Vonk F.J., Scheib H., Ramjan S.F.,
Kuruppu S., Fung K., Blair Hedges S., Richardson M.K., Hodgson W.C.
Ignjatovic V., Summerhayes R., Kochva E.;
"Early evolution of the venom system in lizards and snakes.";
Nature 439:584-588(2006).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AAAB01008944; EAA10278.2; -; Genomic_DNA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Anopheles gambiae Sequence Committee, Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 44; DB 2; Length 149; 84.6%; Pred. No. 92; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                               DB 2; Length 145;
                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Anopheles gambiae Sequence Committee; "Anopheles gambiae re-annotation."; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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149 AA; 15582 MW; 6EA2E6044F4ED59C CRC64;
                                                                                                                                                                                                                                                                                                           145 AA; 14182 MW; A2AEAF2330637142 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-2003, integrated into UniProtKB/TrEMBL. 07-DEC-2004, sequence version 2. 07-FEB-2006, entry version 13. ENSANDP000000020819.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 AA.
                                                                                                                                                                                                                                                                                                                                               ; Score 44; DB
Pred. No. 90;
0; Mismatches
                                                                                                                                                                                                                                                  EMBL; DQ119605; ABA41582.1; -; Genomic_DNA
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PANTHER, PTHR11267; TF T-box, 1.
Pfam; PF00907; T-box; T.
PROSITE; PS50252; TBOX_3; 1.
                                                                                                                                                                                                                                                                                                                                               100.08;
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                                                                                                                                                                                                                                                                                                                                                                 84.6%;
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                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 84.6
les 11; Conservative
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                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
STRAIN=PEST;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI TaxID=180454;
   NCBI_TaxID=51957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q7Q8K9_ANOGA
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                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                 Query Match
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NON TER
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                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Identification of Pax2-regulated genes by expression profiling of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Anguidae;
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                             Score 44; DB 2; Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=15872005; DOI=10.1242/dev.01833;
Bouchard M., Grote D., Craven S.E., Sun Q., Steinlein P.,
                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                 132 132
132 AA; 12324 MW; 2761624E77ABA2CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 143
143 AA; 14137 MW; 5C1818C8EC2121F4 CRC64;
                                                                                                        EMBL; CAAE01007119; CAF89724.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-MAY-2005, integrated into UniProtKB/TrEMBL.
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20-DEC-2005, sequence version 1.
21-FEB-2006, entry version 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 44; DB
84.6%; Pred. No. 89;
tive 0; Mismatches
                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                              84;
                                                                                                                                                                                                                            Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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Development 132:2633-2643(2005).
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07-FEB-2006, entry version 3.
Pou3f3 (Fragment).
                                                                                                                                                                                                       100.08;
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                                                                                                                                                                                                                                84.68;
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Gallus gallus (Chicken).
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                     preliminary data.
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Name=HOXA13;
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NCBI_TaxID=9031;
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RESULT 11
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HOXA13 RESULT 12
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Matches

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1 AAXAAAAAAAA 13
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                                                                                                                                                                                                                                                                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                          Homo sapions (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                  Ottenwaelder B., Obermaier B., Deutschenbaur S., Schaipp A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S., Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Osteoblast;
Dohi Y., Ohgushi H., Nakajima H., Ikeuchi M., Shimaoka H.,
Yonemasu K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                          150 AA; 15110 MW; BOC80E466FCAB03E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004, sequence version 1.
07-FEB-2006, entry version 9.
Core binding factor alphal subunit type I (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ensembl, ENSRNOG00000020193; Rattus norvegicus.
GO; GO:0005634; C:nucleus; IEA.
                                                                                                          01-NOV-1999, integrated into UniProtKB/TrEMBL. 01-NOV-1999, sequence version 1. 07-FBE-2006, entry version 19. 07-FBE-2006, entry version 19. Name-DKFZp586E1621 (Fragment). Name-DKFZp586E1621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      153 AA
                                                                                                                                                                                                                                                                                                                                                                       EMBL, AL080235; CAB45781.1; -; mRNA. PIR; T12547; T12547. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB115745; BAD08305.1; -; mRNA.
SMR; Q765Q0; 93-153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY; PRT;
                                                                                      PRT;
                                                                                     Q9Y4M1 HUMAN PRELIMINARY;
Q9Y4M1;
                                                                                                                                                                                                                                                                        German cDNA Consortium;
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  1 AAXAAAAAAAA 13
                         10 AAAAAAAAAA 22
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les 11; Conserv
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                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                            TISSUE=Uterus
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Q765Q0;
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AC 07650
DT 05-JU
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DD CORE
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PubMed=15377793; DOI=10.1073/pnas.0403306101;
Nierman W.C., Deshazer D., Kim H.S., Tettelin H., Nelson K.E.,
Peldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,
Purkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M.,
Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
Zafar N., Zhou L., Fraser C.M.,
"Structural flexibility in the Burkholderia mallei genome.";
Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
GO, GO:0005524; F:ATP binding; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000040; AML1 Runt.
InterPro; IPR012346; PS3 RUNT DNA_bd.
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07-FBB-2006, entry version 11.
07-FBB-2006, entry version 11.
Name-accB, carboxylase, biotin carboxyl carrier protein.
Name-accB, OrderedLocusNames=BMA2501;
Burkholderia mallei (Pseudomonas mallei).
Burchria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 157;
                                                                                                                                                                                                                                                                                                                                                                                         Score 44; DB 2; Length 153;
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GO; GO: 0009317; C:acetyl-CoA carboxylase complex; IEA.

GO; GO: 0009379; F:bictin binding; IEA.

GO; GO: 0009379; F:bictin binding; IEA.

GO; GO: 0006633; P:fatty acid biosynthesis; IEA.

R GO; GO: 0006633; P:fatty acid biosynthesis; IEA.

InterPro; IPRO01803; AccoAbictinCC.

InterPro; IPRO01803; Bictin_lipoyl.

P Fam; PRO01964; Bictin_lipoyl.

P Fam; PRO01964; Bictin_lipoyl.

P Fam; PRO01964; Bictin_lipoyl.

P Fam; PRO0197; ACOABICTINCC.

PROMITS; PRO1071; ACOABICTINCC.

PROFITE: PS00188; BIOTIN; 1.....
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84.6%; Pred. No. 96;
:ive 0; Mismatches
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TIGR; BMA2501; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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PROSITE, PSS0968; BIOTINYL LIPOYL; 1.
                                                                                                                                                                                              Pfam; PF00853; Runt; 1.
PRINTS; PR00967; ONCOGENEAMLI.
PROSITE; PS51062; RUNT; 1.
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GO; GO:000786; C:nucleosome; IEA.
GO; GO:000786; C:nucleosome; IEA.
GO; GO:0005634; C:nucleosome; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003701; P:chromosome organization and biogenesis (sen. . .; IEA.
GO; GO:0007001; P:chromosome organization and biogenesis (sen. . .; IEA.
InterPro; IPR007124; Hist TAE.
InterPro; IPR007125; Histone—H2B.
InterPro; IPR00558; Histone—H2B.
PANTHER; PTHR11425; Histone—H2B.
PANTHER; PTHR11425; Histone—H2B.
InterPro; IPR005584; Histone—H2B.
                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                   MUCLEOTIDE SEQUENCE.
MEDLINE=20252564; PubMed=10794571; DOI=10.1007/s004120050401;
Udda K., Kinoshita Y., Xu Z.-J., Ide N., Ono M., Akahori Y.,
Tanaka I., Inoue M.;
"Unusual core histones specifically expressed in male gametic cells of
Lilium longiflorum.";
Chromosoma 108:491-500(2000).
-!- SUBUNIT: The nucleosome is an octamer containing two molecules
each of H2A, H2B, H3 and H4. The octamer wraps approximately 146
bp of DNA (By similarity).
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                      Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Liliales, Liliaceae, Lilium.
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Culicidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chromosomal protein; DNA-binding; Nuclear protein; Nucleosome core. SEQUENCE 158 AA; 17249 MW; 37A96D6D9117A0BD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                           01-OCT-2000, integrated into UniProtKB/TrEMBL. 01-OCT-2000, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-DEC-2003, integrated into UniProtKB/TrEMBL. 07-DEC-2004, sequence version 2. 07-FEB-2006, entry version 8. 07-FEB-2006, entry version 8. OR-SANCPO0000015660 (Fragment).
                                                                      158 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 44; DE
84.6%; Pred. No. 96;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB003780; BAA96095.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q7Q9M3 ANOGA PRELIMINARY; PRT; Q7Q9M3;
                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00621; HISTONEH2B.
ProDom; PD000497; Histone H2B; 1.
                                                                                                                                            Lilium longiflorum (Trumpet lily).
                                                                                                                    21-FEB-2006, entry version 25
                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 84.00,
          64 AASAAAAAAAA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AAXAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAAAAAAAAA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00125; Histone; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00427; H2B; 1
                                                                                                                                                                              NCBI_TaxID=4690;
                                                                    Q9MBF7_LILLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
                                                           LILLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANOGA
                                                                                 Q9MBF7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 18
0709M3 ANO
0709M3 ANO
0709M
DT 0709M
DT 07-DE
DT 07-FE
DE ENSAM
GN ORFNA
OS ANOPH
OC NEOPT
          셤
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Carninci P., Kacukawa T., Kataphama S., Gough J., Frith M.C., Maeda N., Carninci P., Kacukawa T., Kataphama S., Gough J., Frith M.C., Maeda N., Bajic V.B., Brenner S.E., Batalov S., Fortest A.R., Zavolan M., Davis M.J., Wilming L.G., Aidinis V., Allen J.E., Allen J.E., Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L., Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., Chiu K.P., Choudhary V., Christoffelb A., Clutterbuck D.R., Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., Ai Fletcher C.F., Fukushima T., Pruruno M., Futaki S., Gariboldi M., Goorgii-Hemming P., Gingera T.R., Gojobori T., Green R.E., Gostincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa T., Hill D., Huminjecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T., Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Alathow M., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2003, integrated into UniProtKB/TrEMBL.
01-MAR-2003, sequence version 1.
07-FEB-2006, entry version 13.
9 days embryo whole body cDNA, RIKEN full-length enriched library,
clone:D030067F24 product:hypothetical protein, full insert sequence.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                             "Anopheles gambiae re-annotation.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                STRAIN=PEST,
The Anopheles gambiae Sequence Committee,
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 AA; 16803 MW; 2D1BAC62C087BBAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AAAB01008900; EAA09564.2; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUE=Whole body;
PubMed=16141072; DOI=10.1126/science.1112014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.6%; Pred. No. 99;
ive 0; Mismatches
                                                                                                                                                                            The Anopheles gambiae Sequence Committee;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QBBNHS_MOUSE PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Conservative
Anophelinae; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 AAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                preliminary data.
                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
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                                                                                               NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TER
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Kurcchkin I.V. Lateau L.F., Lazarevic D., Lipovich L., Liu J.,
Liuni S., Mchillan S., Wadan labu W., Nadera R., Nashondhail E.,
Liuni S., Mchillan S., Wadan labu W., Nadera R., Nashondhail E.,
R. Maracanawa dar. Nishisan Kignona Bach, Mr. R., Parchail S.,
R. Maracanawa dar. Nishisan Kignona S., Noris R., Maracanawa S., Noris R., Sabarda C., Sanada C., Sesaa L., Sanada S., Noris R., Sabarda C., Sanada S., Sanada S

Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License STRAIN=C57BL/6J; TISSUE=Whole body; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., Muramatsu M., Hayashizaki Y., Itoh M., Bayashizaki Y., Itoh M., Bayashizaki Y., Dibataki Y., Muramatsu M., Hayashizaki Y., Dibataki Y., Muramatsu M., Hayashizaki Y., Itoh M., Dibataki Y., Muramatsu M., Hayashizaki Y., Hayas Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Stahli S., Mateuo Y., Nikaido I., Pasole G., Quackenbush J., Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Bakai K., Okido T., Frunno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Gustincich S., Hill D., Hoffmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wasshias, N., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayatuu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya K., Kurihara C., Matsuyama T., Miyazaki A., Murate M., Nakamura M., Nishi K., Nomura K., Numazaki R., Murate M., Ohato N., Okazaki Y., Salto R., Saltoh H., Sakai C., Sakai K., Sahzame N., Sano H., Sakai D., Shibata K., Shinagawa A., Shiraki T., Soqabbe Y., Tagami M., Tagawa A., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases. Gaps MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Nagadoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Alzawa K., Nagadoka S., Sasaki N., Carninci P., Sunbata M., Itoh M., Alzawa K., Nagadoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumioto H., Sakaguchi S., Ikegami T., Rashiwagi K., Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara B., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rikike integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000). Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001). ö 100.0%; Score 44; DB 2; Length 164; 84.6%; Pred. No. 99; 2; Indels ive 0; Mismatches 2; Indels EMBL; AK083689; BAC38994.1; -; mRNA. Ensembl; ENSMUSG0000015882; Mus musculus. Hypothetical protein. SEQUENCE 164 AA; 18462 MW; FD764AE704780A28 CRC64; STRAIN=C57BL/6J; TISSUE=Whole body; 100.08; 11; Conservative NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE Query Match Best Local Similarity Matches 

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1 AAXAAAAAAAA 13

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RESULT 20

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Q96NI3 HUMAN
ID Q96NI3_HUMAN
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             Gramene;
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10550945 ORY
10 DT 01-FE
DT 0
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        SERBERRES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia, Butheria, Buarchoncoglires, Glires; Rodentia, Sciurognathi;
Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP clade,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ensembl; ENSRNOG0000020193; Rattus norvegicus.
Ensembl; ENSRNOG0000020193; Rattus norvegicus.
GO; GO:000554; C:nucleus; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000040; AML1 Runt.
InterPro; IPR012346; P53 RUNT_DNA_bd.
PANTHER; PTHR1950; AML1_Runt; 1.
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Wing R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Saski
Currie J., Collura K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dohi Y., Ohgushi H., Nakajima H., Ikeuchi M., Shimaoka H.,
Yonemasu K.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167 AA; 18085 MW; E3C437F8F04BE74A CRC64;
                                                                                                                                                                                                       07-FEB-2006, entry version 9.
Core binding factor alpha1 subunit type II (Fragment).
Name=CBFA1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003, integrated into UniProtKB/TrEMBL.
01-MAR-2003, sequence version 1.
21.FBB-2006, entry version 1.0.
Putative KNOX family class 2 homeodomain protein.
                                                                                                                         05-JUL-2004, integrated into UniProtKB/TrEMBL
                                           167 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QBH8GG ORYSA PRELIMINARY; PRT; 171 AA.
Q8H8GG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AC098695; AAN74840.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB115746; BAD08306.1; -; mRNA.
                                           PRT;
                                                                                                                                                                05-JUL-2004, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00967; ONCOGENEAML1.
                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS51062; RUNT; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 AAAAAAAAAAAA 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Rice Genomic Sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Osteoblast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=0J1126B12.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=39947;
                                       0765P9 RAT
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SEQUENCE
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08H8G OR1
1D OR1-MP
01-MP

Q765P9
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MEDLINE=2233736; PubMed=12447438; DOI=10.1038/nature01184; Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y., M. U., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H., Hosokawa S., Magukawa M., Arikawa K., Chiden Y., Hayashi M., Akamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C., Hishama S., Honda M., Ichikawa Y., Idonuma A., Ilijima M., Ikeda M., A Ikeno M., Ito Y., Ito Y., Iwabuchi A., Kamiya K., Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I., Machita K., Machara T., Mizuno H., Mizubayashi T., Mukai Y., Nakamura M., Anamiki N., Negishi M., Noha I., Ono N., Saji S., Sakai K., Shibata M., Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Teuji K., Waki K., Yamagata H., Yamane H., Yashiki S., Yoshihara R., Yukawa K., A Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.-I., Eun M.-Y., A Yano M., Jiang J., Gojobori T.;
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (japonica cultivar-group).
Bukaryoct; Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
Ehrhartoideae; Oryzaa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                     Score 44; DB 2; Length 171;
Pred. No. 1e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44; DB 2; Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The genome sequence and structure of rice chromosome 1."; Nature 420:312-316 (2002).
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SEQUENCE 175 AA; 18520 MW; 2FFF4E34C0E89871 CRC64;
                                                                                                                                                                                                                 171 AA; 17982 MW; 647C830E1C22B8F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.6%; Pred. No. 1e+02;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 AA.
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR005540; KNOXI.
InterPro; IPR005541; KNOXI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-FEB-2006, entry version 5.
Hypothetical protein P0406G08.29.
Name=P0406G08.29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-2005, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.08;
                                                                                                                                                                                                                                                                           100.08;
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 84.6%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                        Pfam; PF03790; KNOX1; 1.
Pfam; PF03791; KNOX2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=39947;
                                                                                                                                                                                  Nuclear protein.
SEQUENCE 171 A
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IISSUE=Brain;

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A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Rachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hisheh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uddin T.B., Toshivuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brossk S.A., McKernan R.J., Maramon R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Yillalon D.K., Murny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Schwultz J., Myers R.M.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
M. Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y PubMed=14702039; DOS=10.1038/ng1285;

X PubMed=14702039; DOS=10.1038/ng1285;

X Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,

X Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

Yamamoto U., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,

X Mamamoto U., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,

X Manasahi K., Yaku Y., Kodaira H., Kondo H., Sugawara M.,

X Jakahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,

X Abe K., Kamihara K., Yatsuta N., Sato K., Tanikawa M., Yamazaki M.,

Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,

X Anehori K., Takahashi-Fujii A., Hara H., Murakawa K., Fujimori K.,

X Ranehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,

X Ranehori K., Yauki H., Oshima A., Sasaki N., Imose N.,

Musashino K., Yuuki H., Oshima A., Sasaki N., Aotesuka S.,

Yoshikawa Y., Matsunawa H., Satoh N., Takami S., Tersahima Y., Suzuki O.,

Nomiyama H., Kimada H., Satoh N., Takami S., Tersahima Y.,

X Nomiyama H., Sainahabe K., Kumagai A., Itakura S., Fukuzumi Y.,

X Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,

Hishigaki H., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,

X Namazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,

X Namazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,

X Namazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,

X Namazaki M., Watanabe T., Saidana M., Sasaki M.,

A Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,

Matsushima-Sugano G., Satoh T., Shirai Y., Takahashi Y., Yamashita R.,

Nokumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,

Nokumura K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,

Nokumura K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,

Nokumura K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,

Nokumura K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,

Nokumura K., Yada T., Nakama M., Sasaki M.,

Nokumura K., Yada T., Nakama M., Sasaki M.,

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                               01-DEC-2001, integrated into UniProtKB/TrEMBL.
01-DEC-2001, sequence version 1.
07-MAR-2006, entry version 21.
Hypothetical protein FLJ30829 (Hypothetical protein RBM24)
(OTTHUMP00000016067).
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                                                                                                                                                                                                                                                                                                                                                                                                           Name=RBM24; ORFNames=RP1-259A10.1-002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=14702039; DOI=10.1038/ng1285;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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NUCLEOTIDE SEQUENCE

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The pubmed=1546914; DOI=10.1038/nature03025;

The bubmed=1546914; DOI=10.1038/nature03025;

The bubmed=1546914; DOI=10.1038/nature03025;

The bubmed=1546914;

The bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

Mauceli E., Bouneau L., Fischer C., Lutfalla G., Dossat C., Segurens B.,

The basilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,

Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

Anthouard V., Salanoubat S., Brottier P., Coutance U., P., Gouzy J.,

Relis M., Volff J.-M., Guigo R., Zody M.C., Mesirov J.,

Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Scarpelli C.,

Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.,

"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
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                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUL-2005, sequence version 1.
07-FEB-2006, entry version 3.
Chromosome 2 SCAFIS012, whole genome shotgun sequence. (Fragment).
ORFNAmes=GSTENG0003100001;
Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Tetradontoidea; Tetraodontidae; Tetraodon.
NCBI_TaxID=99883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             which is
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 44; DB 2; Length 191; 84.6%; Pred. No. 1.1e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry whi
                  to the EMBL/GenBank/DDBJ databases.
                                                                                                  Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                              191 AA; 19599 MW; 89E4D14E3DA941F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0833; POAALLERGEÑ. -
PROSITE; PSO0178; AA_TRNA_LIGASE_I; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUL-2005, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    199 AA.
                                                                                                                                                                                                                                                                 EMBL, BC104810; AA104811.1; -; mRNA.
EMBL, AL136305; CA119958.1; -; Genomic_DNA.
Ensembl; ENSG0000112183; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1.1e
0; Mismatches
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Nature 431:946-957(2004).
                                                                                                                                                                                                                     EMBL; AK055391; BAB70914.1; -; mRNA.
EMBL; BC104808; AAI04809.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                             InterPro; IPR001778; POA allergen_C.
InterPro; IPR001412; tRNA-synt_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
SEQUENCE 191 AA; 1
                Submitted (SEP-2005)
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NIH MGC Project;
                                                                                     Babbage A.;
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Mamm. Genome 11:151-158(2000).
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213
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NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                 Best Local Similarity
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NON_TER
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Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Mortlock D.P., Sateesh P., Innis J.W.;
"Evolution of N-terminal sequences of the vertebrate HOXA13 protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Metatheria, Didelphimorphia, Didelphidae, Monodelphis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Falvella F.S., Manenti G., Spinola M., Pignatiello C., Ravagnani Conti B., Pastorino U., Dragani T.A.;
"Population-based association study on two candidate lung adenocarcinoma modifier genes flanking the Di2Si034 locus.";
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                 Length 199;
                                                                                                                                               , Score 44; DB 2; Length 19
Pred. No. 1.2e+02;
0; Mismatches 2; Indels
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Ensembl; ENSG00000123095; Homo sapiens.
SEQUENCE 203 AA; 19438 MW; 02625F0B557CB263 CRC64;
                                                                                                          199 AA; 21690 MW; FB839A4F470FFD5D CRC64;
                                                         EMBL; CAAE01015032; CAG11205.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                     QSSCI4_HUMAN PRELIMINARY; PRT; 203 AA. QSSCI4; 21-DEC-2004, integrated into UniProtKB/TrEMBL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-DEC-2004, sequence version 1.
07-FEB-2006, entry version 5.
Basic helix-loop-helix protein 3 isoform 2.
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Best Local Similarity 84.6%;
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Q9TUC8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=BHLHB3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rissue=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=HOXA13;
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OSSCI4 HUM
OGSSCI4 HUM
DT 21-DE
DT 21-DE
DT 21-DE
DT 07-FE
DB Basic
GN HOMO-
OC BUKAT
OC BUK
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Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98038986; PubMed=9373149; DOI=10.1016/S0378-1119(97)00411-3; Suzkiki Y., Yoshitomo K., Maruyama K., Suyama A., Sugano S.; Construction and characterization of a full length-enriched and a S'end-enriched cDNA library.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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MEDLINE=94171032; PubMed=8125298; DOI=10.1016/0378-1119(94)90802-8;
Martyama K., Sugano S.;
"Oligo-capping: a simple method to replace the cap structure of eucaryotic mRNAs with oligoribonucleotides.";
Gene 138:171-174(1994).
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NUCLEOTIDE SEQUENCE.
Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,
Tanaka A., Yokoyama S.,
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                               100.0%; Score 44; DB 2; Length 213; 84.6%; Pred. No. 1.2e+02; Live 0; Mismatches 2; Indels
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Ensembl; ENSG00000139239; Homo sapiens.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005840; C:ribosome; IEA.
GO; GO:0003735; F:structural constituent of ribosome; IEA.
GO; GO:000412; P:protein biosynthesis; IEA.
                                                                                                                                                                                                                                                                     213 AA; 19165 MW; EDEC8B40FCACADE9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218 AA.
                                                                                                EMBL; AF083097; AAD54642.1; -; Genomic_DNA.
GO; GO:0005634; C:nucleus; IEA.
Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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150 AAAAAAAAAAA 162

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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Rlausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F.; Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Gadin T.B., Donaldo M.F., Casavant T.L., Scheetz T.E.,
Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Nhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rochield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
T. "Generation and initial analysis of more than 15,000 full-length human
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Tanaka A., Yokoyama S.;
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Dermoid cancer;
MEDLINE=98038986; PubMed=9373149; DOI=10.1016/S0378-1119(97)00411-3;
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MEDLINE=94171032; PubMed=8125298; DOI=10.1016/0378-1119(94)90802-8;
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Director MGC Project;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                             10-MAY-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                          10-MAY-2005, sequence version 1.
07-MAR-2006, entry version 8.
RPL14 protein (Ribosomal protein L14 variant)
Name-RPL14;
                                                                        220 AA.
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                                                                        PRT;
                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                        QEIPH7_HUMAN
Q6IPH7;
                                       HUMAN
RESULT 28

OS INT 10-MA

DI 10-MA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=15620360; DOI=10.1016/j.cell.2004.11.040;
Dorus S., Vallender B.J., Evans P.D., Anderson J.R., Gilbert S.L.,
Mahowald M., Wyckoff G.J., Malcom C.M., Lahn B.T.;
"Accelerated evolution of nervous system genes in the origin of Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-FEB-2005, sequence version 1.
07-FEB-2006, entry version 6.
Achaete-scute complex protein (Fragment).
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens.";
Cell 119:1027-1040(2004).
-i- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
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                                                                                                                                                                                                                                                                                                                                                              ; Score 44; DB 2; Length 220;
Pred. No. 1.2e+02;
0; Mismatches 2; Indels
EMBL; AK222750; BAD96470.1; -; mRNA.
Ensembl; ENSG00000139239; Homo sapiens.
GO; GO:0005840; C:ribosome; IEA.
GO; GO:0003735; F:structural constituent of ribosome; IEA.
GO; GO:0006412; F:protein biosynthesis; IEA.
InterPro; IPR005824; KOW.
InterPro; IPR002784; Ribosomal_L14e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AY650320; AAV67352.1; -; mRNA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0030528; F:transcription regulator activity; IEA.
GO; GO:0045449; P:regulation of transcription; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23804 MW; CD0D8E7C9F4F1063 CRC64;
                                                                                                                                                                                                                                                                                                           220 AA; 23787 MW; 0FD8AA7FC191E864 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-FEB-2005, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cercopithecidae, Cercopithecinae, Macaca.
NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                               Pfam; PF00467; KOW; 1.
Pfam; PF01929; Ribosomal_L14e; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001092; HLH basic.
InterPro; IPR011598; HLH DNA_bd
                                                                                                                                                                                                                                                                                                                                                                           100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                       84.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR011598; HLHT
Pfam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
PROSITE; PS50888; HLH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AAXAAAAAAAAA 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AAXAAAAAAAA 13
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Best Local Similarity 84.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 84.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                 Ribosomal protein.
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Q7Q706 ANOGA
Q7Q706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OSISRO MACFA
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NON TER
SEQUENCE
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Q7Q706_ANO
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                                                                         R GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0005634; C:nucleus; IEA.

R GO; GO:00005635; F:DNA binding; IEA.

R GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

R GO; GO:0006350; P:regulation of transcription, DNA-dependent; IEA.

R GO; GO:0006350; P:regulation of transcription, DNA-dependent; IEA.

R InterPro; IPR011991; Wing_hIx_DNA_bd.

R InterPro; IPR011991; Wing_hIx_DNA_bd.

R RMAT; SN00321; PAX; 1.

R SMART; SN00321; PAIREDBOX.

R RMAT; SN00321; PAIREDBOX.

R DNA-binding; Developmental protein; Nuclear protein; Paired box;

M Transcription; Transcription regulation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae; Potexvirus; unclassified Potexvirus.
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PubMed=16096710; DOI=10.1007/s00705-005-0586-x;
Tzanetakis I.E., Postman J.D., Martin R.R.;
"Mint virus X: a novel potexvirus associated with symptoms in 'Variegata' mint.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 44; DB 2; Length 228; 84.6%; Pred. No. 1.3e+02; 1.ve 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 44; DB 2; Length 228; 84.6%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7CCA50757B2ACDE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228 AA; 23774 MW; B1D3877B7B11313B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AY921610; AAX19351.1; -; Genomic_RNA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IPP000052; Pltvir_coat.
Pfam; PR00236; Virus P-coat; 1.
PRINTS; PR00232; POTXCARLCOAT.
PROSITE; PS00418; POTEX_CARLAVIRUS_COAT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-APR-2005, integrated into UniProtKB/TrEMBL.
12-APR-2005, sequence version 1.
07-FBB-2006, entry version 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
                         EMBL; AJ579865; CAE30302.1; -; mRNA.
SMR; Q5K4L2; 1-103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arch. Virol. 151:143-153(2006).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 228
228 AA; 24289 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QSBQDS_9VIRU PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   || ||||||| ||
129 AAAAAAAAAAA 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 84.6
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NUCLEOTIDE SEQUENCE
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=301865;
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SEQUENCE 228
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Mint virus X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON TER
SEQUENCE
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QSBQD5_9VI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anopheles gambiae str. PEST.
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
Anophelimae; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Duplicated, Pax6 genes in Glomeris marginata (Myriapoda: Diplopoda), an arthropod with simple lateral eyes."; 2001ogy 108:47-53(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glomeris marginata.
Bukaryota, Metazoa, Arthropoda, Myriapoda, Diplopoda, Pentazonia,
Glomerida, Glomeridae, Glomeris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 44; DB 2; Length 22
84.6%; Pred. No. 1.38+02;
ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                   The Anopheles gambiae Sequence Committee; "Anopheles gambiae re-annotation."; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227 227
227 AA; 25069 MW; C14D4245AF45563C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AAAB01008960; EAA11077.2; -; Genomic_DNA.GO; GO:0005634; C:nucleus; IEA.GO; GO:0003676; F:nucleuc acid binding; IEA.GO; GO:0003207; F:rucleic acid binding; IEA.InterPro; IPR007087; Znf_C2H2.Pro; PR00096; Ze-C2H2; 3.PROSITE; PS00028; ZnF_C2H2; 3.PROSITE; PS00028; ZnC_FINGER_C2H2; 3.PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.NON_TER.Pro; Z27 Z27 NON_TER.S27 Z27 SEQÜENCE 227 AA; 25069 MW; C14D4245AF45563C CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=16351954; DOI=10.1016/j.zool.2004.11.003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-FEB-2005, integrated into UniProtKB/TrEMBL.
15-FEB-2005, sequence version 1.
17-FEB-2006, entry version 8.
Pax6.2 protein (Fragment).
15-DEC-2003, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Anopheles gambiae Sequence Committee;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                      07-DEC-2004, sequence version 2 07-FEB-2006, entry version 10. ENSANGP00000017596 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                        ORFNames=ENSANGG00000015107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 AAAAAAAAAAA 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preliminary data.
                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q5K4L2_9MYRI
Q5K4L2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=pax6.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=PEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prpic N.M.;
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ASCL1 RAT
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Distributed under the Creative Commons Attribution-NoDerivs License
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Distributed under the Creative Commons Attribution-NoDerivs License
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Potexvirus; unclassified Potexvirus.
                                                                                                                                                                                                                                Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
Potexvirus; unclassified Potexvirus.
NCBI_TaxID=301865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=15664053; DOT=10.1016/j.jviromet.2004.11.006; Tzanetakis I.E., Keller K.E., Martin R.R.; "The use of reverse transcriptase for efficient first- and secondstrand cDNA synthesis from single- and double-stranded RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Maryland;
PubMed=16096710; DOI=10.1007/s00705-005-0586-x;
Pranetexkis I.E., Postman J.D., Martin R.R.;
"Mint virus X: a novel potexvirus associated with symptoms in 'Variegata' mint.";
Arch. Virol. 151:143-153(2006).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tzanetakis I.E., Postman J.D., Martin R.R.; ^{\prime} "Mint virus X: a novel potexvirus associated with symptoms in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 44; DB 2; Length 22
84.6%; Pred. No. 1.3e+02;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228 AA; 23843 MW; 8076F49DE5EB1A96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AY921609; AAX19348.1; -; Genomic_RNA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000062; Pltvir_cat.
Pfouse; PF00286; Virus_P-coat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Oregon;
PubMed=16096710; DOI=10.1007/800705-005-0586-x;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAR-2005, integrated into UniProtKB/TrEMBL. 01-WAR-2005, sequence version 1. 07-FEB-2006, entry version 7.
                                                                                        12-APR-2005, integrated into UniProtKB/TrEMBL 12-APR-2005, sequence version 1. 07-FEB-2006, entry version 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228 AA.
                                  228 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00232; POTXCARLCOAT.
PROSITE; PS00418; POTEX_CARLAVIRUS_COAT; 1.
                                  PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OSG7G9_9VIRU PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       templates.";
J. Virol. Methods 124:73-77(2005)
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Arch. Virol. 151:143-153(2006).
                                                                                                                                                          entry version 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AAXAAAAAAAA 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coat protein.
Mint virus X.
                               QSBQD8_9VIRU
QSBQD8;
                                                                                                                                                                                          Coat protein.
Mint virus X.
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Q5G7G9_9VI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi;
Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILĀRITY: Contains 1 basic helix-loop-helix (bHLH) domain.
                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                              Score 44; DB 2; Length 228;
Pred. No. 1.38+02;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Sprague-Dawley;
MEDLINE=90363294; PubMed=2392153; DOI=10.1038/346858a0;
                                                                                                                                                                                                       228 AA; 23834 MW; A56CCC8FD0F12A81 CRC64;
EMBL; AY789138; AAW67750.1; -; Genomic_RNA.
EMBL; AY921611; AAX19354.1; -; Genomic_RNA.
GO; GO: 00190219; C: viral capsid; IEA.
InterPro; IPR000519; F: structural molecule activity; IEA.
InterPro; IPR00052; Pltvir_coat.
Pfam; PR00286; Virus_P-coat; 1.
PRINTS; PR00232; POTXCRALCOAT.
PRODOM; PD000603; Pltvir_coat; 1.
PROSITE; PS00418; POTEX_CARLAVIRUS_COAT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1990, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X53725; CAA37760.1; -; mRNA.
PIR; S11563; S11563.
TRANSFAC; T00484; -.
Ensembl; ENSRNOG0000004294; Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 AA.
                                                                                                                                                                                                                                                                   Pred. No. 1.3e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGD; 71010; Ascll.
GO; GO:0007399; P:neurogenesis; IDA.
InterPro; IPR001092; HLH_basic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1990, sequence version 1.07-WAR-2006, entry version 46.
Achaete-scute homolog 1.
Name=Ascll; Synonyms=Ashl, Mash-1;
                                                                                                                                                                                                                                                    100.08;
                                                                                                                                                                                                                                                                       84.68;
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                                                                                                                                                                                                                                                                     Sest Local Similarity 84.6
Matches 11; Conservative
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                                                                                                                                                                                          Capsid protein.
SEQUENCE 228
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HUMAN
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                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (japonica cultivar-group).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li X., Zhu J., Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y., Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhao G., Xing K., Yu Z., Tang Y., Wu Y., Lu T., Li T., Hu H., Guan J., Wu M., Zhang R., Zhuu B., Chen Z., Chen L., Jin Z., Wang R., Yin H., Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y., Chen J., Xang H., Chen X., Shao C., Sun Y., Hu Q., Zhang Y., Lan L., Ling C., Sheng H., Gu J., Chen S., Ni L., Zhang Y., Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li Ji, Hong G., Xue Y., Han B.;
                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
         Pfam; PF00010; HLH; 1.

SMART; SW00353; HLH; 1.

PROSITE; P550888; HLH; 1.

Developmental protein; Differentiation; DNA-binding; Neurogenesis; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        factor activity; IEA.
transcription, DNA-dependent; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22337377; PubMed=12447439; DOI=10.1038/nature01183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 44; DB 2; Length 233; 84.6%; Pred. No. 1.3e+02; Live 0; Mismatches 2; Indels
                                                                                                                                                         Length 233;
                                                                                                                                             Score 44; DB 1; Length 23.
Pred, No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMAKI; SHUGSOV, ....., PROSITE; D. PROSITE; PS51032; AP2 ERF; 1.
CERTENCE 233 AA; 25434 MW; 90B3BF38A3A4A419 CRC64;
                                                                                                                                    036BDAC8E2D23274 CRC64;
                                                                Achaete-scute homolog 1.
/FTId=PRO 0000127128.
Helix-loop-helix motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Sequence and analysis of rice chromosome 4.";
                                                                                                                                                                                                                                                                                                         01-OCT-2003, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                   233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AL606635; CAD41708.2; -; Genomic_DNA.
HSSP; 080337; 1GCC.
                                                                                                 Basic motīf.
Poly-Ala.
Poly-Gln.
                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                   Q7XTV6_ORYSA PRELIMINARY; PRT;
Q7XTV6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grames, Q7XTV6; -
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription i
GO; GO:0006355; P:regulation of
InterPro; IPR001471; TF_ERF.
                                                                                                                                                                                                                                                                                                                 01-MAR-2004, sequence version 2.
07-FEB-2006, entry version 14.
OSJNBa0010D21.10 protein.
InterPro; IPR011598; HLH_DNA_bd
                                                                                     129 168 He
118 128 Baa
30 44 Po
48 54 Po
233 AA; 24972 MW; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00367; ETHRSPELEMNT.
ProDom; PD001423; TF ERF; 1.
SMART; SM00380; AP2; 1.
                                                                                                                                                         100.0%;
84.6%; 1
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                                                                                                                                                                                                                            32 AAAAAAAAAAAA 44
                                                                                                                                                                               11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Conservative
                                                                  233
                                                                                                                                                                                                                                                                                                                                                       Name=OSJNBa0010D21.10;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                DNA BIND
COMPBIAS
                                                                                                                                    SEQUENCE
                                                                                                                        COMPBIAS
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                                                                                       DOMAIN
                                                                 CHAIN
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RACKAN WATTTTTO
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MEDINES SEQUENCE LUARDS SCALE FRANT.

NOTICE 20186257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Straubberg R.L., Fearingold E.A., Grouse L.H., Derge J.G.,

Alusener R.D., Collins F.S., Wagner L., Schemmen C.M., Schuler G.D.,

Alusener R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,

Alusener R.D., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

And Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.W.,

Rabas S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., García A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gübbs R.A.,

Richards S., Worley K.C., Hale S., García A.M., Gay L.J., Hulyk S.W.,

Alledon B., Ketteman M., Madan A., Rodrigues S., Sanchez A.M.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLECTIDE SEQUENCE INEXNA].
MEDLINE=91296195; PubMed=8190674;
Ball D.W., Azzoli C.G., Baylin S.B., Chi D., Dou S., Donis-Keller H.,
Cumaraswamy A., Borges M., Nelkin B.D.;
"Identification of a human achaete-scute homolog highly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             binding to the B box (5 -CANNTG-31).
-!- SUBUNIT: Efficient DNA binding requires dimerization with another bHLH protein. Forms a heterodimer with E12/E47.
-!- SUBCELLULAR LOCATION: Nucleus (Probable).
-!- SUBLIARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
                                                                                                                                                                                                                                                                            PSD553; 098030; 01-02T-1996, integrated into UniProtKB/Swiss-Prot. 02-MAY-2002, sequence version 2. ACHAR-2006, entry version 46. Achaeve-scute homolog 1 (HASH1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neuroendocrine tumors.";
Proc. Natl. Acad. Sci. U.S.A. 90:5648-5652(1993)
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EMBL; BC001638; -; NOT ANNOTATED CDS; mRNA.
EMBL; BC002341; AAH02241.1; -; mRNA.
EMBL; BC004425; AAH04425.1; -; mRNA.
EMBL; BC004425; AAH04425.1; -; mRNA.
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Ensembl; ENSG00000139352; Homo sapiens.
                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HASH1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=ASCL1; Synonyms=ASH1;
Homo sapiens (Human).
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14 AASAAAAAAAA 26
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Gaps

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Indels

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Mismatches
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                                                                                                     O9BX46_HUMAN PRELIMINARY;
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Q6CNB7;
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                                            209 AAAAAAAAAAA 221
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                      1 AAXAAAAAAAA 13
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  11; Conservative
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                   Gaps
             HGNC; HGNC:738; ASCLI.

MIM; 100790; gene.
GO; GO:0003700; F:ranscription factor activity; NAS.
InterPro; IPR011598; HLH basic.
InterPro; IPR011598; HLH DNA_bd.
Pfam; PF00010; HLH; 1.
SWART; SMO0153; HLH; 1.
Developmental protein; Differentiation; DNA-binding; Neurogenesis;
Nuclear protein; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
This, Zhong G., Wang C., Shen C., Ke R., Li M., Xiao W. Lin L., Yang S.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                          ; Score 44; DB 1; Length 236;
Pred. No. 1.3e+02;
0; Mismatches 2; Indels
                                                                                                                                                                           Poly-Ala.
Poly-Gln.
E -> G (in dbSNP:1803157).
FrId=VAR 013179.
Q -> QQQ (in Ref. 1).
W; A7D784329305B49A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
SEQUENCE 236 AA, 24740 MW; 9B550B5232E3AA3D CRC64;
                                                                                                                              Achaete-scute homolog 1.
/FTId=PRO 0000127126.
Helix-loop-helix motif.
Basic motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 44; DB 2;
84.6%; Pred. No. 1.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0833; POAALLERGEN.
SMART; SM00360; RRM; 1.
PROSITE; PS00178; AA TRNA_LIGASE_I; UNKNOWN_1.
PROSITE; PS50102; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HGNC; HGNC: 21539; RBM24.

GO; GO:0003676; F:nuclecide binding; IEA.

GO; GO:000166; F:nuclectide binding; IEA.

InterPro; IPR01267; a b plait_nuc bd.

InterPro; IPR001778; POA allergen_C.

InterPro; IPR001778; POA allergen_C.

InterPro; IPR001478; RNPI_RNA_bd.

InterPro; IPR001412; tRNA_Synt_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AX547318; AAS55633.1; -; mRNA.
Ensembl; ENSG00000112183; Homo sapiens.
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25454 MW;
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131
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62
158
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    H-InvDB; HIX0010931;
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236 AA;
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Best Local Similarity
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Best Local Similarity
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COMPBIAS
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Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes, Saccharomycetales, Saccharomycetales, Saccharomycetales, Saccharomycetales, Saccharomycetales, Saccharomycetales, MillaxID=28985,
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STRANI=CBS 2359 / IFO 1267 / NRRL Y-1140 / WM37;
PubMed=15229592; DOI=10.1038/nature02579;
Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 44; DB 2; Length 236; 84.6%; Pred. No. 1.3e+02;
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16-AUG-2004, sequence version 1.
07-FEB-2006, entry version 11.
Similarities with sp|Q9YAC5 Aeropyrum pernix Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE. Babbage A.; Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 AA; 24776 MW; 1CFB5AEBD4E3AA24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ensembl; ENSGO000112183; Homo sapiens.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:000166; F:nucleicide binding; IEA.
GO; GO:000166; F:nucleicide binding; IEA.
InterPro; IPR012677; a b plait nuc bd.
InterPro; IPR001778; PŌA_allergen_C.
InterPro; IPR001712; RRM! RNA_bd.
InterPro; IPR00112; LRMA_Synt_I.
PRINTS; PR00833; PŌAALLERGEN.
SWART; SW00336; RRM; 1.
PROSITE; PS00178; AA TRNA_LIGASE_I; UNKNOWN_I.
PROSITE; PS00102; RRW; 1.
EROSITE; PS50102; RRW; 1.
                                                         01-JUN-2001, integrated into UniProtKB/TrEMBL. 01-JUN-2001, sequence version 1. 01-EB-2006, entry version 28. OTTHUMPO0000016066.
236 AA.
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HSSP; P09651; 1L3K.
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0; Mismatches
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Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
Boisrame A., Bloyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.-M., Nikolski M., Oztas S., Ozter-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
Swennen D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Wincker P., Souciet J.-L.;
I'm Genome evolution in yeasts.",
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Complete proteome; Hypothetical protein.
SEQUENCE 244 AA; 24930 MW; CC83CACE35423EE2 CRC64;
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                                     9, 2006, 22:48:41; Search time 14.8101 Seconds (without alignments) 84.457 Million cell updates/sec
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                               283416 segs, 96216763 residues
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Maximum Match 100%
Listing first 100 summaries
                          protein search, using sw model
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Gaps

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A;Residues: 1-470 <WIL>
A;Cross-references: UNIPROT:Q9XUY1; UNIPARC:UP100007519F; EMBL:Z81552; PIDN:CAB04486.1;
A;Experimental source: clone.F56G4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: ĴH0797
R;Mellerick, D.M.; Kassis, J.A.; Zhang, S.D.; Odenwald, W.F.
Meuron 9, 789-803, 1992
A;Title: Castor encodes a novel zinc finger protein required for the development of a su
A;Reference number: JH0797; MUID:93040222; PMID:1418995
A;Accession: JH0797
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Aparthors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; McAuthors: Kreft, J.; Kuhn, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Molecule type: DNA
A,Rosidues: 1-79 CMEL.
A;Cross-references: UNIPROT:07M3M8; UNIPARC:UPI000017BEED; GB:L04487
C;Comment: This protein is required for the development of embryonic CNS neurons.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C,Species: Listeria monocytogenes
C,Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Drosophila sp.
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                 A;Introns: 17/3; 152/1; 241/3; 339/1; 449/3
C;Superfamily: hypothetical protein F56G4.4; WW repeat homology
F;177-216/Domain: WW repeat homology <WWR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 799;
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39; DB 2;
Pred. No. 69;
3; Mismatches
                                                      A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                .;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39; DB 2
Pred. No. 42;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       castor protein - fruit fly (Drosophila sp.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: FlyBase:FBgn0004878
A;Introns: 284/3; 515/3; 660/3
C;Keywords: metal binding; zinc finger
F;236-242/Region: acidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 75.0%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ASMSAASAASMAA 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F,363-421/Region: zinc finger
F,422-482/Region: zinc finger
F,483-541/Region: zinc finger
F,542-600/Region: zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ASMSAASAASMA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 AKWEAAAASMA 77
A; Reference number: Z19615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                           A; Gene: CESP: F56G4.4
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                                                                                                                                                                                                                                                                                 A;Map position: 1
                                  A;Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                            hypothetical protein lin2792 (imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Species: Listeria innocua
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB1781
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
B;Dominguez-Bernal, G;Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D; Jones, L.M.; Karet, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kunn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mahando, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Varquez-Boland, J.A.; Voss, H.; Wehland, A;Reference number: AB1781
A;Reference number: AB177; MUID:21537279; PMID:11679669
A;Accession: AB1781
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Molecule type: DNA
A;Residues: 1-328 <GLA>
A;Residues: 1-328 <GLA>
A;Cross-references: UNIPROT:Q927J6; UNIPARC:UPI00000CC998; GB:AL592022; PIDN:CAC98018.1;
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin2792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nuclear protein fkh - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Accession: A32380
R;Weigel, D.; Juergens, G.; Kuettner, F.; Seifert, E.; Jaeckle, H.
Cell 57, 645-658, 1989
A;Title: The homeoric gene fork head encodes a nuclear protein and is expressed in the A;Reference number: A32380; WUID:89249328; PMID:2566386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.8%; Score 42; DB 2; Length 328; 76.9%; Pred. No. 10;
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C;Keywords: DNA binding; transcription regulation
F;210-301/Domain: fork head DNA-binding domain homology <FHD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
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         ALIGNMENTS
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Matches 9; Conservative
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A;Molecule type: DNA; mRNA
A;Residues: 1-510 <WEI>
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Gaps

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hypothetical 31.3K protein in agaI-mtr intergenic region (f286) [imported] - Agrobacter C; Species: Agrobacterium tumefaciens C; Species: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: D97395

R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman R, Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B. Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: D97395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Residues: 1-258 <XUR>
A,Cross-references: UNIPROT:Q8UIJ3; UNIPARC:UPI0000164347; GB:AE007869; PIDN:AAK86117.1
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C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
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C;Species: Galleria mellonella (greater wax moth)
C;Date: 18-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 09-Jul-2004
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                                                                                                                  Length 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 258
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R;Zurovec, M.; Sehnal, F.; Scheller, K.; Kumaran, A.K.
Insect Biochem. Mol. Biol. 22, 55-67, 1992
A;Title: Silk gland specific cDNAs from Galleria mellonella L.
A;Reference number: A61615
                                                                                                                                                                             1; Indels
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A;Residues: 1-268 <ZUR>
A;Cross-references: UNIPROT:Q7M468; UNIPARC:UPI000017CAA4
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                                                                                                                     Score 37;
Pred. No.
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Pred. No.
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A;Map position: circular chromosome
C;Superfamily: methyltransferase, YraL type
     C,Genetics:
A,Gene: YPO3978
C,Superfamily: hypothetical protein HI0093
                                                                                                                        68.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 AGSSAASAASGAA 110
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Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                       9; Conservative
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                          145 SAASVASMAA 154
                                                                                                                                                                                                                                  4 SAASAASMAA 13
                                                                                                                  Query Match
Best Local Similarity
Matches 9; Conserv
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AF2613
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C;Species: Yersinia pestis
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-375 < kUR>
A;Cross-references: UNIPROT:Q8ZA42; UNIPARC:UPI0000DC955; GB:AL590842; PIDN:CAC93439.1;
              A; Molecule type: DNA
A; Residues: 1-328 cGLA>
A; Residues: 1-328 cGLA>
A; Cross-references: UNIPROT; Q8Y431; UNIPARC; UPI00000556C4; GB: NC_003210; PIDN: CAD00721.1
A; Experimental source: strain EGD-e
C; Genetics:
A; Gene: lmo2643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fork head domain protein crocodile - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: D-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Oct-2004
C;Accession: S59870; A46178
R;Haecker, U.; Kaufmann, E.; Hartmann, C.; Juergens, G.; Knoechel, W.; Jaeckle, H.
R;Haecker, U.; Kaufmann, E.; Hartmann, C.; Juergens, G.; Knoechel, W.; Jaeckle, H.
A;Title: The Drosophila fork head domain protein crocodile is required for the establish
A;Reference number: S59870; MUID:96080166; PMID:7489720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Hacker, U.; Grossniklaus, U.; Gehring, W.J.; Jackle, H.
Proc. Natl. Acad. Sci. US.A. 89, 8754-8758, 1992
A;Title: Developmentally regulated brosophila gene family encoding the fork head domain.
A;Reference number: A46178; MUID:92409595; PMID:1356269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPARC:UPI000016BBEC; GB:M96440; NID:g157425; PIDN:AAF02177.1; PID:
A;Note: sequence extracted from NCBI backbone (NCBIP:114222)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.4%; Score 38; DB 2; Length 508; 69.2%; Pred. No. 66; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                  DB 2; Length 328
                                                                                                                                                                                                                                                                                          1; Indels
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F;70-161/Domain: fork head DNA-binding domain homology <FHD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Cross-references: UNIPROT: P32027; UNIPARC: UPI000001B0F
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                                                                                                                                                                                                                                  Score 38;
Pred. No.
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69.2%;
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449 ASVAAASAAAAA 461
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Best Local Similarity 69.2
Best Local 9; Conservative
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Best Local Similarity
Matches 9; Conserve
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A;Status: preliminary
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A;Residues: 1-329 <GLA>
A;Residues: 1-329 <GLA>
A;Cross-references: UNIPROT:Q8Y586; UNIPARC:UPI00005571F; GB:NC_003210; PIDN:CAD00261.1
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo2183
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A;Molecule type: DNA
A;Residues: 1-407 <WIL>
A;Cross-references: UNIPROT: UNIPARC: UPI00000754B2; EMBL: Z54235; PIDN: CAA90977.1;
A;Experimental source: clone C09G9
R;Matthews, P.
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A;Molecule type: DNA
A;Residues: 1-407 <WI2>
A;Cross-references: UNIPARC:UP100000754B2; EMBL:Z54236; PIDN:CAA90986.1; GSPDB:GN00022;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Mesidues: 1-420 <SAU>A;Cross-references: UNIPROT: Q9Z4Y6; UNIPARC: UPI00000DAF36; EMBL: AL035707; PIDN: CAB38889
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T36193
R;Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, March 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein C09G9.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19155; T19510
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A,Introns: 13/2; 69/2; 146/2; 195/3; 273/1
C,Superfamily: Caenorhabditis elegans hypothetical protein ZC513.6
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Pred. No. 1.1e+02;
4; Mismatches 1; Indels
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A,Title: Comparative genomics of Listeria species.
A,Reference number: AB1077; MUID:21537279; PMID:11679669
A,Accession: AG1347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, September 1995
A;Reference number: 219133
A;Accession: T19510
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Pred. No. 92;
3; Mismatches
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347 SSLNAASAAAAA 359
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169 SSQSASSAASLA 180
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Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
8; Conserve
                                                                                    A; Molecule type: DNA
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
S;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
S;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.D.; Jones, L.M.; Karst, U.
B.; Jones, L.M.; Karst, U.
B.; Jones, L.M.; Karst, U.
B.; Arathors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC1718
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Exrichrome ABC transporter (permease) homolog lmo2183 [imported] - Listeria monocytogen
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AG1347
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J. Dominguez-Bernal, G.; Duchaud, E.; Dusaurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.
D.; Jones, L.M.; Karst, U.
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mak, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
                               R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell, Karp, P.; Romero, P.; Zhang, S. Science 284, 2117-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
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                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-313 <KUR>
A;Cross-references: UNIPROT:Q8UIJ3; UNIPARC:UP100000D177D; GB:AE008688; PIDN:AAL41324.1;
A;Experimental source: strain C58 (Dupont)
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                                                                                                                                                                                   ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
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66.7%; Pred. No. 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 313;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
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ilarity 69.2%; Pred. No. 8
Conservative 1; Mismatch
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C,Superfamily: methyltransferase, YraL type
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Best Local Similarity
Matches 8; Conserva
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nes 9; Conserv
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A; Residues: 1-329 <GLA>
                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
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                 C; Accession: AF2613
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A,Gene: lin2287
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Query Match

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C,Accession: A55929
R,Cheah, P.Y.; Meng, Y.B.; Yang, X.; Kimbrell, D.; Ashburner, M.; Chia, W.
R,Cheah, P.Y.; Meng, Y.B.; Yang, X.; Kimbrell, D.; Ashburner, M.; Chia, W.
A,Title: The Drosophila 1(2) 35Ba/nocA gene encodes a putative Zn finger protein involved A,Reference number: A55929; MUID:94119100; PMID:8289824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-537 <CHE>
A;Cross-references: UNIPROT:Q24423; UNIPARC:UPI000007B356; GB:L14009; NID:g431289; PID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: UNIPROT:004982; UNIPARC:UPI00000A2615; EMBL:AF007786; NID:g2198852; A,Experimental source: strain Missouri 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C,Accession: T02942
R,Locke, M.E.H.; Guida, A.D.; Falco, S.C.
submitted to the EMBL Data Library, June 1997
A,Description: Deregulation of the methionine biosynthetic pathway in corn seeds.
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C;Superfamily: cystathionine gamma-synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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N;Alternate names: cystathionine gamma-synthase
C;Species: Zea mays (maize)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 05-Oct-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      zinc finger protein nocA - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004
                                                                                                                                                                                          Gaps
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                                                                                                                  Length 509;
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                                                                                                              Score 36; DB 2; Length 509
Pred. No. 1.4e+02;
2; Mismatches 2; Indels
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Pred. No. 1.4e+02;
4; Mismatches 1; Indels
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       C, Superfamily: cystathionine gamma-synthase C, Keywords: carbon-oxygen lyase
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A,Accession: T02942
A,Status: translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-509 <LOC>
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                                                                                                              Query Match 66.7%;
Best Local Similarity 69.2%;
Matches 9; Conservative
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232 SSMAAAAAAAA 244
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Best Local Similarity 61...
Best Aconservative
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A;Accession: 138240
A;Statuus: preliminary; translated from GB/EWBL/DDBJ
A;Statuus: preliminary; translated from GB/EWBL/DDBJ
A;Residues: 1-474 «RES>
A;Cross-references: UNTRACT:Q06945; UNIPARC:UPI0000047FA0; EMBL:X70683; NID:g36552; PIDN
A;Cross-references: UNTRACT:Q06945; UNIPARC:UPI0000047FA0; EMBL:X70683; NID:g36552; PIDN
B;Cross-references: Unitraction of Sales and Sal
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A;Residues: 70,'P',72-123 <DEN>
A;Cross-references: UNIPARC:UP1000016B04E; EMBL:X65661; NID:936551; PIDN:CAA46612.1; PIQ
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A;Cross-references: UNIPROT:004981; UNIPARC:UPI00000A35C3; EMBL:AF007785; NID:g2198850;
A;Experimental source: strain H99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NiAlternate names: sex-determining region Y box 4 protein
C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence revision 06-Sep-1996 #text_change 05-Oct-2004
C;Accession: 138240; S22938; S21479; S31724
R;Farr, C.J.; Easty, D.J.; Ragoussis, J.; Collignon, J.; Lovell-Badge, R.; Goodfellow,
Amm. Genome 4, 577-584, 1993
A;Title: Characterization and mapping of the human SOX4 gene.
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O-succinylhomoserine (thiol) lyase (BC 4.2.99.9) 1 - maize
O-succinylhomoserine (thiol) lyase (BC 4.2.99.9) 1 - maize
NyAlternate names: cystathionine gamma-synthase
Sybecises: Zea mays (maize)
C;Specises: Zea-mays (maize)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 05-Oct-2004
C;Accession: T02940
A;Description: Deregulation of the methionine biosynthetic pathway in corn seeds.
A;Reference number: Z14785
A;Accession: T02940
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                                                                                                                                                        Similarity 69.2%; Score 36; DB 2; Length 420; 9; Conservative 2; Mismarches
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Pred. No. 1.3e+02;
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A;Molecule type: mRNA
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C;Keywords: DNA binding; transcription regulation
F;56-131/Domain: HMG box homology <HMG1>
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A, Experimental source: strain A3(2)
C, Gennetics:
A, Gene: SCOEDS. SCE29.14c
C, Superfamily: tetracycline 6-hydroxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transcription factor SOX4 - human
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327 ASVSAAAAASAPA 339
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nes 9; Conservative
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Matches 9; Conserva
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A; Gene: GDB: SOX4

Query Match Best Local S Matches 9

g 8

RESULT 19

Genetics:

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A;Cross-references: UNIPROT:P27593; UNIPARC:UPI0000138711; EMBL:X58868; NID:g59965; PIDN A;Note: the source is given as pseudorables virus C;Superfamily: herpesvirus glycoprotein H C;Superfamily: herpesvirus glycoprotein H C;Keywords: glycoprotein; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Cross-references: FlyBase: FBgn0000581
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Best Local Similarity 72.7
Matches 8; Conservative
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490 VSAATAASLAA 500
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Best Local Similarity 61.5
Matches 8; Conservative
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Best Local Similarity
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S15478
S15478
S15478
Cj.Date: 09-Jun-1994 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
Cj.Date: 09-Jun-1994 #sequence of a pseudorabies virus gene homologous to glycoprot A, Reference number: S15478
A,Accession: S15478
A,Accession: S15478
A,Accession: S15478
A,Accession: Lose AMEX-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reddues: 1-686 CARES
A; Cross-references: UNIPROT:Q00660; UNIPARC:UPI0000138710; GB:X61696; NID:g61352; PIDN:G
A; Cross-references: UNIPROT:Q00660; UNIPARC:UPI0000138710; GB:X61696; NID:g61352; PIDN:G
C; Superfamily: herpesvirus glycoprotein; transmembrane protein
C; Keywords: glycoprotein; transmembrane predicted <SIG>
F; 1-10/Domain: signal sequence #status predicted <GFH>
F; 3-1-68f/Product: glycoprotein # #status predicted <GFH>
F; 67-67f/Domain: transmembrane #status predicted <GFH>
F; 67-7, 162, 542, 604, 627/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A,Molecule type: DNA
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-686 <KLU>
A,Cross-references: UNIPROT:P27416; UNIPARC:UPI000013870F; GB:M61196; NID:G334058; PIDN:
A,Cross-references: UNIPROT:P27416; UNIPARC:UPI000013870F; GB:M61196; NID:G334058; PIDN:
C,Superfamily: herpesvirus giveproprotein
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-686/Product: glycoprotein # #status predicted <GPH>
F;447-667/Domain: transmembrane #status predicted <GPH>
F;47,162,542,604,627/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                              glycoprotein H precursor - suid herpesvirus 1 (strain NIA-3)
C;Species: suid herpesvirus 1
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: A42000; S16737
E;Peeters, B.; de Wind, N.; Broer, R.; Gielkens, A.; Moormann, R.
J. Virol. 66, 3888-3822, 1992
A;Title: Glycoprotein H of pseudorabies virus is essential for entry and cell-to-cell as the form of the following particles of the fol
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Clyacoprotein H precursor - suid herpesvirus 1
Clyaces suid herpesvirus 1
Clyacession: A39990
R;Klupp, B.G.; Mettenleiter, T.C.
Virology 182, 732-741, 1991
A;Fitle: Sequence and expression of the glycoprotein gH gene of pseudorabies virus.
A;Reference number: A39990; MUID:91220723; PMID:1850925
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Pred. No. 1.8e+02;
3; Mismatches 2; Indels
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245 AQLSAAHAAALAA 257
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Matches 8; Conserv
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Best Local S
Matches 8
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C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #text_change 09-Jul-2004
C;Date: 11-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Dates: 10-Aug-1999
R;Latenkunas, K.; Berger, J.; Ruse, C.; Sinclair, D.A.; Randazzo, F.; Brock, H.W.
Development 125, 4055-4066, 1998
Development 125, 4055-4066, 1998
A;Title: The enhancer of polycomb gene of Drosophila encodes a chromatin protein conserv
A;Reference number: 217611; MUID:98407961; PMID:9735366
A;Accession: T13154
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A;Molecule type: mRNA
A;Residues: 1-2023 <STA>
A;Cross-references: UNIPROT:096542; UNIPARC:UPI0000083EF3; EMBL:AF079764; NID:g3757889;
A;Experimental source: imaginal disc
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A;Residues: 1-5069 <SCH>
A;Cross-references: UNIPROT:052789; UNIPARC:UPI000055B02; EMBL:AJ223012; NID:e1227119;
A;Experimental source: strain LBG A3136
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C.Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C.Accession: T17464
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                      Length 686;
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Pred. No. 4.8e+02;
2; Indels
Score 36; DB 2; Length 000
Pred. No. 1.8e+02;
2; Indels
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19631-1702/Domain: acyl carrier protein homology <ACP1>
19238-1309/Domain: acyl carrier protein homology <ACP2>
19395-5010/Domain: acyl carrier protein homology <ACP3>
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                                                                                    3; Mismatches
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-339 <WIL>
A;Cross-references: UNIPARC:UPI000017BC34; EMBL:Z79758; NID:e1062260; PIDN:CAB02131.1;
A;Experimental source: clone W10D5
C;Genetics:
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C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: G81655
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg Nucleic Acids Rese 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q9PJG1; UNIPARC:UPI0000057ABA; GB:AE002353; GB:AE002160; NI
A;Experimental source: strain Nigg (MOPn)
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A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia track A;Reference number: A71570; MUID:99000809; PMID:9784136
A;Accession: E71497
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A,Residues: 1-439 <ARN>
A,Cross-references: UNIPROT:084583; UNIPARC:UPI0000139ACF; GB:AE001328; GB:AE001273; NI
A;Experimental source: serotype D, strain UW-3/Cx
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C, Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C, Accession: E71497
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Pred. No. 1.7e+02;
1; Mismatches 3; Indels
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Pred. No. 1.4e+02;
4; Mismatches 1;
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A,Gene: CT579
C,Superfamily: conserved hypothetical protein TC0868
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C;Superfamily: conserved hypothetical protein TC0868
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A;Introns: 18/3; 56/2; 195/2; 269/1
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Best Local Similarity 61.5%;
Matches 8; Conservative 4
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69.2%;
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131 ASAASASAAAVAA 143
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268 AASGAASAASSAA 280
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Matches 9; Conservative
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-436 <TET>
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                                                       ABC transporter (permease) BH2113 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Accession: Bec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: A83914
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Ree. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83914
A;Reference number: A8350; MUID:20512582; PMID:11058132
A;Accession: A83914
A;Residues: 1-308 cSTO>
A;Cross-references: UNIPROT:Q9KB22; UNIPARC:UPI00000D7427; GB:AP001514; GB:BA000004; NIC
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH2113
C;Superfamily: maltose transport protein malG
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A.Molecule type: mRNA
A.Residues: 1.314 **NOMA-
A.Cross-references: UNIPRCT:061425; UNIPARC:UPI0000171F45; DDBJ:D29639
A.Cross-references: UNIPRCT:061425; UNIPARC:UPI0000171F45; DDBJ:D29639
A.Experimental source: embryonal carcinoma F9 cells
C.Comment: This enzyme plays a role in the mitochondrial beta-oxidation of short chain f
C.Comment: This enzyme plays a role in the mitochondrial beta-oxidation of NAD to NADH and exerts its highest activity toward
C.Superfamily: 3-hydroxyacyl-CoA dehydrogenase homology
C.Keywords: fatty acid beta-oxidation; homodimer; mitochondrion; NAD; oxidoreductase
F1-12/Domain: transit peptide (mitochondrion) #status predicted <TPP>
F13-314/Product: 3-hydroxyacyl-CoA dehydrogenase homology and the status predicte
F12-314/Domain: 3-hydroxyacyl-CoA dehydrogenase homology and the status predicte
F12-314/Domain: 3-hydroxyacyl-CoA dehydrogenase homology and the status predicte
F12-314/Domain: 3-hydroxyacyl-CoA dehydrogenase homology and the status predicte
F12-57/Region: beta-alpha-beta NAD nucleotide-binding fold
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                                  bC transporter (permease) BH2113 [imported] - Bacillus halodurans (strain C-125)
;Species: Bacillus halodurans
;Date: 01.Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
;Accession: A83914
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hypochetical protein W10D5.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T26328
R;Kershaw, J.
submitted to the EMBL Data Library, September 1996
A;Reference number: 220200
A;Reference number: 220200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.8%; Score 35; DB 2; Length 308; 69.2%; Pred. No. 1.3e+02;
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Best Local Similarity 66.7%;
Matches 8; Conservative
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les 9; Conservative
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11 SMSSSSSASAAA 22
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Gaps

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Length 646

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R.Haller, J.; Cote, S.; Broenner, G.; Jaeckle, H.
Genes Dev. 1, 862-867, 1987
A.Title: Dorsal and neural expression of a tyrosine kinase-related Drosophila gene durin
A.Reference number: A27041; MJID:88112827; PMID:3428600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Map position: 2R,66F1
A,Introns: 453/1; 497/1
C,Keywords: atchoposphorylation; glycoprotein; phosphoprotein
F;9,65,187,223,224,250,611,660/Binding site: carbohydrate (Asn) (covalent) #status predi
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Eur. J. Biochem. 216, 343-352, 1993
A;Title: Molecular cloning and expression of mouse and human cDNA encoding AES and ESG;
A;Reference number: 835678; MUID:93373944; PMID:8365415
A;Accession: 835681
A;Status: preliminary
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A;Reference number: 222137; MUID:98094274; PMID:9434185
A;Accession: T42296
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-646 < ALO>
A;Cross-references: UNIPROT:048456; UNIPARC:UPI000009B4CA; EMBL:X97918; PIDN:CAA66557.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Oct-2004
C;Accession: S35681; S34162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tyrosine kinase-related protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: A27041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35; DB 2; Length 753; Pred. No. 2.8e+02;
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61.5%; Pred. No. 2.9e+02;
ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-753 <HAL>
A;Cross-references: UNIPROT:P14083; UNIPARC:UPI0000136FEA
                                                                                                                                                                                                     Score 35; DB 2; I
Pred. No. 2.5e+02;
2; Mismatches 3;
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F;613-646/Domain: WD repeat homology «WD3»
F;695-728/Domain: WD repeat homology «WD4»
F;736-769/Domain: WD repeat homology «WD5»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: dTKR
A;Cross-references: FlyBase:FBgn0003715
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                                                                                                                                                                                                        Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     293 AOMHAAAAAAAA 305
                                                                                                                                                                                                                                                                                                                                                                           202 AAOSAANAVKWAA 214
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Best Local Similarity 61.5%
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Best Local Similarity 61.5
Matches 8; Conservative
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A; Residues: 1-771 <MIY>
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C;Species: phage SPP1
C;Species: phage SPP1
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T42296
R;Alonso, J.C.; Luder, G.; Stiege, A.C.; Chai, S.; Weise, F.; Trautner, T.A.
Gene 204, 201-212, 1997
A;Title: The complete nucleotide sequence and functional organization of Bacillus subtil
                                                                                                                                                                                                                                             C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: H8324
C;Accession: H8324,
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q910R3; UNIPARC:UP100000C5747; GB:AE004685; GB:AE004091; NIU A;Experimental source: strain PA01 C;Genetics: A;Genetics:
                                                                                                                                                                                                              probable chemotaxis transducer PA2573 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cranscription factor btd - fruit fly (Drosophila sp.)
C;Species: Drosophila sp.
C;Date: 18-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 07-May-1999
C;Accession: S39356
B;Wimmer, E.A.; Jaeckle, H.; Pfeifle, C.; Cohen, S.M.
Nature 366, 690-694, 1993
A;Title: A Drosophila homologue of human Spl is a head-specific segmentation gene.
A;Reference number: S39356; MUID:94081952; PMID:8259212
A;Accession: S39356
A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-644 <WIM>
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64.8%; Score 35; DB 2; Length 644;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 9; Conservative 1; Mismatches 2; Indels
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Pred. No. 2.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.8%;
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                                                                                271 ATSGAASAASSAA 283
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Matches 9; Conservative
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                            1 ASMSAASAASMAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: H83324
A;Status: preliminary
A;Molecule type: DNA
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Length 771;

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hypothetical protein AGR_L_2329 [imported] - Agrobacterium tumefaciens (strain C58, Cerr
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct_2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                    C;Accession: G98275
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B. Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                        A,Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu
A,Reference number: A97359, MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-1520 (KUR>
A, Cross-references: UNIPROT: Q8U9Q4; UNIPARC: UPI00000D22BA; GB: AE007870; PIDN: AAK89729.1
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A;Cross-references: UNIPROT:O61845; UNIPARC:UPI000007A573; EMBL:AF067617; PIDN:AAC17559
A;Experimental source: strain Bristol N2; clone T04D1
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| Jate: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
| Accession: T33152
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Pred. No. 9.8e+02;
3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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A.Description: The sequence of C. elegans cosmid T04D1.
A.Reference number: Z21292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein T04D1.4 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DB 2; I
Pred. No. 5.3e+02;
2; Mismatches 1;
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61.5%;
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Similarity 72...
Similarity 72...
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Matches 8; Conservative
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484 LSARSAASLAA 494
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SXAD12
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polyketide synthase Atu3672 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

polyketide synthase Atu3672 [imported] - Agrobacterium tumefaciens

[C.Species: Agrobacterium tumefaciens

C.Species: Agrobacterium tumefaciens

C.Bate: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004

C.Accession: AF3008

R;Mood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I R;Mood, D.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell

RAPP, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                probable tail fiber protein GP37 - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C;Accession: G64887; T09189
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cq. A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              moto, Y.; Horiuchi, T.

DNA Res. 3, 363-377, 1996

A;Title: A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the A;Reference number: 216603; MUID:97251357; PMID:9097039

A;Accession: T09189

A;Accession: T09189

A;Accession: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 3-1122 <AIB>
A;Cross-references: UNIPARC:UPI00001360ED; GB:AE000234; GB:U00096; NID:g1787633; PIDN:AA

A;Cross-references: UNIPARC:UPI00001360ED; GB:AE000234; GB:U00096; NID:g1787633; PIDN:AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1122 <BLAT>
A;Cross-references: UNIPROT:P76072; UNIPARC:UP10000168098; GB:AE000234; GB:U00096; NID:q
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A;Molecule type: DNA
A;Residues: 1-150 «KUR>
A;Cross-references: UNIPROT:Q8U9Q4; UNIPARC:UPI0000D22BA; GB:AE008689; PIDN:AAL4484.1;
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Experimental source: strain K-12, substrain MG1655
R, Aiba, H.; Baba, T.; Fujita, K.; Hayashi, K.; Inada, T.; Isono, K.; Itoh, T.; Kasai, H
.; Motomura, K.; Nakade, S.; Nakamura, Y.; Nashimoto, H.; Nishio, Y.; Oshima, T.; Saito
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A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AF3008
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Pred. No. 5.3e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.8%; Score 35; DB 2; Length 1122; 75.0%; Pred. No. 4.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: G64887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
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1 ASMSAASAASMA 12

Best Local Similarity 75.0 Matches 9; Conservative

Query Match

64.8%;

Conservative

3 MSAASAASMAA 13

A, Map position: linear chromosome

C;Genetics: A;Gene: Atu3672

Gaps

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Length 211; 4; Indels

Score 34; DB 2; I Pred. No. 1.3e+02; ); Mismatches 4;

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A;Cross-references: UNIPROT:Q9NTF4; UNIPARC:UPI000066CFFC; EMBL:AL137304 A;Experimental source: adult testis; clone DKFZp434H247 C;Genetics:
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                                                                                                                                                                                                                                                            63.0%;
69.2%;
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Best Local Similarity 69.2
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A; Reference number: Z23037
                                             A Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-211 <AAA>
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                        A; Accession: T46497
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C; Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C; Accession: T03033
R; Radowaki, R; Kubo, N; Ozawa, K.; Hirai, A.
EMBO J. 15, 6652-6661, 1996
A; Reference number: Z14829; MUID:97133294; PMID:8978691
A; Recession: T03033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPARC:UPI00004007E; EMBL:X73487; NID:g313361; PIDN:CAA51880.1; PIC;Genetics:
A;Map position: 9.4-10.7
C;Superfamily: adenovirus hexon-associated protein (IX)
                                                                        A,Cross-references: UNIPROT:P03284, UNIPARC:UPI000004007E
R;Kimura, T.; Sawada, Y.; Shinawawa, M.; Shimizu, Y.; Shiroki, K.; Shimojo, H.; Sugisaki
Nucleic Acids Res. 9, 6571-6589, 1981
A;Title: Nucleotide sequence of the transforming early region Elb of adenovirus type 12
A;Reference number: A93745; MUID:82105565; PMID:6275367
                                                                                                                                                                                                         A;Accession: A93745
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-144 «KIM»
A;Cross-references: UNIPARC:UPI000004007E; GB:X73487; NID:g313361; PIDN:CAA51880.1; PID:
B;Sprengel, J.
submitted to the EMBL Data Library, June 1993
A;Reference number: S33928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-169 «KAD»
A;Cross-references: UNIPROT:P92683; UNIPROT:Q8LQX9; UNIPARC:UPI000008B4C4; EMBL:D85381;
A;Experimental source: cultivar Nipponbare
C;Genetics:
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hypothetical protein DKFZp434H247.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 04-Fb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accesion: T46497
R;Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, January 2000
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Pred. No. 1e+02;
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C;Superfamily: mammalian cytochrome-c oxidase chain Vb
C;Keywords: mitochondrion; oxidoreductase
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16 ASASASAASGAA 28
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Best Local Similarity 69.2
Best Local 9, Conservative
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  A; Accession: A90814
A; Molecule type: mRNA
A; Residues: 1-144 <BOS>
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A,Status: preliminary
A,Molecule type: DNA
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32 39 72.2 793 1 CAS DROME 33 39 72.2 1014 2 Q2UQFO ASPOR 34 39 72.2 4574 2 Q63LK9-BURPS 35 38 70.4 129 2 Q2QLK1 ORYSA 36 38 70.4 166 2 Q84JTZ-ORYSA	38 70.4 169 2 38 70.4 172 2 38 70.4 172 2	38 70.4 174 2 38 70.4 328 2 50 70.4 328 2	38 70.4 328 2 38 70.4 328 2 38 70.4 328 2 38 70.4 330 2	38 70.4 332 2 38 70.4 343 2 38 70.4 376 2	38 70.4 434 2 38 70.4 472 2 20 70 4 500 1	38 70.4 508 2	38 70.4 545 2 38 70.4 545 2 38 70.4 847 2	38 70.4 1090 2 38 70.4 1090 2 38 70.4 3360 2 37 68.5 76 2	37 68.5 104 2 37 68.5 131 2 37 68.5 151 2 37 68.5 197 2	37 68.5 199 2 37 68.5 234 2 37 68.5 266 2 37 68.5 285 2	37 68.5 286 2 37 68.5 290 2	37 68.5 293 2 37 68.5 293 2 37 68.5 294 2	37 68.5 375 2 37 68.5 375 2	37 68.5 376 2 37 68.5 394 2 37 68.5 426 2	37 68.5 457 2 37 68.5 462 2	37 68.5 518 2	37 68.5 533 2 Q3JXI 37 68.5 536 2 Q2STI	37 68.5 540 2 37 68.5 551 2	37 68.5 554 2 37 68.5 575 2	37 68.5 640 2 37 68.5 653 2	37 68.5 735 2 37 68.5 761 2	37 68.5 818 2 37 68.5 818 2	37 68.5 868 2	37 68.5 1144 2 37 68.5 2178 2	37 68.5 2601 36 66.7 110	PTNAMID I I &	סיימווייס
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GenCore v Copyright (c) 1993	Sea		Title: US-10-617-568-5 Perfect score: 54 Sequence: 1 ASMSAASAASMAA 13	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 2849598 seqs, 925015592 residues	Total number of hits satisfying chosen parameters: 28.	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries	<pre>Database : UniProt_7.2:* 1: uniprot_sprot:* 2: uniprot_trembl:*</pre>	sults predicted be the score of the total score	SUMMARIES	Result Query No. Score Match Length DB ID	43 79.6 272 2 QC	3 42 77.8 207 2 Q2N062 9STRA 4 42 77.8 328 2 Q927JG_LISIN 5 42 77.8 417 2 Q9VJXS_DROME	42 77.8 910 2 QC	9 42 77.8 1258 2 Q	1 42 77.8 1326 2 Q. 22 41 75.9 324 2 Q.	3 41 75.9 805 2 Q	5 40 74.1 210 2 Q0 6 40 74.1 510 1 F)	7 40 74.1 510 2 8 40 74.1 1839 2	9 39 72.2 181 2 Q	1 39 72.2 216 2 QC	3 39 72.2 301 2 0	5 39 72.2 378 2 Q	39 72.2 395 2 39 72.2 441 2 30 72 2 441 2	39 72.2 470 2 00	1 39 72.2 724 2 Q

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oryza sativ corynebacte argone aur azoarcus sp candida alb phytophthor frankia sativ purkholderi oryza sativ burkholderi oryza sativ purkholderi burkholderi cryptococcu triomicrosp spergillus spergillus spergillus spergillus burkholderi cryptococcu triomicrosp streptococcu triomicrosp

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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
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NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phytophthora sojae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=67593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1642;
[1]
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Q2N062;
                                                                                                                                                                                                                                                                                                                                                                  Local Sim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=CBS 2359 / IFO 1267 / NRRL Y-1140 / WM37;

Pubmed=15225592; DOI=10.1038/nature02579;

Budon B., Sherman D., Fischer G., Durrens P., Casaregola S.,

A Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,

Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,

Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,

Barnay S., Blanchin S., Beckerich J.-M., Geyne E., Bleykasten C.,

Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,

Baliaray S., Banchin S., Pairhead C., Ferry-Dumazet H., Groppi A.,

Hantraye F., Hennequin C., Jauniau N., Joyet P., Kachouri R.,

M. Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,

Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,

Rellarz S., Potler S., Richard G.-F., Straub M.-L., Suleau A.,

Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,

Wincker P., Souciet J.-L.;

W. "Genome evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Eukaryopts, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                           Anuyvercomyces lactis (reast).
Bukaryota; Fungi, Ascomycota; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
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07-FEB-2006, entry version 7.
Hypothetical protein OSJNBa0018M09.16 (Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Length 272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T., Katayose Y.; to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome.
SEQUENCE 272 AA; 25696 MW; BC0464D2994066D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=OSJNBa0018M09.16; Synonyms=OJ1115_D03.3;
                                                                                                                                                                   integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004, integrated into UniProtKB/TrEMBL
                                                                                                        272 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79.6%; Score 43; DB
76.9%; Pred. No. 56;
iive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; CR382122; CAH02414.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
Sasaki T., Matsumoto T., Yamamoto K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                        PRT;
                                                                                                                                                                                                           sequence version 1.
                                                                                                                                                                                                                                                                                             OrderedLocusNames=KLLA0B11055g;
                                                                                                                                                                                                                                        07-FEB-2006, entry version 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QČK4T3_ORYSA PRELIMINARY;
Q6K4T3;
                                                                                                                                                                                                                                                                                                                                 Kluyveromyces lactis (Yeast)
                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ASVSAASAASVAS 133
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hes 10; Conservative
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Submitted (JUL-2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=28985;
                                                                                                     QECVLB_KLULA
QECVLB;
                                                                                                                                                                       16-AUG-2004,
16-AUG-2004,
                                                                                                                                                                                                                                                                      Similarity.
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1006K473 OR
1006K473 OR
1007 OS-4
1007 OS-4
1007 OS-4
1007 OS-6
100
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QGCVL8 KA

DD QGCV

AC QGCV

BD 16-A

DT 16-A

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Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jiang R.H., Tyler B.M., Whisson S.C., Hardham A.R., Govers F.; "Ancient Origin of Blicitin Gene Clusters in Phytophthora Genomes."; Mol. Biol. Evol. 23:338-351(2006).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=P6497;
Jiang R.H.Y., Tyler B.M., Whisson S.C., Hardham A.R., Govers F.;
Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 207;
                                                                                                                                                                                                                        Length 285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Listeria innocua.
Bacteria, Firmicutes, Bacillales, Listeriaceae, Listeria.
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                                                                                                                                                                                                                                                                           Indels
                                                                                                                           Gramene, O6K4T3; -.
Hypothetical protein.
SEQUENCE 285 AA; 30341 MW; E955D01FD443ED22 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; DQ229265; ABB56018.1; -; Genomic DNA.
SEQUENCE 207 Aa; 19497 MW; F467E939F266199A CRC64;
                                                                                                                                                                                                                      Score 43; DB 2;
Pred. No. 59;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 42; DB 2;
Pred. No. 62;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001, integrated into UniProtKB/TrEMBL.
01-DEC-2001, sequence version 1.
07-FBB-2006, entry version 14.
07-FBP-2005, protein.
OrderedLocusNames=lin2792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-FEB-2006, integrated into UniProtXB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207 AA
                                                                           EMBL; AP005533; BAD22199.1; -; Genomic_DNA.
EMBL; AP004001; BAD21485.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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07-FEB-2006, entry version 1.
Elicitin-like protein SOLIA.
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0
                                                                                                                                                                                                                             79.6%;
84.6%;
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Q927J6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        || ||:|:|||||
180 ASASASSSASMAA 192
                                                                                                                                                                                                                                                                                                                                                                           173 ASRCAASAASMAA 185
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nes 10; Conservative
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Lewis S.E.;
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     MEDLINES-2019606; Pubbed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li Pw., Hookins R.A., Galle R.F., Amanatides P.G., Scherer S.E., Li Pw., Hookins R.A., Galle R.F., Amanatides R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Manatides G., Halt G., Nelson C.R., Miklos G.L.G., Man K.H., Doyle C., Barter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Bansal W., Bana A., Baxendale J., Bayakarsolu L., Beasley B.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Abrits K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Abrits K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Aboson K., Coule E., Connes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Dodon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn R., Cadek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harvey D.A., Heiman T.J., Wei M.-H., Ibegwam C., Ratchum K.A., Howleton K.A., Howland T.J., Wei M.-H., Ibegwam C., Ratchum K.A., Galali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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            STRAIN=CIIP 11262 / Serovar 6a;
MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fshih H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maltournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterayota; Dittera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.8%; Score 42; DB 2; Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                          Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A. Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.; "Comparative genomics of Listeria species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     328 AA; 36670 MW; F2E1A0F2C6D98622 CRC64;
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 417 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; ALS96173; CAC98018.1; -; Genomic_DNA. PIR; AB1781; AB1781. ListLiist; LIN2792; -. BioCyc; LINN1642:LIN2792-MONOMER; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76.9%; Preu. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000, sequence version 1.
07-FEB-2006, entry version 19.
CG16850-PA.
                                                                                                                                                                                                                                                                                                                                                                    Science 294:849-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 AAMSAAAAAAAAA 325
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Matches 10; Conservative
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09VJX5 DR
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01-M
DT 01-
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Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Li J.H., McIntcoh T.C., McLeod M.D., Morbherson D.D., Markulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Pollard J., Puri V., Reese M.G., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Ashinet K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Strong R., Sun B., Shire B., Spradling A.C., Stapheton M., Strong R., Sun B., Ashires R., Tector C., Turner R., Venter B., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Zhong X.H., Zhong F.N., Zhou M., Zhou K., Zhou K., Zhu S., Zhu K., Smith H.O., Ching R.A., Myers B.W., Rubin G.M., Venter J.C.;
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MEDIJNE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22426065; PubMed=12537568; Carlson J.W., Halpern A., Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoekins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleron M., Suton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finishing a whole-genome shotgun: release 3 of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
Yu C., Rubin G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases
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FlyBase; FBgn0032527; CG16850.
SEQUENCE 417 AA; 44286 MW; 42EA717B5604565F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a genomics perspective.";
Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
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Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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NUCLEOTIDE SEQUENCE.
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Score 42; DB 2; Length 417;

77.88;

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                                        STRAIN=2603 V/R / ATCC BAA-611 / Serotype V;
MEDLINE=2222988; PubMed=12200547; DOI=10.1073/pnas.182380799;
MEDLINE=22222988; PubMed=12200547; DOI=10.1073/pnas.182380799;
Messels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
Radune D., Fedorova N.B., Scanlan D., Khouri H.M., Mulligan S.,
Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome analysis of multiple pathogenic isolates of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         agalactiae: implications for the microbial 'pan-genome'.";
Proc. Natl. Acad. Sci. U.S.A. 102:13950-13955(2005).
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                            "Complete genome sequence and comparative genomic analysis of ar emerging human pathogen, serotype V Streptococcus agalactiae."; Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77.8%; Score 42; DB 2; Length 970
69.2%; Pred. No. 2.9e+02;
iive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-NOV-2005, integrated into UniProtKB/TrEMBL.
22-NOV-2005, sequence version 1.
07-FEB-2006, entry version 5.
06-Il wall surface anchor family protein.
Name=clfB; ORFNames=SAM 1428;
Streptococcus agalactia CJB111.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO, GO:000596; C:cell surface; IEA.
GO; GO:0005618; C:cell wall; IEA.
InterPro; IPRO0189; Gram pos_anchor.
Pfam; PF00746; Gram pos_anchor; 1.
TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
PROSITE; PS50847; GRAM_POS_ANCHORNING; 1.
Cell wall; Complete protecome; Peptidoglycan-anchor.
SEQUENCE 970 AA; 99433 MW; OE817044FGEE9CE6 CRC64;
                         NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QBDFZ9 STRAG PRELIMINARY, PRT; 1130 AA.
QBDFZ9;
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881 ASMSASTSASMSA 893
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Matches 9; Conservative
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NCBI_TaxID=342617;
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                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome analysis of multiple pathogenic isolates of Streptococcus agalactiae: implications for the microbial 'pan-genome'."; Proc. Natl. Acad. Sci. U.S.A. 102:13950-13955 (2005).
-:- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus agalactiae serotype V.
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          910 AA; 94148 MW; C7F57665B2C99CFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AAJO01000001; EAO63494.1; -; Genomic_DNA.
GO; GO:0009986; C:cell surface; IEA.
GO; GO:0005618; C:cell wall; IEA.
     Pred. No. 1.2e+02;
2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OBDYL7 STRAS PRELIMINARY; PRT; 970 AA. 08DYL7; 01-MAR-2003, integrated into UniProtKB/TrEMBL. 01-MAR-2003, sequence version 1. 01-MAR-2006, entry version 18. Cell wall surface anchor family protein. OrderedLocusNames=SAG1462;
                                                                                                                                                                                                                                                                                             22-NOV-2005, integrated into UniProtKB/TrEMBL. 22-NOV-2005, sequence version 1. 27-NOV-2005, esquence version 5. Cell wall surface anchor family protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=18RS21;
PubMed=16172379; DOI=10.1073/pnas.0506758102;
                                                                                                                                                                                                                                                   910 AA.
                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell wall; Peptidoglycan-anchor. SEQUENCE 910 AA; 94148 MW; C
                                                                                                                                                                                                                                                                                                                                                                                                 ORFNames=SAJ 1458;
Streptococcus agalactiae 18RS21
                                                                                                                                                                                                                                                   PRELIMINARY;
76.9%;
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821 ASMSASTSASMSA 833
                                                                                                      1 ASMSAASAASMAA 13
                                                                           1 ASMSAASAASMAA 13
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nes 9; Conservative
  Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=216466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI TaxID=342613;
                                                                                                                                                                                                                                                Q3DVC9_STRAG
Q3DVC9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fraser C.M.;
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Length 970;

PRT; 1310 AA.

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                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=REMAI6 / Serotype III;
STRAIN=22242508; PubMed=1135421;
Glaser P., Rusniok C., Buchrisesr C., Chevalier F., Frangeul L.,
Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Genome sequence of Streptococcus agalactiae, a pathogen causing
                                                                                                                                                                                                                         Streptococcus agalactiae serotype III.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                   01-MAR-2003, integrated into UniProtKB/TrEMBL. 01-MAR-2003, sequence version 1. 07-FBB-2006, entry version 17. 07-PBP-2006, entry version 17. orderedLocusNames=gba1529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AL766851; CAD47188.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Microbiol. 45:1499-1513(2002).
                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invasive neonatal disease.
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                                                                                                                                                                                                                                                                                                     NCBI_TaxID=216495;
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73_STRA3
Q8E473_STRA3
Q8E473_
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     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-A909 / ATC2 2751 / Serotype Ia;
PubMed=16172379; DOI=10.1073/pnas.0506788102;
PubMed=16172379; DOI=10.1073/pnas.0506788102;
Tettelin H., Masignani V., Cieslewicz M.J., Donati C., Medini D., Ward N.L., Angiuoli S.V., Crabtree J., Jones A.L., Durkin A.S., DeBoy R.T., Davidsen T. M., Mora M., Scarselli M., Margarit y Ros I., Peterson J.D., Hauser C.R., Sundaram J.P., Nelson W.C., Madupu R., Brinkac L.M., Dodson R.J., Rosovitz M.J., Sullivan S.A.,
Daugherty S.C., Haft D.H., Selengut J., Gwinn M.L., Zhou L., Zafar N., Smith S., Utterback T.R., White O., Rubens C.E., Grandi G., Madeit L.C., Kasper D.L., Telford J.L., Wessels M.R., Rappuoli R.,
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                                                                                                                                                                                                                                          Score 42; DB 2; Length 1130;
Pred. No. 3.4e+02;
4; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ULGK; SAL. 1172).

GO; GO:0009986; C:cell surface; IEA.

GO; GO:0005886; C:cell wall; IEA.

InterPro; IPR001899; Gram_pos_anchor.

Fram; PF00746; Gram_pos_anchor; 1.

TIGRFAMS; TIGR01167; LFXTG_anchor; 1.

PROSITE: PSSO847; GRAM POS_ANCHORING; 1.

Cell wall; Complete protecome; Peptidoglycan-anchor.

SEQUENCE 1258 AA; 124927 MW; AF0CC314FFBAB9BF CRC64;
                                                                           EMBL; AAJQ01000008; EAO73831.1; -; Genomic_DNA.
GO; GO:0009986; C:cell surface; IEA.
GO; GO:0005618; C:cell wall; IEA.
Cell wall; Peptidoglycan-anchor.
SEQUENCE 1130 AA; 113624 MW; 264E398D72562EGE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-NOV-2005, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1258 AA.
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                                                                                                                                                                                                                                                   77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                      945 ASMSASTSASMSA 957
                                                                                                                                                                                                                                       Query Match
Best Local Similarity 69.2°
Matches 9, Conservative
                                                                                                                                                                                                                                                                                                                                                          1 ASMSAASAASMAA 13
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Best Local Similarity 69.27
Best Local 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 STRA1
Q3K052 STRA1
Q3K052;
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03K052 ST
10D AC
03K052 ST
10D AC
03K0 ON EN
DT 08-N
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Tettelin H., Masignani V., Cieelewicz M.J., Donati C., Medini D.,
Ward W.L., Angluoli S.V., Crabtree J., Jones A.L., Durkin A.S.,
DeBOY R.T., Davidsen T.M., Mora M., Scarselli M., Margarit y Ros I.,
Peterson J.D., Hauser C.R., Sundaram J.P., Nelson W.C., Madupu R.,
Brinkac L.M., Dodson R.J., Rosovitz M.J., Sullivan S.A.,
Daugherty S.C., Haft D.H., Selengut J., Gwinn M.L., Zhou L., Zafar N.,
Khouri H., Radune D., Dimitrov G., Warkins K., O'Connor K.J.,
Smith S., Utterback T.R., White O., Rubens C.E., Grandi G.,
                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                           77.8%; Score 42; DB 2; Length 1310;
BIOCYC; SAGAZIIII0:GBS1529-MONOMER; -.
BIOCYC; SAGAZIIII0:GBS1529-MONOMER; -.
GO; GO:000986; C:cell surface; IEA.
GO; GO:0005618; C:cell wall; IEA.
InterPro; IPRO10189; Gram_pos anchor; 1.
FIGREAMS; TIGR01167; LPXTG anchor; 1.
PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
Cell wall; Complete profesome; Peptidoglycan-anchor.
SEQUENCE 1310 AA; 129398 MW; 9FB7A8BE89B8F155 CRC64;
                                                                                                                                                                                                                                               Pred. No. 3.9e+02;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-NOV-2005, integrated into UniProtKB/TrEMBL. 22-NOV-2005, sequence version 1. 77-FEB-2006, entry version 5. Cell wall surface anchor family protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1326 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=sdrE; ORFNames=SAI_1566;
Streptococcus agalactiae H36B.
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Q3D424;
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781 ASMSASTSASMSA 793
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AAJS01000004; EA078954.1; -; Genomic_DNA.
GO; GO:0009961; C:cell surface; IEA.
GO; GO:0005618; C:cell wall, IEA.
Cell wall; Peptidoglycan-anchor.
SEQUENCE 1326 AA; 131101 MW; 2866221DCFBD528E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Madoff L.C., Kasper D.L., Telford J.L., Wessels M.R., Rappuoli R.,
Fraser C.M.;
                                                                                                Genome analysis of multiple pathogenic isolates of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-AUG-2004, integrated into UniProtKB/TrEMBL.
16-AUG-2004, sequence version 1.
07-FEB-2006, entry version 12.
07-FEB-2006, 
                                                                                                                                           agalactiae: implications for the microbial 'pan-genome'.";
Proc. Natl. Acad. Sci. U.S.A. 102:13950-13955(2005).
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.9%; Score 41; DB 2; Length 324; 83.3%; Pred. No. 1.4e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324 AA; 35095 MW; 69775D1A260C9908 CRC64;
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685 ASMSASTSASMSA 697
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Best Local Similarity 83.3
Matches 10; Conservative
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hes 9, Conservative
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                                                                                                                                                                                                                                                                                                                                                     preliminary data.
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06C1D7 YAR
10C1D AC
06C1D DT
16-AU
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RA ATTERN B.W. Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,

RA ATTERN B.W., Allen T., An P., Anderson M., Anderson S.,

Ant-Zahra M., Allen T., An P., Anderson M., Anderson S.,

Ant-Zahra M., Allen T., An P., Alderson M., Anderson S.,

Blitshictor B. Bloom T., Blye J., Boguslavskiy L.,

B. Borowsky M., Boukhgalter B., Brunache A., Boguslavskiy L.,

B. Citroen M., Comisting M., Considing T., Cook A., Cooke P., Corum B.,

Citroen M., Collymore A., Considing T., Cook A., Cooke P., Corum B.,

R. Citroen M., Collymore A., Campen T., Dugray S., Dodges S., Dodges P.,

B. Dorje P., Dorjec K., Dorrisi L., Duffey N., Dupes A., Elkins T.,

R. Fickson J., Farina A., Faro S., Perreira P., Flacher H.,

R. Angopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,

R. Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliav I.,

R. Anderson J., Farina P., Kodira C., Kulbokas E., Lebutt K.,

R. Anderson M., Romen P., Kodira C., Kulbokas E., Lebutt K.,

R. Anderson M., Mabbit R., Maru K., Markless E., Malora C., Major J.,

R. Morzell S., Marabella R., Maru K., Matthews C., Malora C., Major J.,

R. Morzell W., McDhoudy S., McGhee T., Mikkelsen T., Minega V., Moru K.,

Morzethy W., McDonough S., McGhee T., Mikkelsen T., Minega V., Moru K.,

R. Morzethy M., Mulrain L., Munson G., Naylor J., Newson C., Settipal B.,

R. Well K., Soman S., Parker S., Perrin D., Phunkhang P., Piqani B.,

R. Weltz R., Richardson S., Rise C., Roditage Z., Roger S., Rogers D.,

R. Retts R., Richardson S., Rise C., Roditage Z., Roger S.,

R. Retts R., Richardson S., Rise C., Roditage Z., Roger S.,

R. Retts R., Mithardson S., Rise C., Roditage S., Roger S.,

R. Persing S., Taender S., Theodore J., Thollulasang Y., Tobham K.,

R. Tesma S., Yang S., Yang S., Yang S., Wang S., Wangchuk T.,

R. Persing S., Taender S., Theodore S., Perrin D., Wassiltev H.,

R. Tesmon S., Yang S., Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Fungi, Basidiomycota, Ustilaginomycetes;
Ustilaginomycetidae, Ustilaginales; Ustilaginaceae; Ustilago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The genome sequence of Ustilago maydis.";
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AACPO1000242; EAK82947.1; -; Genomic_DNA.
GO; GO:0044249; P:cellular biosynthesis; IEA.
INTERPRO; IPR000649; IF-2B_related.
PANTHER; PTHR10233; IF-2B, IF-2B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                  19-JUL-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                           805 AA.
                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                           19-JUL-2005, sequence version 1.
07-FEB-2006, entry version 4.
                                                                                                                                                                                                                                                                                                                         07-FEB-2006, entry version 4. Hypothetical protein.
                                                                                                                                                                           PRELIMINARY;
179 SMSKAQAASMAA 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Ustilago maydis 521
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RESULT 14 Q7S1A6\_NEU

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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
A manatides P.G., Scherer S.E., I. P.W., Hoskins R.A., Galle R.E.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
A Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Banos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=89249328; PubMed=2566386; DOI=10.1016/0092-8674(89)90133-5;
Weigel D., Juergens G., Kuettner F., Seifert E., Jaeckle H.;
"The homeotic gene fork head encodes a nuclear protein and is
expressed in the terminal regions of the Drosophila embryo.";
Cell 57:645-658(1989).
                                                                                                                                                                                              Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L. Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R., Gibbon J.E., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C., Harrison F.H., Gibbon J., Harwood C.S., "Complete genome sequence of the metabolically versatile photosynthetic bacterium Rhodopseudomonas palustris.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoda, Arthropoda, Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                          Rhodopseudomonas palustris.
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB 2; Length 210;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome; Hypothetical protein.
SEQUENCE 210 AA; 21813 MW; 07F77C85CCABFFE5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FKH DROME STANDARD; PRT; 510 AA. P1734; Q9VAVO; 01-ARE-1990, integrated into UniProtKB/Swise-Prot. 01-APR-1990, sequence version 1. 07-FBB-2006, entry version 57. Fork add protein. Name-fkh; ORFNames-CG10002;
                                                                                                                                      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=CGA009 / ATCC BAA-98;
PubMed=14704707; DOI=10.1038/nbt923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; BX572594; CAE25971.1; -; Genomic_DNA.
BioCyc; RPAL258594:RPA0527-MONOMER; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                               Bradyrhizobiaceae; Rhodopseudomonas
                                                                                                                                                                                                                                                                                                                    Nat. Biotechnol. 22:55-61(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74.1%;
83.3%;
                      OrderedLocusNames=RPA0527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 ASASASASIA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ASMSAASAASMA 12
      protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7227;
                                                                                                   NCBI_TaxID=1076;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41, DB 2; Length 1293;
Pred. No. 5.6e+02;
0; Mismatches 2; Indels
                                    Score 41; DB 2; Length 805;
Pred. No. 3.5e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000886; ER target S.
PROSITE; PS00014; ER TARGET; UNKNOWN 1.
SEQUENCE 1293 AA; 136804 MW; C85AF94F062EB449 CRC64;
  86248 MW; 5A4CC28D1060ACD6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AABX01000455; EAA29126.1; -; Genomic_DNA.
InterPro; IPR000886; ER target S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                          15-DEC-2003, integrated into UniProtKB/TrEMBL.
15-DEC-2003, sequence version 1.
07-FEB-2006, entry version 10.
ORFOILCTED PROTEIN.
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05-JUL-2004, sequence version 1.
07-FEB-2006, entry version 8.
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                                    Query Match 75.9%;
Best Local Similarity 76.9%;
Matches 10; Conservative
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Q7S1A6;
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Matches 11; Conservative
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805 AA;
                                                                                                                                                                                                                                                                                                                                                                                                    Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=5141;
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QENCES;
SEQUENCE
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RESULT 15 QENCES RHO ID QENCE AC QENCE DT 05-JU DT 05-JU

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Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
A Foelier C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
A dalain M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Krafe C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D. L.,
Morkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Alazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Klamos II., Simpson M., Strong R., Sun E.,
Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
Syriskas R., Tector C., Turner R., Venter E., Wang S., Yao Q. A.,
Wang Z.-Y., Massarman D.A., Weinsteck G.M., Weissenbach J.,
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Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
Glibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195 (2000).
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Genome Biol. 3.RESEARCH0083.1-RESEARCH0083.22(2002).

-!- FUNCTION: Fkh promotes terminal as opposed to segmental

-i- Function: In the absence of kth, this development switch does

not occur. The nuclear localization of the fkh protein suggest

that fkh regulates the transcription of other, subordinate, genes.
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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m c}
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GO; GO: 00005515; F: protein binding; IPI.
GO; GO: 00005439; P: erctodermal gut development; TAS.
GO; GO: 00007439; P: endoderm formation; TAS.
GO; GO: 00007439; P: endoderm formation; TAS.
GO; GO: 0000720; P: malphghian tubule morphogenesis; TAS.
GO; GO: 00007435; P: salivary gland morphogenesis; IMP.
InterPro; IPRO11991; Wing hix_DNA_bd.
PEam; PF00250; Fork head.
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PIR; A32380; A32380.
HSSP; Q99958; 1DSV.
SMR; P14734; 210-300.
IntAcc; P14734; -.
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Ensembl; CG10002; Drosophila melanogaster.
FlyBase; FBgn0000659; fkh.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rrown; PD000425; TF_Fork_head; 1. SMART; SM00339; FH; 1.
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0005155; P:regulation of transcription, DNA-dependent; IEA.
DNA-binding; Nuclear protein.
SEQUENCE 510 AA; 54242 MW; 3089574C2BE7981B CRC64;
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PROSITE; PS00657; FORK HEAD_1; 1.
PROSITE; PS00658; FORK HEAD_2; 1.
PROSITE; PS50039; FORK HEAD_3; 1.
Complete proteome; Developmental protein; DNA-binding;
Nuclear protein; Transcription; Transcription regulation.
Nuclear protein; Fork head protein.
//FIId=FRO_000091896.
                                                                                                                                                                                                                                                                                      Length 510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stapleton M., Carlson J., Chavez C., Frise E., George R., Park S., Wan K., Yu C., Celniker S., Submitted (OCT-2005) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                             510 AA; 54286 MW; 2B86E807CBF7881B CRC64;
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69.2%; Pred. No. 3.2e+02;
iive 3; Mismatches 1;
                                                                                                                                                                                                                                                                                                          Pred. No. 3.2e+02;
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13-SEP-2005, sequence version 1.
07-FEB-2006, entry version 2.
Hypothetical protein.
O*Promes=Becep1808DRAFT 7796,
Burkholderia vietnamiensis G4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-DEC-2005, integrated into UniProtKB/TrEMBL. 06-DEC-2005, sequence version 1.
                                                                                                                                                                                                                                                                                         Score 40; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             510 AA.
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                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                               Fork-head.
                                                                                                                                                                                                     Gly-rich.
His-rich.
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101 ASMSASMSASMSA 113
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101 ASMSASMSASMSA 113
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                                                                                                                                                                                    300
40
356
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COMPBIAS
COMPBIAS
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Q4B6Z4_B
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STRAIN=BisB18;
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Q6Z461_ORYSA
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                                                                                                                                                                                                                                                                                                                                              Larimer F., Land M.; "Annotation of the draft genome assembly of Burkholderia vietnamiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
Enthartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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07-DEC-2004, sequence version 1.
21-FEB-2006, entry version 7.
Hypothetical protein P0679C08.7-2 (Hypothetical protein P0493C11.25-
                                                                                                                                         Detter C., Glavina T., P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina Hammon N., Israni S., Pitluck S., Richardson P.;
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
                                                                                                             US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavi Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome and assembly of Burkholderia vietnamiensis G4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sasaki T., Marsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.1%; Score 40; DB 2; Length 1839; 76.9%; Pred. No. 1.2e+03; ive 1; Mismatches 2; Indels
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"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1839 AA; 185155 MW; 0DADC47988CEC299 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                              Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
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InterPro; IRRO003006; IG MHC.
DAGSITE; PS00290; IG MHC; UNKNOWN_1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>OŠVRP3 ORYSA PRELIMINARY; PRT; 181 AA.</u>
QSVRP3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=P0679C08.7-2; Synonyms=P0493C11.25-2;
                                                                                                                                                                                                                                                                                                   STRAIN-G4;
US DOE Joint Genome Institute (JGI-ORNL);
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Sasaki T., Matsumoto T., Yamamoto K.
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                                                                  NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone:P0679C08."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=G4;
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OGSVRP3 ORY
DG OGSVRP3
DT 07-DE
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                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=BisB18;
US DOE Joint Genome Institute (JGI-ORNL);
Larimer F., Land M.;
"Annotation of the draft genome assembly of Rhodopseudomonas palustris
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome and assembly of Rhodopseudomonas paluetris BisBl8.";
Submitted (OCT-2005) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-DEC-2005, sequence version 1.
07-FEB-2006, entry version 3.
Cell wall surface anchor family protein (Fragment).
ORFNAMES-RPCDRAFT 08/19; BisB18.
Bacteria, Proteobacteria, Alphaproteobacteria; Rhizobiales,
Bradyrhizobiaceae; Rhodopseudomonas.
                                                                                                                                                                                                                                                                                                                                                72.2%; Score 39; DB 2; Length 181; 69.2%; Pred. No. 1.7e+02; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.2%; Score 39; DB 2; Length 201; 76.9%; Pred. No. 1.8e+02; ive 1; Mismatches 2; Indels
clone:P0493C11.", Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BisB18.";
Submitted (NOV-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                            Hypothetical protein.`
SEQUENCE 181 AA; 18397 MW; A5CAB7C54081C7D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 AA; 17690 MW; A28DC1EFB43DF437 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AALR01000022; EAP10010.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-DEC-2005, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                        EMBL; AP002542; BAD67872.1; -; Genomic_DNA.
EMBL; AP000559; BAD67675.1; -; Genomic_DNA.
Gramene; Q5VRP3; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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50 AAMSASSAAAAAA 62
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NUCLEOTIDE SEQUENCE.
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Q4IBZ8_GIBZE
Q4IBZ8;
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STRAIN=CLIB 122 / B 150.

A Dulon B., Sherman D., Fischer G., Durrens P., Casaregola S.,

A Dulon B., Sherman D., Fischer G., Durrens P., Casaregola S.,

A Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,

Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,

Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,

Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,

Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,

A Rerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,

A Nicaud J.-M., Nikolski M., Oztar S., Ozier-Kalogeropoulos O.,

Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,

Swennen D., Tekaia F., Wesolowski Louvel M., Westhof E., Wirth B.,

Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,

Mincker P., Souciet J.-L.;

Mincker P., Souciet J.-L.;
                                                                                                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                    Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP clade,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OrderedLocusNames=XALIOA18524g;
Yarrowia lipolytica (Candida lipolytica).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
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                                                                                                                                                                                  Sasaki T., Mařsumoto T., Katayose Y.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC
                                                                                                                                                                                                                                                                                                                                                                                          72.2%; Score 39; DB 2; Length 216;
69.2%; Pred. No. 2e+02;
ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                        Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                               GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPRO4333; SBP.
Pfam; PF03110; SBP; 1.
SEQUENCE 216 AA; 22044 MW; AF74A6B47B498E60 CRC64;
                         05-JUL-2004, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-AUG-2004, integrated into UniProtKB/TrEMBL
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 216 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 AA
                                                                Putative squamosa-promoter binding protein.
                                                                                                                                                                                                                                                                                        EMBL; AP005186; BAC84006.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
 PRT;
                                     05-JUL-2004, sequence version 1.
07-FEB-2006, entry version 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-AUG-2004, sequence version 1. 07-FEB-2006, entry version 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome evolution in yeasts.";
Nature 430:35-44(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
Q6Z461_ORYSA PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ASMSAASAASMAA 13
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                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 69.2
nes 9; Conservative
                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
                                                                            Name=P0430F03.47;
                                                                                                                                           NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                     Gramene; Q6Z461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4952;
                                                                                                                                                                                                           clone: P0430F03.
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OGCGKG;
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Burkgalter B.W. Nusbaum C., Abouelleil A., Allen N., Anderson S.,
Rh Arachchi H.M., Barna N., Bastien V., Bloom T., Boguelavkiy L.,
Rh Arachchi H.M., Barna N., Calvo S.E., Camarata J., Chang J.,
Chopel Y., Collymore A., Cooke P., Cooke P., Chang J.,
Chopel Y., Collymore A., Cook P., Cooke P., Conum B., DeArellano K.,
Rh Buits J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
Ra Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D.,
Rh Hafez N., Hagopian D., Hagos B., Hall J., Horton L., Hulme W.,
Rh Hafez N., Halgos B., Johnson R., Jones C., Kamal M., Kamat A.,
Rh Hafez N., Mathews C., Landers T., Levine R., Lindblad-Toh K., Liu G.,
Rh Manning J., Matthews C., Mauceli E., McCarthy M., Meldrim J.,
Rh Manning J., Matthews C., Mauceli E., McCarthy M., Meldrim J.,
Rh Morol B., Nihova T., Nlenga V., Murphy T., Naylor J., Nguyen C.,
Rh Morol B., Nihova T., Peterson K., Phunkhang P., Pierre N.,
Rh Nicoll S., Rachupka A., Ramasamy U., Raymon C., Retta R., Rise C.,
Smirnov S., Smith C., Spencer B., Schupback R., Seaman S., Severy P.,
Rh Lanama J., Talamas J., Tesfaye S., Theodore J., Travers M.,
Rh Janama J., Talamas J., Tesfaye S., Theodore J., Tayham K., Travers M.,
Rh Junder E.S., Viel R., Vol. X., Wang S., Wilson B.,
Rh Lander E.S., Viel R., Vol. X., Wang S., Wilson B.,
Rh Lander E.S., Wanger S., Wielk R., Samer S., Samin S.,
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Distributed under the Creative Commons Attribution-NoDerivs License
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Submitted (FBE-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Bukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,

Hypocreomycetidae, Hypocreales, Nectriaceae, Gibberella.
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                                                                                                                                                                                                                                                                                                                                                                                       Length 298;
                                                                                                                                                                                                                                                                                                                                                   Score 39; DB 2; Length 295 Pred. No. 2.7e+02;
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Complete proteome; Hypothetical protein.
SEQUENCE 301 AA; 32281 WW; E5838FC4C947BA3B CRC64;
                                                                                                                                                                                                                                                                                                  298 AA; 29325 MW; 50660B6CAC94A883 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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                                                                                                                        EMBL, CR382127, CAG84139.1, -; Genomic_DNA.
InterPro; IPR001778; POA allergen_C.
PRINTS; PR000833; POAALLERGEN.
Complete protecome.
SEQUENCE 298 AA; 29325 MW; 50660B6CAC94
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Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        76.98;
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Best Local Similarity
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone: P0679C08
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-ATCC 23344;

PubMed=15377793; DOI=10.1073/pnas.0403306101;

Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E., Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,

Daugherty S.C., Davideen T.D., DeBoy R.T., Dimitrov G., Dodson R.J., Nougherty S.C., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F., Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M., Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N., Zhou L., Fraser C.M., Structural flexkbility in the Burkholderia mallei genome."; Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
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                                                                                                                                                                                                                                                                                     OrderedLocusNames=BMA157;
Burkholderia mallei (Pseudomonas mallei).
Burkholderia; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; pseudomallei group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.2%; Score 39; DB 2; Length 378; 69.2%; Pred. No. 3.4e+02; ive 3; Mismatches 1; Indels
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Pfam; PF03807; F420 oxidored; I.

Complete proteome; Hypothetical protein.

SEQUENCE 378 AA; 38312 MW; E714B642803AD906 CRC64;
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                                                                                                                                                                                                       25-OCT-2004, integrated into UniProtKB/TrEMBL.
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                                                                                                                                                            PRT;
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Q63RN7;
                                                                                                                                                                                                                       25-0CT-2004, sequence version 1.
07-FEB-2006, entry version 8.
Hypothetical protein.
                                                                                                                                                          PRELIMINARY;
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MSAASAASMAA 13
                                          LSAASAASMVA 56
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Best Local Similarity
9; Conserve
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Q62HU5;
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©58NM6 OB4ZZ1;

01-MAY-2000, integrated into UniProtKB/TrEMBL.

01-MAY-2000, sequence version 1.

21-FEB-2006, entry version 20.

Putative OSNAC7 protein (Putative NAM (No apical meristem) protein).

Name=P0493C11.25-1; Synonyme=134P10.2, P0679C08.7-1;

Oryza sativa (japonica cultivar-group).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; BEP Clade; Ehrhartoideae; Oryzaa.
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Chillingworth T., Cronin A., Crossett B., Davis P., DeShazer D., Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K., Keith K.E., Maddison M., Moule S., Price C., Quail M.A., Sabbinowitsch E., Rutherford K., Sanders M., Simmonds M., Songsivilai S., Stevens K., Tumapa S., Vesaratchavest M., Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J., Witcholderia pseudomallei."; Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245 (2004).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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GO; GO:0006118; P:electron transport; ĪEA.
InterPro; IPR04455; NADPoxred F420.
Pfam; PF03807; FQ oxidored; Ī.
Complete proteome; Hypothetical protein.
SEQUENCE 378 AA; 38429 MW; 846216FB210C015E CRC64;
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GO; GO:0045449; P:regulation of transcription; IEA.
InterPro; IPR003441; NAM.
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EMBL; AP002542; BAB19365.1; -; Genomic_DNA.
EMBL; AF488413; AAO33144.1; -; Genomic_DNA.
HSSP; Q9C932; 1UT7.
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36 ASRSSASAALAA 48
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                             NUCLEOTIDE SEQUENCE.
STRAIN=H12424;
US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Burkholderia cenocepacia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Larimer F., Land M.; "Annotation of the draft genome assembly of Burkholderia cenocepacia
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI TaxID=6239;
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MEDLINE-99069613; PubMed-9851916; DOI=10.1126/science.282.5396.2012;
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
NCBI_TaxID=331272;
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PIR; T22785; T22785.
Ensembl; F5664.4; Caenorhabditis elegans.
Wormbase; WBGene0010159; F5664.4.
Wormpep; F5664.4; CE18758.
GO; GO:0005674; C:nucleus; IEA.
GO; GO:0008270; F:nucleic acid binding; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
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US DOE Joint Genome Institute (JGI-ORNL);
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Science 282:2012-2018(1998).
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Matches 10; Conservative
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US DOB Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Burkholderia cenocepacia
AU 1054.";
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Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
NCBI_TaxID=331271;
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                                                                                                                                      Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AAHIO1000002; EAM14373.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 441 AA, 46730 MW; 81765FDA8EF6B8D5 CRC64;
                  Pfam; PF02365; NAM; 1.
PROSITE; PS51005; NAC; 1.
SEQUENCE 395 AA; 42027 MW; 907916BE379EE14C CRC64;
                                                                                                                                   72.2%; Score 39; DB 2; L
69.2%; Pred. No. 3.6e+02;
tive 3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-AUG-2005, integrated into UniProtKB/TrEWBL. 02-AUG-2005, sequence version 1. 07-FEB-2006, entry version 2. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-SEP-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       441 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US DOE Joint Genome Institute (JGI-ORNL);
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q45C13_9BURK PRELIMINARY; PRT;
Q45C13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-SEP-2005, sequence version 1.
07-FEB-2006, entry version 2.
Hypothetical protein.
ORFNames=BcenDRAFT 5768;
Burkholderia cenocepacia AU 1054.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORFNames=Bcen2424DRAFT 0493;
Burkholderia cenocepacia HI2424.
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264 AAMSASSAAAAA 276
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                                                                                                                                                                                                                                                          1 ASMSAASAASMAA 13
                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preliminary data.
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                                                                                                                                                                  Local Similarity
nes 9; Conserv
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Q4LHN7;
                                                                                                                                         Query Match
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CAS_DROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Frager C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., Lathigra R., White O., Ketchum K.A., Palner N., Dodgon R., Hickey E.K., Gwinn M., Dougherty B., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M., van-Vugt R., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C., Garland S., Fujii C., Cotton M.D., Horst K., Tomb J.-F., Roberts K., Hatch B., Smith H.O., Venter J.C.,
                                                                                                                                                                                                       Gaps
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Saccharomycetales, Saccharomycopsidaceae, Saccharomycopsis.
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Burkholderiaceae, Burkholderia, pseudomallei group.
                                                                                                                                                     72.2%; Score 39; DB 2; Length 470; 75.0%; Pred. No. 4.3e+02; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72.2%; Score 39; DB 2; Length 629; 76.9%; Pred. No. 5.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                               470 AA; 53845 MW; 91F3A5A0A433E37A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           629 AA; 65145 MW; 305D2666A67EC6EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             24-JAN-2006, integrated into UniProtKB/TrEMBL.
24-JAN-2006, sequence version 1.
07-FEB-2006, entry version 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2002, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    724 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; CP000086; ABC37984.1; -; Genomic_DNA.
GO; GQ:0016740; F:transferase activity; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                        Pfam; PF06220; zf-U1-C.
SMART; SM00451; ZrF-U1; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 470 AA: Flase was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomycopsis fibuligera (Yeast).
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07-FEB-2006, entry version 15.
Acetolactate synthase (EC 4.1.3.18)
                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gamma-glutamyltransferase.
ORFNames=BTH_10389;
Burkholderia_thailandensis E264.
    InterPro; IPR013085; Znf_Ul.
InterPro; IPR013085; Znf_Ul-C.
                                                                                                                                                                                                                                                                                                                                                                                                    QZT1K2_BURTH PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                 Query Match
Best Local Similarity 75.u-
Conservative
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Matches 10; Conservative
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66 AKMEAAAASMA 77
                                                                                                                                                                                                                                              1 ASMSAASAASMA 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=271848;
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Q8NJ49;
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Q8NJ49-SAC
Q8NJ49-SAC
DD OBD O1-OC
DT O1-OC
DT O7-FP
DE Acetc
GN Names
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OC Bukar
OC Bukar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO, GO:003884; F:acetolactate synthase activity, IEA.
GO; GO:0016829; F:lyase activity; IEA.
GO; GO:0016829; F:lyase activity; IEA.
GO; GO:0030976; F:thiamin pyrophosphate binding; IEA.
GO; GO:0030902; F:thiamin pyrophosphate binding; IEA.
InterPro; IPR012846; Acetolac syn lg.
InterPro; IPR001846; Acetolac syn lg.
InterPro; IPR00199; TPP bd enzyme N.
InterPro; IPR012001; TPP bd enzyme N.
InterPro; IPR012001; PPP—enzyme M.
InterPro; IPR012001; PPP—enzyme M.
PANTHER; PTHR1868:SF61; Acolac_synthlrg; 1.
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
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NUCLEOTIDE SEQUENCE, FUNCTION, TISSUE SPECIFICITY, AND DEVELOPMENTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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24-MAY-2004, integrated into UniprotKB/Swiss-Prot.
24-MAY-2004, integrated into UniprotKB/Swiss-Prot.
24-MAY-2004, sequence version 2.
77-MAY-2004, entry version 2.
77-MAY-2004, mainty version 3.
77-MAY-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=1418995; DOI=10.1016/0896-6273(92)90234-5; Mellerick D.M., Kassis J.A., Zhang S.-D., Odenwald W.F.; "Castor encodes a novel zinc finger protein required for the development of a subset of CNS neurons in Drosophila."; Neuron 9:789-803(1992).
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NUCLECTIDE SEQUENCE.
STRAIN=8014;
NG Li.H., Nga B., Tan K.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           724 AA; 77781 MW; 678EC6021FC874DF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AJ491151; CAD36014.1; -; Genomic_DNA.
HSSP; P07342; INOH.
SMR; Q8NJ49; I17-724.
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Pfam; PF02705; TPP—enzyme M; 1.
Pfam; PF02776; TPP—enzyme M; 1.
PIRSF; PIRSF500108; Acetolac syn lg; 1.
PIRSF; PIRSF500370; ThDP depend ac; 1.
TIGRPAMs; TIGR00118; acolac lg; 1.
PROSITE; PS00187; TPP_ENZYMES; 1.
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No. N. K. Doyle C., Buxter E.G., Helt C., Nelson C.R., Mkkos G.L.G.,

No. Bartin J. S., Agbowni, Barkon it. S., Marterstronkool, Bean Schain.

No. Beacen K.Y., Beacen P.Y., Beamen P.Y., Beamen P., Bolishakov S. M.,

Beacen K.Y., Charam D.A., Buller H., Deldieu E., Conter A., Chandra I.,

No. Beacen K.Y., College E., Warsh A.D., Bollen H.,

Burtis K.C., Wannen D.A., Buller H., Derg S., Mays A.D. De Millotter P.,

Burtis K.C., Burtis M. College E., Deldieu E., Conter A., Chandra I.,

Burtis K.C., Deldieu E., Charam D.A., Buller H., My A.D. De Millotter P.,

Burtis K.C., College E., Deldieu E., Conter D., Charam D.,

B. Glock M., College E., Garrell J.H., Gul Z., Gabar H., H., Ingere P.,

B. Glock M., College E., Markon D. M., Hermander J. H., Houck J.,

B. Maldin E., Gorrell J.H., Gul Z., Gabar H., H., Ingere M.,

Harris N.L., Astroy D.A., Heiman T.J., Rewitz B., Link K.,

Harris N.L., Astroy D.A., Heiman T.J., Rewitz B., Maldon D.,

Harris N.L., Stone F., Wentley M. M., Maldon D.,

Harris N.L., Stone F., Wentley M. M., Maldon D.,

Harris N.L., Stone F., Wentley M. M., Maldon D.,

Harris N.L., Stone F., Maldon P., Link Y., Maldon D.,

Harris N.L., Stone F., Maldon P., Link Y., Maldon D.,

Harris N.L., Stone F., Maldon M., Maldon D.,

Harris N.L., Stone F., Maldon M., Maldon D.,

Harris N.L., Stone F., Maldon M., Maldon D.,

Maldon P., Lei Y., Mendison M., Shapen M., Skupski M.P., Saile T.,

B. Mount S.M., Woy M., Murphy B., Marphy L., Marry D., Maldon D.,

B. Maldon D.R., Maldon M.A., Maldon J., Maldon D.,

B. Maldon D.R., Maldon M.A., Maldon J., Maldon J., Maldon J.,

B. Maldon D.R., Maldon M.A., Maldon J., Maldon J., Maldon J.,

B. Maldon D.R., Maldon M.A., Maldon J., Maldon M., Sand M.,

B. Maldon D.R., Maldon M.A., Maldon J., Maldon M., Sand M.,

B. Maldon J.R., Maldon M.A., Maldon J., Maldon M., Sand M.,

B. Maldon D.R., Maldon M.A., Maldon J., Maldon M., Sand M.,

B. Maldon M.M., Maldon M., Maldon J., Maldon M., Maldon J.,

B. Maldon M.M., Maldon J., Maldon M., Maldon J., Maldon M.,

B. Maldon M., Maldon M.
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Mandradid N. F. Kollumi K., Stivers C., Nagle J., Foole S.J.,

"Regulation of FOU genes by castor and hunchback setablishes layered
RY Genes Bow. 12:44-560(1998).

RE HISTORY CONTRIBUTION OF DULI ON SCOS25-4773 (01)0012-4;

RA HISTORY SECRIFICITY.

RA HISTORY CONTRIBUTION CASTOR THE SPOCIATION DATE of the Mandradid M. Pract T.;

RA HISTORY STATEMENT CASTOR Sensitive That Spociates approach of key control of the Mandrad M. Pract T.;

RY Genes Bow. 12:143-14(201).

RY Genes Bow. 12:144-560(1998).

RY Genes Bow. 12:144-560(19
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                                                                                                                                                                                                                                                        A Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.-M.,
A Holden M.T.G., Titball R.W., Thomson N.R., Bason N., Bascham I.R.,
Bentley S.D., Sabaihia M., Thomson N.R., Bason N., Bascham I.R.,
Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
Chillingworth T., Cronin A., Crossett B., Davis P., DeShazer D.,
A Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
A Rabbinowitesch E., Rutherford K., Sanders M., Simmonds M.,
Songsivilai S., Stevens K., Tumapa S., Vesaratchavest M.,
Mhitchead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.,
"Genomic plasticity of the causative agent of melioidosis,
I Burkholderia pseudomallei.",
I Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
                                                                                  Burkholderia pseudomallei (Pseudomonas pseudomallei).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; pseudomallei group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.2%; Score 39; DB 2; Length 4574; 76.9%; Pred. No. 4.2e+03; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4574 AA; 484884 MW; F8FA0909D2D9C75F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, BX571966; CAH18467.1; -; Genomic DNA.
GO, GO:0048037; F:cofactor binding; IEA.
GO, GO:0016829; F:lyase activity; IEA.
GO, GO:0016829; F:lyase activity; IEA.
GO, GO:0006220; P:amino acid metabolism; IEA.
GO, GO:000633; P:fatty acid biosynthesis; IEA.
GO, GO:0008152; P:metabolism; IEA.
InterPro; IPR000981; ACP like.
InterPro; IPR001597; Beta_elim_lyase.
InterPro; IPR001597; Beta_elim_lyase.
InterPro; IPR001597; Beta_elim_lyase.
InterPro; IPR00163; Phsphopanteth_bd.
InterPro; IPR002199; SDR.
PNTHRR; PRTRI1712; Receacyl_synth; 8.
PATHER; PRTRI1712; Receacyl_synth; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pfam; PP00106; adh short; 1.—
Pfam; PP01212; Beta_elim_lyase; 2.
Pfam; PP010109; Ketoacyl-synt; 3.
Pfam; PF02801; Ketoacyl-synt C; 3.
Pfam; PF0580; PP-binding; 2.
Probom; PS00592; Beta_elim_lyase; 1.
PROSITE; PS000606; ACP_DOMAIN; 2.
PROSITE; PS00606; B KETOACXL SYMTHASE; 1.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_2.
                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JAN-2006, integrated into UniProtKB/TrEMBL. 24-JAN-2006, sequence version 1. 07-FEB-2006, entry version 2. 07-FEB-2006, entry version 2. ORFNames-LOC_0512943610;
                                                                                                                                                                                                                    STRAIN-K96243;
PubMed=15377794; DOI=10.1073/pnas.0403302101
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Q2QLR1;
    25-OCT-2004, sequence version 1.
07-FEB-2006, entry version 10.
Putative polyketide synthase.
OrderedLocusNames=BPSS1006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3959 ASASAASAASAAS 3971
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Matches 10; Conservative
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                                                                                                                                                        NCBI_TaxID=28450;
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Q2QLR1_ORY
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                                                                                                                                                                                                                                                                                                           Gaps
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Burotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
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                                                                                                                                                                                                                                                            72.2%; Score 39; DB 1; Length 793; 69.2%; Pred. No. 7.2e+02;
                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AP007151; BAE56215.1; -; Genomic DNA.
SEQUENCE 1014 AA; 109950 MW; 29FB09A9CAB2F5EA CRC64;
                                                            0 -> E (in Ref. 1).
R -> A (in Ref. 1).
A -> G (in Ref. 1).
G -> R (in Ref. 1).
S -> T (in Ref. 1).
S -> T (in Ref. 1).
A -> R (in Ref. 1).
C -> R (in Ref. 1).
E35DE18DD3C37671 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-JAN-2006, integrated into UniProtKB/TrEMBL.
24-JAN-2006, sequence version 1.
07-MAR-2006, entry version 3.
MRNA cleavage and polyadenylation factor II complex.
ORFNames=A6099005501277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QG31K9 BURPS PRELIMINARY; PRT, 4574 AA. Q631K9; 25-0CT-2004, integrated into UniProtKB/TrEMBL.
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                                                                                                                                                                                                                                                                                                       3; Mismatches
                                               Ala-rich
                                                                   0440040
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| 758 AALSAASAAAAA 770
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                                                                                                                                                                                                                                                                                 Best Local Similarity 69.2
Matches 9; Conservative
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583
710
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758
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                                        COMPBIAS
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Q63LK9 BURPS
ID Q63LK9 Bt
AC Q63LK9;
DT 25-OCT-20
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Q2UKI7 ASE
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                                                                                                                                                                                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=OSJNBB0096M04.140; Synonyms=OSJNBb00043P23.4;
Oryza sativa (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP Glade;
Ehrhartoideae; Oryzeae; Oryza.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Duell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M., Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S., Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J., Mitc O., Salzberg S.L., Fraser C.M.;

"Oryza sativa chromosome 3 BAC OSJNBO0968004 genomic sequence."; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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21-FEB-2006, entry version 13.
Hypothetical protein OSJNBb0096M04.140 (Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                       70.4%; Score 38; DB 2; Length 129; 75.0%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
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Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                             Buell C.R., Wing R.A., McCombie W.A., Ouyang S.;
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                      EMBL; DP000011; ABA99936.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 129 AA; 13507 MW; 61F89A3E8FF8AA49 CRC64;
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Matches 9; Conservative
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                                                                                                NCBI_TaxID=39947;
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084.712_0RYSA
084.712_0RYSA
07 01.-UUN-20
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DE HYDOCHECL
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X PubMed=16772010, DOI=10.1038/nature04300;

A Rusumoto K., Arima T., Akita O., Kashiwagi Y., Abe K., Gomi K.,

A Kusumoto K., Atima T., Akita O., Kashiwagi Y., Abe K., Gomi K.,

Horiuchi H., Kitamoto K., Kobayashi T., Takeuchi M., Denning D.W.,

A Galagan J.E., Nierman W.C., Yu J., Archer D.B., Bennett J.W.,

B hatnagar D., Cleveland T.E., Fedorova N.D., Gotoh O., Horikawa H.,

Hosoyama A., Ichinomiya M., Igarashi R., Iwashita K., Juvvadi P.R.,

A Kato M., Kato Y., Kin T., Kokubun A., Maeda H., Maeyama N.,

A Maruyama J., Nagasaki H., Nakajima T., Oda K., Okada K., Paulsen I.,

Sakamoto K., Sawano T., Takahashi M., Takase K., Terabayashi Y.,

A Wortman J.R., Yamada O., Yamagata Y., Anazawa H., Hata Y., Koide Y.,

Komori T., Koyama Y., Minetoki T., Suharnan S., Tanaka A., Isono K.,

Kuhara S., Ogaasawara N., Kikuchi H.,

Kenoma J.S., Salama J.S., Kikuchi H.,

Kenoma J.S., Ogaasawara M., Kikuchi H.,

Kenoma J.S., Ogaasawara M., Kikuchi H.,

Kenoma J.S., Ogaasawara M., Kikuchi H.,

Kenoma J.S., Janaka A., Isono K.,

Kenoma J.S., Ogaasawara M., Kikuchi H.,

Kenoma J.S., Ogaasawara M., Kikuchi H.,
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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                                                                                                                                                                                                                                                                                        Length 166;
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SEQUENCE 169 AA; 17228 NW; 3A2A8F472804F675 CRC64;
                                                                                                                                                                                                                         166 AA; 17181 MW; 6EC080E8429A16DB CRC64;
                                                                                                                                                                                                                                                                                        70.4%; Score 38; DB 2; I
75.0%; Pred. No. 2.2e+02;
iive 2; Mismatches 1;
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20-DEC-2005, sequence veraion 1.
20-EBB-2006, entry version 3.
CG13448 (Fragment).
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EMBL; AC092559; AAO37944.1; -; Genomic_DNA.
EMBL; AC099324; AAO73278.1; -; Genomic_DNA.
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                                           EMBLI, noveral
Gramene; Q84JT2; -.
TwietPro; IPRO00095; PAK_box_Rho_bd
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Q2UKI7;
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                                                                                                                        Pfam, PF00786; PBD; 1.
PROSITE, PS50108; CRIB; 1.
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ORFNames=A0090003000790;
                                                                                                                                                                                              Hypothetical protein. SEQUENCE 166 AA; 1
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Matches 9; Conserv
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20-DEC-2005, integrated into UniProtKB/TrEMBL.
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Job time: 125.139 secs
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                                                                                                                                                                                                                                                                                                                     Comeron J.M., Guthrie T.B.;
"Intragenic Hill-Robertson Interference Influences Selection Intensity on Synonymous Mutations in Drosophila.";
Mol. Biol. Evol. 22:2519-2530(2005).
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Comeron J.M., Guthrie T.B.;
"Intragenic Hill-Robertson Interference Influences Selection Intensity
on Synonymous Mutations in Drosophila.";
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                                 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38; DB 2; Length 172;
Pred. No. 2.3e+02;
2; Mismatches 1; Indels
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Pred. No. 2.3e+02;
2; Mismatches 1; Indels
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20-DEC-2005, sequence version 1.
07-FEB-2006, entry version 3.
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75.0%; Pred. No. ...
                                                                                                                                                                                                                                                  STRAIN=T33;
PubMed=16120803; DOI=10.1093/molbev/msi246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; DQ138774; ABA86380.1; -; Genomic_DNA
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Drosophila yakuba (Fruit fly)
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Q2XX89;
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SYSAATAAAMAA 62
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174 AA.

PRT;

QZXY87\_DROER PRELIMINARY;

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                                                                                                                                                                                                                                                     PubMed=16120803; DOI=10.1093/molbev/msi246;
Comeron J.M., Guthrie T.B.;
"Intragenic Hill-Robertson Interference Influences Selection Intensity
on Synonymous Mutations in Drosophila.";
Mol. Biol. Evol. 22:2519-2530(2005).
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0
                                                                        Drosophila erecta (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 38; DB 2; Length 174;
Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 AA; 17861 MW; 76E5A0CDB39E7C7E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; DQ138775; ABA86381.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
20-DEC-2005, sequence version 1. 07-FEB-2006, entry version 3.
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Best Local Similarity 75...
6 Conservative
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51 SYSAATAAAMAA 62
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NUCLEOTIDE SEQUENCE.
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255	8 6 6	2 1 2 8 6		m w 4.	1442	2 4 4 4 2 4 4 4	0 4 4 4 6 C C C C C C C C C C C C C C C C	6 4 2 8 6 6 0 1 1 1	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	, 6, 6, 6, 4, 4, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6,	68 70 71 71	72	7 4 7 7 7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8
5.1.9 Biocceleration Ltd.		7; Search time 97.4177 Seconds (without alignments) 61.014 Million cell updates/sec			m.	rs: 2589679				cted by chance to have a of the result being printed, score distribution.		Description	Adv78640 Cell atta Adv86538 Silk pept Adv8641 Cell atta Aed86539 Silk pept Abr38361 Human can Abr38360 Human can Abr38364 Human can Abr38365 Human can Abr38365 Human can Abr38365 Human can Adv386540 Silk pept Aed86540 Silk pept Aed786542 Cell atta Adv32224 Beta-shee Adv32226 Beta-shee Adv32226 Beta-shee Adv363090 Human ARX Adh58940 Silk prot Aef40057 Polyalani Aao30392 Human ARX Adv78647 Cell atta
GenCore version 5.1 Copyright (c) 1993 - 2006 Bio	GenCore version (c) 1993 - 2006, using sw model	September 9, 2006, 22:37:17 ; S (with	US-10-617-568-36 44 1 AAXAAAAAAAA 13	BLOSUM62 Gapop 10.0 , Gapext 0.5	2589679 seqs, 457216429 residues	hits satisfying chosen parameters	length: 0 length: 2000000000	Minimum Match 0% Maximum Match 100% Listing first 100 summaries	A_Geneseq_8:* 1: geneseqp1990s:* 2: geneseqp1990s:* 3: geneseqp2000s:* 4: geneseqp2001s:* 5: geneseqp2001s:* 7: geneseqp2003as:* 7: geneseqp2004s:* 9: geneseqp2005s:* 9: geneseqp2005s:*	ults predi the score the total	\$ Query	Match Length DB ID	
	OM protein - pro	Run on:	Title: Perfect score: Sequence:	Scoring table:	Searched:	Total number of	Minimum DB seg 1 Maximum DB seg 1	Post-processing:	<b>Database</b> :	Pred. No. score grea and is der	Result	Score	1 1 2 2 2 3 3 2 2 3 3 2 2 3 3 3 3 3 3 3

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Composition useful for producing fibers or films, comprises hybrid multiblock copolymer derived from Nephila clavipes or Bombyx mori silks.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell attachment; cell culture; transplantation; vaccine; antibiotic.
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Pred. No. 1.8;
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0; Mismatches
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AED86538 standard; peptide; 13 AA.
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                                                                                                         Silk peptide linker, SEQ ID 10
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                                                                                                                                                                                                                                                                                                                                13-MAY-2002; 2002US-0380502P.
                                                                                                                                                                                                                                                                                               25-APR-2005; 2005US-00113494
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 Ade10624 8
Ade10677 8
Ade10681 8
Ade10626 8
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Pred. No. 1.8;
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); Mismatches
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                                                                                                               ALIGNMENTS
 ADE10624
ADE10677
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ADV

Synthetic.

ADV78640;

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Gaps

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Query Match Best Local ( Matches

8 셤 RESULT 2 AED86538

Length 13; Indels

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                                                                                                                                                                                                                                                                                                          The invention relates to a novel cell attachable polypeptide comprising an auxiliary amino acid sequence (Y) chemically bonded to a cell attachable minimal amino acid sequence (X), where (Y) contains 1-50 amino acids and the sum total content of Gly and Ala in (Y) is 42-100% with cacids and the sum total content of Gly and Ala in (Y) is 42-100% with respect to the total number of amino acids in (Y). The polypeptide of the invention may be utilized during culturing of cells for use in various experiments, including toxicity studies, gene transfer and production of useful substances such as cytokines, thrombolytic agents, vaccines, hormones and antibiotics. Furthermore, the polypeptide may be useful for culturing cells for transplantation of skin, cranial bones, muscles, skin tissue, bone marrow and retina. The polypeptide exhibits extremely potent cell adhesion properties and can attach cells, such as NHDF and VERO cells, more efficiently onto a base material, relative to conventional methods. The polypeptide also exhibits had steability, thus sterilization in autoclaves can be performed conveniently. The current sequence is that of a cell attachment-related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Composition useful for producing fibers or films, comprises hybrid multiblock copolymer derived from Nephila clavipes or Bombyx mori silks.
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                  Cell attachable polypeptide useful for culturing cell, comprises auxiliary amino acid sequence having specific amount of Gly and A chemically bonded to cell attachable minimal amino acid sequence,
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1.9;
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); Mismatches
                                                                                                                          Disclosure; SEQ ID NO 105; 20pp; Japanese
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                                                                                                                                                                                                                                                                                                                                         auxillary peptide of the invention
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21-MAY-2003; 2003JP-00144125.
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                      (SANN ) SANYO CHEM IND LID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Silk peptide linker,
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                                              WPI; 2005-053150/06
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                                                                                                                                                                                                                                                                                                                                                                 Sequence 14 AA;
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Best Local S
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                                                         The present invention relates to a novel composition (C1) comprising a hybrid multiblock copolymer. The multiblock copolymer comprise peptide linkers, which are derived from peptide sequences found in native silk biomacromolecules or the crystalline domains of Nephila clavipes or Bombyx mori silks. The present sequence is one such peptide linker. (C1 is useful for producing films or fibers utilized in tissue-engineering scaffolds, cell culture substrates, biocompatible coatings, sutures, membranes, grafts and drug delivery systems. (C1) enables to produce fibers or films having increased stiffness and tensile strength.
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Pred. No. 1.9;
0; Mismatches 2;
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Disclosure; SEQ ID NO 11; 27pp; English.
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10-APR-2001; 2001US-0283112P.
25-APR-2001; 2001US-0286630P.
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human leukocyte antigen.
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Best Local Similarity
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ABR38360;
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sequence is a human leukocyte antigen (HLA) peptide, used in an example
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human leukocyte antigen.
                                                                                                            2; Indels
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Pred. No. 2;
0; Mismatches
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                                                                               Score 44;
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Morrison K, Morrison RK, Raitano AB,
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1 Similarity 84.6%; 1
11; Conservative 0;
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10-APR-2001; 2001US-0283112P.
25-APR-2001; 2001US-0286630P.
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Best Local Similarity
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The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosits of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example
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Pred. No. 2;
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orrison RK, Raitano AB;
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10-APR-2001; 2001US-0283112P.
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Matches 11; Conservative
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The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example from the invention
                                                                                                                                                                                                                                                                                                           New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in cancer patients.
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Morrison K, Morrison RK, Raitano AB;
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10-APR-2001; 2001US-0283112P.
25-APR-2001; 2001US-0286630P.
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10-APR-2001; 2001US-0283112P.
25-APR-2001; 2001US-0286630P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; cytostatic; vacci
human leukocyte antigen.
                                                                                                                                                                        (AGEN-) AGENSYS INC.
                                                                                                                                                                                                                                                                     WPI; 2003-075555/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200283921-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-MAY-2003
                       24-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABR38362;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to novel human cancer-related genes and proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic, grognosic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                        W, Hubert RS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 6; Length 15;
                                                                           Human; cytostatic; vaccine; cancer; immune response; HLA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cytostatic; vaccine; cancer; immune response; HLA;
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                                   Human cancer-related protein 187P3F2 HLA peptide #1495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cancer-related protein 187P3F2 HLA peptide #1496.
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        Faris M,
                                                                                                                                                                                                                                                                                                                                                                                                                         Morrison RK, Raitano AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 13; Page 618; 1021pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                      Challita-Eid PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                               10-APR-2002; 2002WO-US011654.
                                                                                                                                                                                                                                                                                     10-APR-2001; 2001US-0282739P.
10-APR-2001; 2001US-0283112P.
25-APR-2001; 2001US-0286630P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                             human leukocyte antigen
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                                                                                                                                                                                                                                                                                                                                                                (AGEN-) AGENSYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15 AA;
                                                                                                                                                                      WO200283921-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200283921-A2
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Morrison K, N
                                                                                                                                  Homo sapiens
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19-MAY-2003
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                                                                                                                                                                                                         24-OCT-2002
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RESULT 9 ABR38365

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Gaps

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2; Indels

Disclosure; SEQ ID NO 3; 23pp; English.

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The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ781561). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic multiblock copolymer; linker; peptide block; native silk biomacromolecule; crystalline domain; structural biopolymer; silk; beta-sheet forming crystalline segment; film; fibre; high tensile strength; spider; beta-sheet crystalline segment.
                                                                             New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in cancer patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spider beta-sheet crystalline segment found in silk biopolymer.
            Hubert RS;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44; DB 6; Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
            Ge ™,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 2;
0; Mismatches
            Challita-Eid PM, Faris M,
           Jakobovits A, Challita-Eid PM, Farıs
Morrison K, Morrison RK, Raitano AB;
                                                                                                                                                                    Claim 13; Page 618; 1021pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADO58104 standard; peptide; 15 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                         100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.68;
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                                                        WPI; 2003-075555/07.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                               from the invention
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                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
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ID ADO
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Multiblock copolymer useful for producing fibers and films having high tensile strength, comprising linkers and peptide blocks derived from peptide sequences found in native silk biomacromolecules of Nephila clavipes.

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The invention relates to a novel cell attachable polypeptide comprising an auxiliary amino acid sequence (Y) chemically bonded to a cell attachable minimal amino acid sequence (X), where (Y) contents is 1-50 amino acids and the sum total content of Gly and Ala in (Y) is 42-100% with respect to the total number of amino acids in (Y). The polypeptide of the invention may be utilized during culturing of cells for use in various experiments, including toxicity studies, gene transfer and production of useful substances such as cytokines, thrombolytic agents, vaccines, normones and antibiotics. Furthermore, the polypeptide may be useful for culturing cells for transplantation, particularly, transplantation of skin, cranial bones, muscles, skin tissue, bone marrow and retina The polypeptide exhibits extremely potent cell adhesion properties and can attach cells, such as NHDP and VERO cells, more efficiently onto a base material, relative to conventional methods. The polypeptide also exhibits
                                                                                                                                                                                                                                                                                                                                                                          ö
                        The present invention relates to synthetic multiblock copolymers comprising linkers and peptide blocks derived from peptide sequences found in native silk biomacromolecules such as the crystalline domain of the spider, Nephila clavipes, or the silkworm, Bombyx mori. The synthetic multiblock copolymers are produced by replacing the amorphous peptide domain of a structural biopolymer such as silk with a nonpeptide segment while maintaining the beta-sheet forming crystalline segments. The multiblock copolymers have solid-state structures and mechanical properties similar to the naturally occurring structural biopolymers. The copolymers are useful for producing films or fibres with high tensile strength. The present sequence represents a spider beta-sheet crystalline segment found in the silk biopolymer.
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell attachable polypeptide useful for culturing cell, comprises auxiliary amino acid sequence having specific amount of Gly and Ala, chemically bonded to cell attachable minimal amino acid sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell attachment; cell culture; transplantation; vaccine; antibiotic.
                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                   8; Length 15;
                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell attachment-related auxillary peptide - SEQ ID 106.
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                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                       Score 44;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADV78642 standard; peptide; 15 AA.
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                                                                                                                                                                                                                                                                                                                                   100.0%;
84.6%; )
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                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                Sequence 15 AA;
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                                                                                                                                                                                                                                                                                                                                     Query Match
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ADV78642
ID ADV78
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RESULT 13

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The invention relates to determining, monitoring and/or controlling the quality of a sample comprising at least one peptide and/or protein, comprising providing at least one protease-sensitive standard and/or at least to me modification-sensitive standard and/or at least one standard and/or at least one standard and/or peptide loss, adding sample comprising at least one eavage for monitoring peptide loss, adding sample comprising at least one eavage and/or protein, and determining the level of proteolytic cleavage and/or modification and/or peptide loss of the standard. The proteolytic cleavage is due to the presence of at least one protease selected from carvage is due to the presence of at least one proteases, appartic cleavage is due to the presence of at least one proteases, proteases, thiol proteases, metallo proteases, coproteases, thiol proteases, metallo proteases, concascade and proteases involved in the clotting cascade and proteases involved in the classical and/or alternative complement cascade. The protease sensitive standard is at least one protease complement cascade. The protease sensitive standard is at least one protein, capacity of a sample comprising at least one cleavage site for at least one protein, capacity of a sample comprising at least one peptide and/or potein, complication and/or peptide loss of the standard with time. The present sequence is an Arg-C digest peptide from a hypothetical standard peptide (containing an Asp-N endoproteinase site and an Arg-C proteinase (clostripain and trypsin) site) useful in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Determining, monitoring and/or controlling the quality of a sample comprising at least one peptide and/or protein comprises determining the level of proteolytic cleavage and/or modification, and/or peptide loss of
                                                                                                           Arg-C proteinase digest peptide SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 2;
); Mismatches
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Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Lamping N,
                                                                                                                                                    Protein degradation; protein detection.
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                                                                                                                                                                                                                                                                                                                     14-JUL-2005; 2005WO-EP007684.
                                                                                                                                                                                                                                                                                                                                                              15-JUL-2004; 2004EP-00016696.
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                                                                  23-MAR-2006 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kellmann M, Menzel C,
                                                                                                                                                                                                                                                                                                                                                                                                       (BIOV-) BIOVISION AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2006-109952/11.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the standard.
                                                                                                                                                                                                                                                                          19-JAN-2006.
                                                                                                                                                                                           Synthetic.
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high heat stability, thus sterilization in autoclaves can be performed conveniently. The current sequence is that of a cell attachment-related auxillary peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Composition useful for producing fibers or films, comprises hybrid multiblock copolymer derived from Nephila clavipes or Bombyx mori silks.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a novel composition (CI) comprising a hybrid multiblock copolymer. The multiblock copolymer comprise peptide linkers, which are derived from peptide sequences found in native silk biomacromolecules or the crystalline domains of Nephila clavipes or Bombyx mori silks. The present sequence is one such peptide linker. (Clis useful for producing films or fibers utilized in tissue-engineering scaffolds, cell culture substrates, biocompatible coatings, sutures, membranes, grafts and drug delivery systems. (CI) enables to produce fibers or films having increased stiffness and tensile strength.
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                                                                                                                              Length 15;
                                                                                                                                                                     2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2;
                                                                                                                              ٠.
د.
                                                                                                         100.0%; Scc...
84.6%; Pred. No. c.
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 12; 27pp; English,
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                                                                                                                                                                                                                                                                                                                                                       AED86540 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Silk peptide linker, SEQ ID 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
84.6%; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-MAY-2002; 2002US-0380502P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-APR-2005; 2005US-00113494.
                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                            1 AAXAAAAAAAAA 13
                                                                                                                                                                                                                                                  1 AAAAAAAAAAA 13
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                                                                                                                                                                   11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rathore O, Sogah DY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2006-008467/01.
                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nephila clavipes.
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                                                                                     Sequence 15 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JAN-2006
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                                                                                                                        Query Match
Best Local
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Zucht H, Hess

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Gaps

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Length 15; 2; Indels

DB 10;

12-FEB-1998

AEF42853 standard; peptide; 15 AA.

RESULT 14

g

8

AEF42853 ID AEF4

Beta sheet; circular dichroism spectroscopy; glycosidase activity; phosphodiesterase activity; drug screening; hydrolysis; neurodegenerative disease; Alzheimer's disease; amyloid deposition.

Beta-sheet forming peptide #2.

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This sequence represents a specific example of a polypeptide, which forms a beta sheet in an aqueous environment and has the general formula a beta sheet in an aqueous environment and has the general formula con Jahmilkukmalln-NH2, in which A = D- or L-alanine amino acid, m. m2 = 0.40; ml+m2 = 10.40; J = a charged amino acid; n = 1 or 2; X = any amino acid except prolline; u = 0 or 1; J1 lysine, hydroxylysine, arginine, histidine, aspartic acid, glutamic acid or gamma-carboxyglutamic acid; Ac = an acylation modification to the carboxylic acid terminus; NH2 = an amidation modification to the carboxylic acid terminus; and X1 = cysteine, threonine, tyrosine or serine. The peptides have thosphodiesterase activity and readily hydrolyse nucleic acids. They also have glycosidase activity and readily hydrolyse sugar phosphates. Further they can cause amine-catalysed decarboxylation (e.g. decarboxylation of call constituents), and they can hydrolyse phospholipids. They can be used for screening drugs for the prevention or treatment of neurodegenerative diseases, e.g. Alzheimer's disease, which result in amplication deposition. They can also be used to screen for drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polypeptide(s) which form stable beta sheets in aq. environment - having phosphodiesterase and glycosidase activity and useful in bio:engineering.enzymatic and drug screening applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                             Beta sheet; circular dichroism spectroscopy; glycosidase activity; phosphodiesterase activity; drug screening; hydrolysis; neurodegenerative disease; Alzheimer's disease; amyloid deposition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Length 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
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Pred. No. 2.1;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           (TORR-) TORREY PINES INST MOLECULAR STUDIES.
                                                                                                                                                                                      'note= "N-terminal acetyl"
                                                                                                                                                                                                                         "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           which inhibit or disrupt the beta sheet
                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 14; 35pp; English
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                 Beta-sheet forming peptide #1
                                                                                                                                                                                                                                                                                                                           96WO-US007564.
                                                                                                                                                                                                                                                                                                                                                                                                                             Perez-Paya E,
                                                                                                                                                                                                                                                                                                                                                            95US-00452043
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                                                                                                                                                                                                                                                                                                                                                                                                                             Blondelle SE,
                                                                                                                                                        Key
Modified-site
                                                                                                                                                                                                       Modified-site
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                                                                                                                                                                                                                                                                                                                           23-MAY-1996;
                                                                                                                                                                                                                                                        WO9637212-A1
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                                                                                                                                                                                                                                                                                         28-NOV-1996
                                                                                                                     Synthetic
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AAW32226
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This sequence represents a specific example of a polypeptide, which forms a beta sheet in an aqueous environment and has the general formula unhaltvuma2n or A-11nam1xuma2n-NHF, in which A = D- or L-alamine amino acid; ml, m2 = 0.40; ml+m2 = 10-40; J = a charged amino acid; n = 1 or 2; x = any amino acid except proline; u = 0 or 1; J1 lysine, hydroxylysine, arginine, histidine, aspartic acid, glutamic acid or gamma-carboxyglutamic acid; Ac = an acylation modification to the amino terminus; NH2 = an amidation modification to the carboxylic acid terminus; and X1 = cysteine, threonine, tyrosine or serine. The peptides have phosphodiesterase activity and readily hydrolyse nucleic acids. They also have glycosidase activity and readily hydrolyse sugar phosphates. Further they can cause amine-catalysed decarboxylation (e.g. decarboxylation of oxalacetate), and they can hydrolyse phospholipids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polypeptide(s) which form stable beta sheets in aq. environment - having phosphodiesterase and glycosidase activity and useful in bio:engineering.enzymatic and drug screening applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bioengineering, enzymatic and drug screening applications. In particular they can be used for screening drugs for the prevention or treatment of neurodegenerative diseases, e.g. Alzheimer's disease, which result in amyloid protein deposition. They can also be used to screen for drugs
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Pred. No. 2.1;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                              Perez-Paya E, Forood B, Houghten RA;
                                                                                                                                                                                                                                                                                                                                                               (TORR-) TORREY PINES INST MOLECULAR STUDIES.
                                                                                                                                                            note= "N-terminal acetyl"
                                                                                                                                                                                             /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             which inhibit or disrupt the beta sheet
                                                                                                                            Location/Qualifiers
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les 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                              Blondelle SE,
                                                                                                                                               Modified-site
                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                23-MAY-1996;
                                                                                                                                                                                                                                                                                                                              26-MAY-1995;
                                                                                                                                                                                                                                 WO9637212-A1
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                                                                                               Synthetic
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ID ADV7
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Cell attachment-related auxillary peptide - SEQ ID 107

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RESULT 19
AAO30390
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                                                                                                                                                                                                                                                                                  The invention relates to a novel cell attachable polypeptide comprising an auxiliary amino acid sequence (Y) chemically bonded to a cell attachable minimal amino acid sequence (X), where (Y) contains 1-50 amino acids and the sum total content of G1y and Ala in (Y) is 42-100% with respect to the total number of amino acids in (Y). The polypeptide of the invention may be utilized during culturing of cells for use in various experiments, including toxicity studies, gene transfer and production of useful substances such as cytokines, thrombolytic agents, vaccines, hormones and antibiotics. Furthermore, the polypeptide may be useful for
                                                                                                                                                                                                                                                                                                                                                                                             culturing cells for transplantation, particularly, transplantation of skin, cranial bones, muscles, skin tissue, bone marrow and retina. The polypeptide exhibits extremely potent cell adhesion properties and can attach cells, such as NHDF and VERO cells, more efficiently onto a base material, relative to conventional methods. The polypeptide also exhibits high heat stability, thus sterilization in autoclaves can be performed conveniently. The current sequence is that of a cell attachment-related auxillary peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                 Cell attachable polypeptide useful for culturing cell, comprises auxiliary amino acid sequence having specific amount of Gly and Ala, chemically bonded to cell attachable minimal amino acid sequence,
           cell attachment; cell culture; transplantation; vaccine; antibiotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beta sheet, circular dichroism spectroscopy; glycosidase activity, phosphodiesterase activity; drug screening; hydrolysis; neurodegenerative disease; Alzheimer's disease; amyloid deposition.
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Pred. No. 2.1;
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0; Mismatches
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                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 107; 20pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.08;
                                                                                                       20-MAY-2004; 2004JP-00150510
                                                                                                                             21-MAY-2003; 2003JP-00144125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.68;
                                                                                                                                                     (SANN ) SANYO CHEM IND LTD.
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Matches 11; Conserv
                                                          JP2005002106-A.
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                                                                               06-JAN-2005
                                  Synthetic.
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This sequence represents a specific example of a polypeptide, which forms a beta sheet in an aqueous environment and has the general formula and the abeta sheet in an aqueous environment and has the general formula and the abeta sheet in an aqueous environment and has the general formula and the acid, ml.m2 = 10-40; J = a charged amino acid; n = 1 or 2; x = any amino acid except proline, u = 0 or 1; J1 lysine, hydroxylysine, arginine, histidine, aspartic acid, glutamic acid or gamma-carby, Ac = an acylation modification to the amino cramboxylutamic acid, Ac = an acylation modification to the carboxylic acid terminus; NH2 = an amidation modification to the carboxylic acid terminus; and X1 = cysteine, threonine, tyrosine or serine. The peptides have bosphodiesterase activity and readily hydrolyse nucleic acids. They also have glycosidase activity and readily hydrolyse sugar phosphates. Further they can cause amine-catalysed decarboxylation (e.g. decarboxylation of coxalacetate), and they can hydrolyse phospholipids. They can be used for screening applications. In particular they can be used for screening applications or treatment of neurodegenerative diseases, e.g. Alzheimer's disease, which result in amiliar in the contraction and protein and prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polypeptide(s) which form stable beta sheets in aq. environment - having phosphodiesterase and glycosidase activity and useful in bio:engineering.enzymatic and drug screening applications.
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Pred. No. 2.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Houghten RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TORR-) TORREY PINES INST MOLECULAR STUDIES.
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0; Mismatches
/note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Forcod B,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 16; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAO30390 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                                                                                                                              95US-00452043
                                                                                                                                                                                                                                                                                                  96WO-US007564
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                                                                                                WO9637212-A1
                                                                                                                                                                                                                                                                                             23-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Silk; genetically modified; silk-like protein; polymer; silkworm fibroin; elastin; fibronectin; textile; food; industry; cosmetics; pET-SLP(n); pET-SLP(2; 4; 6); SLP6.
                                                                                                                                                                              The invention relates to human orthologue of Aristaless homeobox gene, ARX. ARX gene is associated with infantile spasms (IS), non-specific X-linked mental retardation, X-linked myoclonic epilepsy and Partington syndrome. ARX gene is useful for diagnosing ARX-related disorders e.g., mild mental retardation, infantile spasms or dystonia. The present sequence is human ARX (GCG)10+7 mutant cDNA fragment encoded peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mass production of silk protein and silk-like protein having imparted function by employing genetically-modified Escherichia coli, useful in textiles, food industry and cosmetics.
                                                                                                                         New ARX gene, useful for diagnosing ARX-related disorders e.g., mild mental retardation, infantile spasms or dystonia.
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                                                                                                                                                                                                                                                                                      100.0%; Score 44; DB 7; Length 18;
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Silk protein related peptide #SEQ ID 9.
                                             (WOME-) WOMEN'S & CHILDREN'S HOSPITAL.
                                                                                                                                                            Disclosure; Fig 2a; 74pp; English.
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26-NOV-2002; 2002WO-AU001599
                      26-NOV-2001; 2001AU-00009095
                                                                                                                                                                                                                                                                                                   84.68;
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                                                                                         WPI; 2003-505184/47.
N-PSDB; AAL61167.
                                                                    Stromme P;
                                                                                                                                                                                                                                                                                                 Similarity
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Best Local (
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The invention relates to a method for producing silk or genetically-modified silk-like protein, comprising designing a silk or silk-like polymer containing e.g. domesticated silkworm fibroin and synthesizing

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the minimum unit of the silk or the thus designed polymer for integration into expression vectors and transfer into Escherichia coli prior to growing in a medium. Also disclosed is a method for producing silk or certainty and silk-like protein, comprising designing a silk or silk-like polymer containing at least one protein selected from certainced silkworm fibroin, wild silkworm fibroin, elastin and Cf fibronectin and essentially comprising the domesticated from cf fibronectin and essentially comprising the domesticated or wild silkworm fibroin. The produced silk and silk-like protein are useful in textiles, food industry and cosmetics. Using this method, expression efficiency is greatly improved, thus providing silk-like protein with designed functionallities easily in large quantities. The SLP gene, PUC-link and SLP(n) were constructed for producing expression vector pEr-SLP(n) with cexpression of pET-SLP(2,4,6). The target protein SLP6 was obtained after CC cleavage of the tag sequence with use of cyanogens bromide. The sequences given in records for ADHS8932-ADHS8971 represent silk-like protein creation of the vector of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides a method for mass production of silk protein and gene recombinant silk-like protein (SLP). The method involves integrating a silk like polymer selected from e.g. domestic silkworm fibroin, wild silkworm fibroin, elastin and fibronectin of the minimum unit into an expression vector selected from expression vectors containing T7 promoter. The method is useful for mass producing silk or silk-like proteins with improved cellular adhesiveness, elasticity or hardness and is also useful in clothing, food and cosmetic industries. The present sequence is a polyalanine peptide which is similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Producing silk or silk-like protein comprises integrating a silk like polymer comprising the minimum unit into an expression vector selected from expression vectors containing T7 promoter.
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEF40057 standard; peptide; 18 AA.
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22-NOV-2004; 2004US-00515264.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18 AA;
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AAO30392

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The invention relates to a novel cell attachable polypeptide comprising an auxiliary amino acid sequence (Y) chemically bonded to a cell attachable minimal amino acid sequence (X), where (Y) contains 1-50 amino acids and the sum total content of Gly and Ala mino 3-2-1003 with cacids and the sum total content of Gly and Ala mino 3-2-1003 with crespect to the total number of amino acids in (Y). The polypeptide of the invention may be utilized during culturing of cells for use in various experiments, including toxicity studies, gene transfer and production of useful substances such as cytokines, thrombolytic agents, vaccines, hormones and antibiotics. Furthermore, the polypeptide may be useful for culturing cells for transplantation, particularly, transplantation of skin, cranial bones, muscles, skin tissue, bone marrow and retina. The collypeptide exhibits extremely potent cell adhesion properties and can attach cells, such as NHDF and VERO cells, more efficiently onto a base convention and methods. The polypeptide also exhibits for material, relative to conventional methods. The polypeptide also exhibits conveniently. The current sequence is that of a cell attachment-related conveniently. The current sequence is that of a cell attachment-related auxillary peptide of the invention.
                                                                                                                                              cell attachment; cell culture; transplantation; vaccine; antibiotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell attachable polypeptide useful for culturing cell, comprises auxiliary amino acid sequence having specific amount of Gly and Ala, chemically bonded to cell attachable minimal amino acid sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell adhesion property polypeptide auxiliary amino acsequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell adhesion; cytokine; hormone; antibiotic; heat tolerance.
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                                                                                                      Cell attachment-related auxillary peptide - SEQ ID 51.
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0; Mismatches
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                                                                                                                                                                                                                                                                                                         20-MAY-2004; 2004JP-00150510.
                                                                                                                                                                                                                                                                                                                                                 21-MAY-2003; 2003JP-00144125.
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                                                                                                                                                                                                                           JP2005002106-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alternatively
                                                                24-MAR-2005
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                                                                                                                                                                                      Synthetic.
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                         ADV78587;
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polyalanine region in wild silk worm and is used in the formation of SLPA (Silk-like protein with polyalanine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to human orthologue of Aristaless homeobox gene, ARX. ARX gene is associated with infantile spasms (IS), non-specific X-linked mercal retardation, X-linked myoclonic epilepsy and Partington syndrome. ARX gene is useful for diagnosing ARX-related disorders e.g., mild mental retardation, infantile spasms or dystonia. The present sequence is human ARX 428-451dup(24bp) mutant cDNA fragment encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homeobox gene; ARX; ARX-related disorder; X-linked myoclonic epilepsy; infantile spasm; mental retardation; Partington syndrome; diagnosis; dystonia; human; mutant; mutein.
                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New ARX gene, useful for diagnosing ARX-related disorders e.g., mild
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human ARX 428-451dup(24bp) mutant cDNA fragment encoded peptide.
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                                                                                                    Score 44; DB 10; Length 18;
Pred. No. 2.3;
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                                                                                                                           Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 2b; 74pp; English
                                                                                                      100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-NOV-2002; 2002WO-AU001599.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-NOV-2001; 2001AU-00009095.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity 84.6%;
11; Conservative
                                                                                                                             84.68;
                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                    1 AAXAAAAAAA 13
                                                                                                                                                                                                                         AAAAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AAXAAAAAAAA 13
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                                                                                                                                            11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2003-505184/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stromme P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAL61169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003045989-A1
                                                              Ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sapiens
                                                              Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                           22-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                   AA030392;
                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gecz J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide
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Homo

WPI;

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Gaps

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Indels

2

SEQ 63.

ADV78587 standard; peptide; 19 AA.

RESULT 23 ADV78587 ID ADV

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8

Matches

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                                                                                                                                                                               The invention relates to a novel polypeptide having cell adhesion property. The polypeptide comprises a minimum amino acid sequence and an auxiliary amino acid sequence capable of expressing a cell adhesion property and having a molecular weight of 1500-15000. The invention further comprises a cell adhesion property polypeptide base material. The cell adhesion property polypeptide base material is useful for producing a cell. The cell adhesion property polypeptide is useful for culturing and analyzing cells, screening assays, and producing bloactive substances such as cytokines, hormones, antibiotics, etc. The cell adhesion property polypeptide has excellent cell adhesion property, heat stability and has low immunogenicity. This sequence represents a human adhesion property polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis A virus; HAV; immunogen; immunostimulant; virucide; vaccine; antigen; major structural capsid polypeptide; HAV antibody detection.
                                                                                                                                  polypeptide having cell adhesion property, useful for culturing
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                          Length 19;
                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                        ; Score 44; DB 9;
Pred. No. 2.4;
0; Mismatches 2;
                                                                                                                                                                 Disclosure; SEQ ID NO 63; 26pp; Japanese.
                                                                                                                                              cells and producing bioactive substances.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic HAV peptide, SEQ ID NO: 89.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB69489 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                          100.0%;
84.6%; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JUL-2000; 2000WO-US019267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0144412P
                                       09-DEC-2003; 2003JP-00409854.
                                                         09-DEC-2003; 2003JP-00409854.
                                                                            (SANN ) SANYO CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                   AAAAAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fields HA, Khudyakov YE;
                                                                                                                                                                                                                                                                                                                                                                                1 AAXAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                             11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-112681/12.
                                                                                                                 WPI; 2005-514832/53.
                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis A virus
                                                                                                                                                                                                                                                                                                                        Sequence 19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200105824-A2
JP2005170810-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1999;
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                    30-JUN-2005
                                                                                                Kurokawa Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB69489;
                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                     Novel
                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 25
AAB69489
                                                                                                                                                                                                                                                                                                                                                             Matches
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The present sequence is one of a number of synthetic peptides which are immunoreactive with hepatitis A virus (HAV) antibodies. The peptides comprise antiquence epitopes of the major structural capsid polypeptides or non-structural polypeptides of HAV with one or more glutamine con accuses at the carboxy end of the peptide. The peptides are used to detect the presence of antibodies against HAV in mammalian serum, to caect the presence of HAV in a human or animal through the binding of the peptide to an antibody, to detect acute phase infection by detecting cy antibodies in mammalian serum and detecting convalescence in a mammal. The peptides are used to detect or quantify HAV antibodies in samples in clinical or research-based assays using immunoblotting, fluorescence in situ hybridisation analysis, gel-mobility shift assays, tracking of radioactive or bioluminescent markers, chromatography or electrophoresis. The peptides are used to induce an immune response to HAV when administered to a human or animal. Glutamine at the carboxy end the peptides enhances the IgM antibody reactivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lung cancer; tumour; cytostatic; immunostimulant; vaccine; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to novel compositions and methods for the therapy and diagnosis of cancer, particularly lung cancer. The compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptides and encoding polynucleotides, useful for diagnosing, preventing and/or treating lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Synthetic peptides used as antigen sources for enzyme immunoassays detecting anti-hepatitis A virus and as vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Fanger GR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 4; Length 20;
Pred. No. 2.5;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human lung tumour clone peptide, SEQ ID No 2122.
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Durham M, Carter D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 2122; 258pp; English.
                                                                                                   Disclosure; Page 127; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADH47641 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
84.6%; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-OCT-2002; 2002WO-US034777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-OCT-2001; 2001US-00017754.
28-MAR-2002; 2002US-00113872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AAXAAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AAAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 84.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Henderson RA, Wang T,
Johnson JC, Retter MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mcnabb A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-468346/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003037267-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human; clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Johnson JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bangur CS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADH47641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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ADH47641
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The invention relates to a method for producing silk or genetically-
modified silk-like protein, comprising designing a silk or silk-like
protein, comprising designing a silk or silk-like
polymer containing e.g. domesticated silkworm fibroin and synthesizing
the minimum unit of the silk or the thus designed polymer for integration
into expression vectors and transfer into Bscherichia coli prior to
growing in a medium. Also disclosed is a method for producing silk or
growing in a medium. Also disclosed is a method for producing silk or
silk-like polymer containing at least one protein selected from
constituted silk-like protein, wild silkworm fibroin, elastin and
fibroin. The produced silk and silk-like protein are useful in textiles,
food industry and cosmetics. Using this method, expression efficiency is
greatly improved, thus providing silk-like protein with designed
functionalities easily in large quantities. The SLP gene, PUC-link and
                                                                                                                                                                                                                                                                                                                            ö
comprise one or more lung tunmour polypeptides, immunogenic portions therof, polymucleotides that encode such polypeptides, antigen presenting cells that express such polypeptides, and T cells that are specific for cells expressing such polypeptides. The novel compositions have cytostatic and immunostimulant activity. The lung tunmour antigens can be used in the creation of a vaccine. The polymucleotides that encode the lung tunmour polypeptides can be used in gene therapy to help in the treatment of lung tunmours. This sequence represents a human lung tumour clone polypeptide of the invention. This sequence was not shown in the specification. It has been taken from a World Intellectual Property
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Silk; genetically modified; silk-like protein; polymer; silkworm fibroin; elastin; fibronectin; textile; food; industry; cosmetics; pET-SLP(n); pET-SLP(2; 4; 6); SLP6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mass production of silk protein and silk-like protein having imparted function by employing genetically-modified Escherichia coli, useful in textiles, food industry and cosmetics.
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                 Length 20;
                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                   Organization CD ROM supplied with the specification.
                                                                                                                                                                                                                                                                                                                          5;
                                                                                                                                                                                                                                                                                 Score 44; DB 7;
Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Silk protein related peptide #SEQ ID 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; SEQ ID NO 24; 56pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADH58955 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                 100.0%;
84.6%; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAY-2002; 2002WO-JP005010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002WO-JP005010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYNI-) UNIV JAPAN TOKYO AGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                              1 AAXAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                     AAAAAAAAAA 17
                                                                                                                                                                                                                                                                                                                        11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-108256/11.
                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                            Sequence 20 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADH58955;
                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 27
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SLP(n) were constructed for producing expression vector pET-SLP(n) with expression of pET-SLP(2,4,6). The target protein SLP6 was obtained after cleavage of the tag sequence with use of cyanogens bromide. The sequences given in records for ADH58932-ADH58971 represent silk-like protein related polypeptides and polynucleotides, and primers used in the creation of the vector of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel isolated polynucleotide comprising a
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polynucleotide encoding lung tumor polypeptides, useful for diagnosing, preventing and treating cancer e.g. lung cancer.
                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                      Human lung cancer-related L984P peptide fragment - SEQ ID 2122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sleath PR;
Fanger GR,
                                                                                                                       8; Length 20;
                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                lung tumour; cytostatic; lung cancer; human; L984P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kalos MD,
Carter D,
                                                                                                                       DB
                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 39; SEQ ID NO 2122; 99pp; English.
                                                                                                                       100.0%; Score 44;
                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Watanabe Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Durham M,
                                                                                                                                                                                                                                                                        ADJ21560 standard; peptide; 20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-1999; 99US-00346492.

15-OCT-1999; 99US-00466867.

30-DEC-1999; 99US-00476300.

06-MAR-2000; 2000US-00530077.

10-APR-2000; 2000US-00533077.

10-APR-2000; 2000US-00560406.

05-JUN-2000; 2000US-00560406.

05-JUN-2000; 2000US-00560406.

05-JUN-2000; 2000US-005614124.

29-AUG-2000; 2000US-0056163.

08-SEP-2000; 2000US-00651824.

26-SEP-2000; 2000US-00651325.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-0CT-2000; 2000US-00677419.
30-0CT-2000; 2000US-00702705.
13-DBC-2000; 2000US-0073626.
03-MAY-2001; 2001US-00849626.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-OCT-2002; 2002US-00283017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-JUL-2001; 2001US-00902941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-OCT-2001; 2001US-00017754
28-MAR-2002; 2002US-00113872
                                                                                                                                    84.6%;
                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                           1 AAXAAAAAAAA 13
                                                                                                                                                                                                     3 AAAAAAAAAAA 15
                                                                                                                                                 11; Conservative
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Retter MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bangur CS, Mcnabb A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-167010/16.
                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                     US2003211510-A1.
                                                                                             Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RA,
                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                           04-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Johnson JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Henderson
                                                                                                                                                                                                                                                                                                  ADJ21560;
                                                                                                                       Query Match
                                                                                                                                                 Matches
                                                                                                                                                                                                                                            RESULT 28
                                                                                                                                                                                                                                                          ADJ21560
 8868888888
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The invention relates to a novel cell attachable polypeptide comprising an auxiliary amino acid sequence (Y) chemically bonded to a cell attachable minimal amino acid sequence (X), where (Y) contains 1-50 amino acids and the sum total content of Gly and Ala in (Y) is 42-100% with respect to the total number of amino acids in (Y). The polypeptide of the invention may be utilized during culturing of cells for use in various caperiments, including toxicity studies, gene transfer and production of useful substances such as cytokines, thrombolytic agents, vaccines, or useful substances such as cytokines, thrombolytic agents, vaccines, or culturing cells for transplantation, particularly, transplantation of skin, cranial bones, muscles, skin particularly, transplantation of skin, cranial bones, muscles, skin tissue, bone marrow and retina. The polypeptide exhibits extremely potent cell adhesion properties and can attach cells, such as Nibra and VERO cells, more efficiently onto a base material, relative to conventional methods. The polypeptide also exhibits high heat stability, thus sterilization in autoclaves can be performed conveniently. The current sequence is that of a cell attachment-related
sequence chosen from any one of 40 lung tumour polypeptides or its complements, fragments or degenerate variants. The method of the invention has cytostatic applications and may be useful for detecting and treating lung cancer in a patient, as well as for inhibiting the development of lung cancer in a patient via incubating CD4+ and/or CD8+ cells isolated from a patient with at least one component chosen from a polypeptide, polynucleotide or antigen presenting cell (APC) of the invention and administering an effective amount of the proliferated reals to the patient. The current sequence is that of the human lung cancer-related peptide of the invention. The current sequence is not shown in the specification per se but is available on the USPTO web-site http:seqdata.uspto.gov/sequence.html?DocID=20030211510.
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell attachable polypeptide useful for culturing cell, comprises auxiliary amino acid sequence having specific amount of Gly and Ala, chemically bonded to cell attachable minimal amino acid sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell attachment; cell culture; transplantation; vaccine; antibiotic.
                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 44; DB 8; Length 20;
                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell attachment-related auxillary peptide - SEQ ID 52
                                                                                                                                                                                                                                                                                                                                                                             2.5;
                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 52; 20pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADV78588 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAY-2004; 2004JP-00150510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAY-2003; 2003JP-00144125.
                                                                                                                                                                                                                                                                                                                                                                          84.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AAXAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 AAAAAAAAAAAA 17
                                                                                                                                                                                                                                                                                                                                                                                                  11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SANN ) SANYO CHEM IND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2005-053150/06
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                          Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JP2005002106-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alternatively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-MAR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-JAN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADV78588;
                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 29
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The present invention provides a method for mass production of silk protein and gene recombinant silk-like protein (SLP). The method involves integrating a silk like polymer selected from e.g. domestic silkworm fibrolin, wild silkworm fibroin, elastin and fibronectin of the minimum unit into an expression vector selected from expression vectors containing T7 promoter. The method is useful for mass producing silk or silk-like proteins with improved cellular adhesiveness, elasticity or hardness and is also useful in clothing, food and cosmetic industries. The present sequence is a silk-like protein with polyalanine (SLPA)
                                                                                    ö
                                                                                                                                                                                                                                                                                                           Domestic silkworm silk-like protein with polyalanine peptide SEQ ID: 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Producing silk or silk-like protein comprises integrating a silk like polymer comprising the minimum unit into an expression vector selected from expression vectors containing T7 promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                     Protein production; silk; food; cosmetics; silk-like protein;
polyalanine; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 44; DB 10; Length 20; 84.6%; Pred. No. 2.5; 2; Indels ive 0; Mismatches 2; Indels
                                                        Length 20;
                                                                                     2; Indels
                                                       100.0%; Score 44; DB 9;
84.6%; Pred. No. 2.5;
iive 0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; SEQ ID NO 24; 25pp; English.
auxillary peptide of the invention.
                                                                                                                                                                                                                        AEF40072 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAY-2002; 2002WO-JP005010.
22-NOV-2004; 2004US-00515264.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-AUG-2005; 2005US-00197315.
                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AAXAAAAAAAA 13
                                                                                                                                                4 AAAAAAAAAAA 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Conservative
                                                                                                                   1 AAXAAAAAAAAA 13
                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 11; Conserva'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2006-109210/11.
                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ASAK/) ASAKURA T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AEF40068.
                                                                                                                                                                                                                                                                                                                                                                                                                                    US2006019348-A1.
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                              Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified.
                                                                                                                                                                                                                                                                                  23-MAR-2006
                                                              Mac
Local Sim
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                                                                                                                                                                                                                                                                                                                                                                                         Bombyx mori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Asakura T;
                                                                                                                                                                                                                                                       AEF40072;
                                                           Query Match
                                                                                         Matches
                                                                                                                                                                                              RESULT 30
                                                                                                                                                                                                             AEF40072
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AAY25436

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The present sequence is one of a number of synthetic peptides which are immunoreactive with hepatitis A virus (HAV) antibodies. The peptides comprise antigenic espitopes of the major structural apsid polypeptides of the major structural apsid polypeptides of HAV with one or more glutamine connected to a number of the peptide. The peptides are used to detect the presence of antibodies against HAV in mammalian serum, to detect the presence of AHAV in a human or animal through the binding of the peptide to an antibody, to detect acute phase infection by detecting in mammalian serum and detecting convalescence in a mammalian serum and detecting convalescence in a mammalian serum and actecting convales in clinical or research-based assays using immunoblotting, fluorescence in situ hybridisation analysis, gel-mobility shift assays, tracking of radioactive or bioluminescent markers, chromatography or electrophoresis. The peptides are used to induce an immune response to HAV when administered to a human or animal. Glutamine at the carboxy end of the peptides enhances the IgM antibody reactivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        miniblock polymer; optical response; mid infrared wavelength range; long range ordered fluid; liquid crystals; nanolithography; tresensitive device; If sensor; II filter; night telescope; thermosensitive detector; non-linear chromophore; biomaterial; tissue engineering scaffold; ferroelectric material; artificial muscle;
                                                                                                                                                                                                                                                                                                Synthetic peptides used as antigen sources for enzyme immunoassays detecting anti-hepatitis A virus and as vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 4; Length 21; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                    (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 127; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Self-assembling polymer peptide #67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADJ81212 standard; peptide; 21 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.08;
                                                                                   14-JUL-2000; 2000WO-US019267
                                                                                                                             99US-0144412P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-OCT-2002; 2002WO-US031375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-OCT-2001; 2001US-0326743P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AAXAAAAAAAA 13
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                                                                                                                                                                                                                Khudyakov YE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Conservative.
                                                                                                                                                                                                                                                        WPI; 2001-112681/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         device
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21 AA;
WO200105824-A2.
                                                                                                                             15-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-MAY-2004
                                         25-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-JUL-2003,
                                                                                                                                                                                                                Fields HA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           switching
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes the production of a novel synthetic DNA (1), wf8r, encoding an antifreeze polypeptide, AFPWF8R modelled on the antifreeze peptide (AFP) found in winter flounder. The polypeptides encoded by (1) lower the freezing temperature of water and prevent ice formation, therefore are useful as antifreeze agents. The use of synthetic peptides is less toxic than the use of chemicals (prior art). Naturally occurring antifreeze polypeptides are not available in large quantities, synthetic antifreeze polypeptides are more readily available. The antifreeze polypeptides are produced by recombinant means, a process which is cheaper and less time consuming compared to direct chemical synthesis of synthetic peptides (prior art)
                                                                                                                                                                                                          Antifreeze peptide; AFP; wf8r; AFPWF8R; winter flounder; ice formation; water freezing temperature; antifreeze agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis A virus; HAV; immunogen; immunostimulant; virucide; vaccine; antigen; major structural capsid polypeptide; HAV antibody detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic antifreeze peptide and the gene coding its production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                Synthetic antifreeze protein AFPWF8R insert fragment B2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (VIRG ) VIRGINIA TECH INTELLECTUAL PROPERTIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 44; DB
Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 2.6;
0; Mismatches
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                                   AAY25436 standard; protein; 21 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 8C; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB69490 standard; peptide; 21 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                       91US-00814220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 90US-00588437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAX88104, AAX88105.
                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-418272/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis A virus.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Szumanski MBW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21 AA;
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                                                                                                                        09-SEP-1999
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                                                                                                                                                                                                                                                                                                                 US5925540-A
                                                                                                                                                                                                                                                                                                                                                           20-JUL-1999
                                                                                                                                                                                                        Antifreeze
                                                                            AAY25436;
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Matches

ð 8 RESULT 32

AAB69490

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Gaps

.. 0

2; Indels

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The invention relates to a miniblock polymer (I) comprising a self-
fabricating block and a solubilizing block, a block for triggering self-
ce fabrication by external or environmental conditions, and a block for
incorporating turns in the polymer or for providing sites for chemical
conformations, has a molecular weight of 1000-300000 and, in solution,
can self-fabricate to form 3-dimensional material having long-range
corder, and where (I) has glycine content of at least 20%. (I) is useful
for controlled delivery of a drug which involves incorporating acro
corterial. (II), and administering the self-fabricating material incorporating
the drug. The drug is incorporated within layers of the self-fabricating
content of mid infrared wavelength range which involves applying (II)
contents, which can then undergo very specific structural transitions to
cor forms, which can then undergo very specific structural transitions to
cor forms, which can then undergo very specific structural transitions to
cor forms, which can then undergo very specific structural transitions to
cor forms, which can then undergo very specific structural transitions to
cor forms, which can then undergo very specific structural transitions to
cor forms, which can then undergo very specific structural transitions to
cor forms, which can then undergo very specific structural transitions to
cor forms, which can then undergo very specific structural transitions to
corporated fabricated fransitive devices.

(I) is useful for preparing chemically patterned templates with either
copolymer (II) is useful for modifying and improving performance of IR-
condition, and in optical applications e.g., as matrices to align non-
condition, and in optical applications e.g., as matrices to align non-
linear chromophores which are useful in creating materials for second
coder non-linear orbites. (II) is useful in dreating materials are contained are strictly and contained are strictly and contained are useful in creating materials, second
contains an expecific des
                                                                                                                                                                                                   Miniblock polymer useful in nanolithographic processes, has self-fabricates fabricating block and solubilizing block, has glycine and self-fabricates to form 3-dimensional materials having long-range orders, in solution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               miniblock polymer; optical response; mid infrared wavelength range; long range ordered fluid; liquid crystals; nanolithography; IR-sensitive device; IR sensor; IR filter; night telescope; thermosensitive detector; non-linear chromophore; biomaterial; tissue engineering scaffold; ferroelectric material; artificial muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ferroelectric materials, artificial muscles, switching devices, et sequence represents a peptide used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 44; DB 7; Length 21; Pred. No. 2.6; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                           Claim 31; SEQ ID NO 67; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Self-assembling polymer peptide #197.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADJ81342 standard; peptide; 21 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.08;
04-JUN-2002; 2002US-0385809P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.6%;
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Best Local Similarity 84.6'
....hes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AAXAAAAAAAA 13
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                                                                                                     Valluzzi R, Kaplan DL;
                                                    (TUFT ) TUFTS COLLEGE.
                                                                                                                                                       WPI; 2003-671392/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    switching device
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADJ81342;
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Gaps

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etc. This

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The invention relates to a minibility block, a block for triggering self-
dabricating block and a solubilizing block, a block for triggering self-
fabrication by external or environmental conditions, and a block for
fabrication by external or environmental conditions, and a block for
incorporating turns in the polymer or for providing sites for chemical
can self-fabricate to form 3-dimensional material having long-range
corder, and where (1) has glycine content of at least 20%. (1) is useful
corder, and where (1) has glycine content of at least 20%. (1) is useful
corder, and administering the self-fabricating material incorporating
corder, and administering the self-fabricating actual
corder, and administering the self-fabricating actual
corder. The drug is incorporated within layers of the self-fabricating
corder and infrared wavelength range which involves applying (1)
corder to mid infrared wavelength range which involves applying (1)
corder to mid infrared wavelength range which involves applying (1)
corder surface of the device (all claimed). (1) is useful for preparing
corder fluids (i.e., liquid crystal) in a variety of phases
corder range ordered fluids (i.e., liquid crystal) in a variety of phases
corder ranged materials. (1) can be used as structural transitions to
corder ranged processes. A self-fabricated structure containing the
corder rangely of processes. A self-fabricated structure containing the
colymer (II) is useful for modifying and improving performance of IR-
continger (II) is useful for modifying and improving performance of the modifying and improving performance of the modifying and improving performance of IR-
contingerial devices, IR sensors, IR filters, night telescopes and
continge that absorb specific wavelengthes of infrared
contingent than the contingent in a contingent maniform of the modifying and contingent in a contingent maniform or a self-fabricated arructure or and administration or contingent maniforms. (II) as a martine devices and a manifold of the contingent in a conti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Miniblock polymer useful in nanolithographic processes, has self-fabricates fabricating block and solubilizing block, has glycine and self-fabricates to form 3-dimensional materials having long-range orders, in solution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     radiation, and in optical applications e.g., as matrices to align non-
linear chromophores which are useful in creating materials for second
order non-linear orbits. (II) is useful in hydrogen catalysis, as
coatings for biomaterials, scaffolds for tissue engineering,
ferroelectric materials, artificial muscles, switching devices, etc. The
sequence represents a peptide used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention relates to a miniblock polymer (I) comprising a self-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 198; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADV78589 standard; peptide; 21 AA.
                                                                                                                                                                                                       02-OCT-2001; 2001US-0326743P. 04-JUN-2002; 2002US-0385809P.
                                                                                                                                                         02-OCT-2002; 2002WO-US031375
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                                                                                                                                                                                                                                                                                       (TUFT ) TUFTS COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-671392/63.
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                                                   WO2003056297-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21 AA;
                                                                                                   10-JUL-2003
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Synthetic.
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DT 24-M
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The invention relates to a novel cell attachable polypeptide comprising an auxiliary amino acid sequence (Y) chemically bonded to a cell attachable minimal amino acid sequence (X), where (Y) contains 1-50 amino acids and the sum total content of Gly and Ala in (Y) is 42-100% with caids and the sum total content of Gly and Ala in (Y). The polypeptide of the invention may be utilized during culturing of cells for use in various experiments, including toxicity studies, gene transfer and production of useful substances such as cytokines, thrombolytic agents, vaccines, cueful substances such as cytokines, thrombolytic agents, vaccines, or useful substances such as cytokines, the polypeptide may be useful for culturing cells for transplantation, particularly, transplantation of skin, cranial bones, muscles, skin tissue, bone marrow and retina. The collypeptide exhibits extremely potent cell adhesion properties and can attach cells, such as NHDF and VERO cells, more efficiently onto a base catach relative to conventional methods. The polypeptide also exhibits conveniently. The current sequence is that of a cell attachment-related auxillary peptide of the invention.
                                                                                                                                                                     Cell attachable polypeptide useful for culturing cell, comprises auxiliary amino acid sequence having specific amount of Gly and Ala, chemically bonded to cell attachable minimal amino acid sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell attachable polypeptide useful for culturing cell, comprises auxiliary amino acid sequence having specific amount of Gly and Ala, chemically bonded to cell attachable minimal amino acid sequence, alternatively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell attachment; cell culture; transplantation; vaccine; antibiotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44; DB 9; Length 22;
Pred. No. 2.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell attachment-related auxillary peptide - SEQ ID 55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 2.8;
0; Mismatches
                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 54; 20pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADV78591 standard; peptide; 23 AA.
                            21-MAY-2003; 2003JP-00144125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.68;
                                                                         (SANN ) SANYO CHEM IND LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 84.6
Matches 11; Conservative
                                                                                                                          WPI; 2005-053150/06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22 AA;
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                                                                                                                                                                                                                                                    alternatively
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ADV78591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel cell attachable polypeptide comprising an auxiliary amino acid sequence (Y) chemically bonded to a cell attachable minimal amino acid sequence (X), where (Y) contains 1-50 amino acids and the sum total content of Gly and Ala in (Y) is 42-100$ with cacids and the sum total content of Gly and Ala in (Y) is 42-100$ with crespect to the total number of amino acids in (Y). The polypeptide of the invention may be utilized during culturing of cells for use in various caperiments, including toxicity studies, gene transfer and production of useful substances such as cytokines, thrombolytic agents, vaccines, hormones and antibiotics. Furthermore, the polypeptide may be useful for culturing cells for transplantation, particularly, transplantation of skin, cranial bones, muscles, skin tissue, bone marrow and retina. The polypeptide exhibits extremely potent cell adhesion properties and can attach cells, such as NHDF and VERO cells, more efficiently onto a base material, relative to conventional methods. The polypeptide also exhibits conveniently. The current sequence is that of a cell attachment-related conveniently. The current sequence is that of a cell attachment-related auxillary peptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      auxiliary amino acid sequence having specific amount of Gly and Ala, chemically bonded to cell attachable minimal amino acid sequence,
                                             cell attachment; cell culture; transplantation; vaccine; antibiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cell attachment; cell culture; transplantation; vaccine; antibiotic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          attachable polypeptide useful for culturing cell,
Cell attachment-related auxillary peptide - SEQ ID 53.
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                                                                                                                                                                                                                                                                                             21-MAY-2003; 2003JP-00144125.
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Best Local Similarity
Local Similarity
Local 11; Conservative
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                                                                                                                                            JP2005002106-A.
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                                                                                                Synthetic
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RESULT 36

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Gaps

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an auxiliary amino acid sequence (X) chemically bonded to a cell attachable minimal amino acid sequence (X), where (Y) contains 1-50 amino acids sequence (X), where (Y) contains 1-50 amino acids and the sum total content of Gly and Ala in (Y) is 42-100\$ with respect to the total number of amino acids in (Y). The polypeptide of the invention may be utilized during culturing of cells for use in various experiments, including toxicity studies, gene transfer and production of useful substances such as cytokines, thrombolytic agents, vaccines, commones and antibiotics. Furthermore, the polypeptide may be useful for culturing cells for transplantation, particularly, transplantation of skin, cranial bones, muscles, skin tissue, bone marrow and retina. The polypeptide exhibits extremely potent cells, more efficiently onto a base material, relative to conventional methods. The polypeptide also exhibits high heat stability, thus sterilization in autoclaves can be performed conventiently. The current sequence is that of a cell attachment-related auxillary peptide of the invention. The invention relates to a novel cell attachable polypeptide comprising Disclosure; SEQ ID NO 55; 20pp; Japanese. 

Sequence 23 AA;

Gaps .; 0 Score 44; DB 9; Length 23; Pred. No. 2.9; 2; Indels Pred. No. 2.9; ; 0 84.68; 11; Conservative Best Local Similarity Query Match

1 AAXAAAAAAAA 13

4 AAAAAAAAAAA 16

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8

ADV78592 standard; peptide; 24 AA. 24-MAR-2005 ADV78592; 

(first entry)

Cell attachment-related auxillary peptide - SEQ ID 56.

cell attachment; cell culture; transplantation; vaccine; antibiotic.

Synthetic.

JP2005002106-A.

06-JAN-2005

20-MAY-2004; 2004JP-00150510.

21-MAY-2003; 2003JP-00144125.

(SANN ) SANYO CHEM IND LTD.

WPI; 2005-053150/06.

Cell attachable polypeptide useful for culturing cell, comprises auxiliary amino acid sequence having specific amount of Gly and Ala, chemically bonded to cell attachable minimal amino acid sequence, alternatively.

Disclosure; SEQ ID NO 56; 20pp; Japanese.

The invention relates to a novel cell attachable polypeptide comprising an auxiliary amino acid sequence (Y) chemically bonded to a cell attachable minimal amino acid sequence (X), where (Y) contains 1-50 amino acids and the sum total content of Gly and Ala in (Y) is 42-100% with respect to the total number of amino acids in (Y). The polypeptide of the invention may be utilized during culturing of cells for use in various experiments, including toxicity studies, gene transfer and production of useful substances such as cytokines, thrombolytic agents, vaccines,

hormones and antibiotics. Furthermore, the polypeptide may be useful for culturing cells for transplantation, particularly, transplantation of skin, cranial bones, muscles, skin tissue, bone marrow and retina. The polypeptide exhibits extremely potent cell adhesion properties and can attach cells, such as NHDF and VERO cells, more efficiently onto a base material, relative to conventional methods. The polypeptide also exhibits high heat stability, thus sterilization in autoclaves can be performed conveniently. The current sequence is that of a cell attachment-related auxillary peptide of the invention. 888888888888

Sequence 24 AA;

Gaps ö 100.0%; Score 44; DB 9; Length 24; '84.6%; Pred. No. 3; 2; Indels Pred. No. 3; 0; Mismatches 84.6%; 11; Conservative Query Match Best Local Similarity Matches

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ò g RESULT 39

ABG95821 standard; peptide; 25 AA. ABG95821

ABG95821;

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(first entry) 09-DEC-2002 Transmembrane domain peptide #1.

Transmembrane domain; human; cow; papillomavirus; HIV; psoriasis; composite receptor; cell proliferative disorder; cystic fibrosis; T-cell lymphotropic virus; human immunodeficiency virus; cytostatic; antipsoriatic; respiratory.

Unidentified.

WO200262823-A2

15-AUG-2002.

01-FEB-2002; 2002WO-US002837.

02-FEB-2001; 2001US-0265624P.

(UYYA ) UNIV YALE.

ď Bray-Ward Rabinovich P,

WPI; 2002-723154/78.

ö New isolated peptide and fusion peptide, useful for inserting proteins peptides and nucleic acids into the cell membrane in vivo or in vitro that may be useful in treating cancer or other proliferative disorders, e.g. psoriasis. 

Claim 5; Page 62; 111pp; English.

The invention relates to an isolated peptide used in compositions for expressing a composite receptor on the cell surface. The peptide is a fusion peptide comprising at least one cell penetrating domain which is linked to at least one transmembrane domain or to an adapter domain capable of binding to a molecule, where the orientation of the cell penetrating domain is independent of the orientation of the transmembrane or adapter domain. The peptides are useful for inserting proteins or peptides such as regulatory factors, enzymes, antibodies, drugs or toxins and nucleic acids such as DNA or RNA into the cell membrane either in vivo or in vitro, that may be useful in inhibiting or treating diseases or disorders, which could benefit from the addition of surface receptors to cells, such as cancer and other proliferative disorders like psoriaais and cystic fibrosis. The methods are useful for identifying agents that modulate the activity of a receptor protein and for preparing the fusion

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The invention relates to a miniblock polymer (I) comprising a self-
fabricating block and a solubilizing block, a block for triggering self-
fabrication by external or environmental conditions, and a block for
incorporating turns in the polymer or for providing sites for chemical
modifications, has a molecular weight of 1000-300000 and, in solution,
can self-fabricate to form 3-dimensional material having long-range
order, and where (I) has glycine content of at least 20%. (I) is useful
for controlled delivery of a drug which involves incorporating a drug
within (I), and administering the self-fabricating material incorporating
corporating. The drug is incorporated within layers of the self-fabricating
material. (II) is useful for modifying the optical response of a device
in the near to mid infrared wavelength range which involves applying (II)
co the surface of the device (all claimed). (I) is useful for preparing
long range ordered fluids (i.e., liquid crystals) in a variety of phases
or forms, which can then undergo very specific structural transitions to
form rigid materials. (I) can be used as structural trissue implants, in
claying crystal displays, and for producing high-performance composites.
(I) is useful for preparing chemically pattend templates with either
general features are specific features. (I) is also useful in
nanolithographic processes. A self-fabricated structure containing the
                                                                                                                     ö
peptide. This sequence represents a transmembrane domain of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Miniblock polymer useful in nanolithographic processes, has self-fabricates fabricating block and solubilizing block, has glycine and self-fabricates to form 3-dimensional materials having long-range orders, in solution.
                                                                                                                                                                                                                                                                                                                                                                                                                                          miniblock polymer; optical response; mid infrared wavelength range; long range ordered fluid; liquid crystals; nanolithography; IR-sensitive device; IR sensor; IR filter; night telescope; thermosensitive detector; non-linear chromophore; biomaterial; tissue engineering scaffold; ferroelectric material; artificial muscle;
                                                                                                                   Gaps
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                                                                         Length 25
                                                                                                                 2; Indels
                                                                             2,
                                                                           44; DB
No. 3.1;
                                                                                                                 0; Mismatches
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                                                                                               Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                      Self-assembling polymer peptide #198.
                                                                             Score
                                                                                                                                                                                                                                                                                         ADJ81343 standard; peptide; 26 AA.
                                                                         ch 100.0%;
1 Similarity 84.6%;
11; Conservative · 0
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2002US-0385809P.
                                                                                                                                                                                           AAAAAAAAAAA 18
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                                                                                                                                                     1 AAXAAAAAAAA 13
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                                                                                             Local Similarity
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                                     Sequence 25 AA;
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Matches
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polymer (II) is useful for modifying and improving performance of IR-sensitive devices, IR sensors, IR filters, night telescopes and thermosensitive detectors. (II) can be used for preparing films, membranes or coatings that absorb specific wavelengths of infrared radiation, and in optical applications e.g., as matrices to align nonlinear chromophores which are useful in creating materials for second order non-linear orbits. (II) is useful in hydrogen catalysis, as coatings for blomaterials, scaffolds for tissue engineering, ferroelectric materials, artificial muscles, switching devices, etc. The sequence represents a peptide used in the method of the invention.
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                                                                                                                                                                                                                                                                                                100.0%; Score 44; DB 7; Length 26; 84.6%; Pred. No. 3.2;
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                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                       84.68;
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Job time: 99.4177 secs
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phosphatidylinosit zinc finger protei transcription fact myc-associated zin polyomavirus enhan homeotic protein e	probable YME1 ATP- transcription fact box A-binding fact C14orf4 protein -	hypothetical prote hypothetical prote protein H05C05.1 [ ecdysone-induced p	ecdysone-induced p puff 74E protein - DNA-binding protei	dachshund isolorm dachshund protein dachshund protein	dachshund protein stribe a/b protein	bumetanide sensiti bumetanide sensiti	ovo procein - frui spalt protein - fr related to PAN2 pr sex comb protein -	hypothetical prote fibroin - Chinese protein F5323 6 [i	homeotic protein c	finger protein esc alpha-amylase inhi	finger protein, Sp segmentation prote cytochrome-c perox	homeotic protein e 26S proteasome reg	DNA-Binding procest homeotic protein B Om(1D) protein - f	homeotic protein B	glucan 1,4-aipna-g neurogenic protein	gene Deita protein neurogenic repetit	serine-fich hypothetical prote	eyelid - fruit fly hypothetical prote	Bir repeat contain		antifreeze protein	antifreeze protein antifreeze protein	O E		polyA binding prot hypothetical prote	7 5	9 9	transcription fact paired box protein	The state of the s
30 46 85.2 490 2 T09084 31 46 85.2 494 2 A42170 32 46 85.2 495 1 S31223 33 46 85.2 497 2 JCS076 34 46 85.2 513 2 A48233 35 46 85.2 552 1 WJFFEN	46 85.2 627 2 46 85.2 644 2 46 85.2 779 1 46 85.2 796 2	46 85.2 805 2 46 85.2 82.2 82.2 82.2 82.2 82.2 82.2 82.2	46 85.2 8/3 2 46 85.2 883 2 46 85.2 1028 2	46 85.2 1055 2 46 85.2 1072 2 46 95.3 1074 3	46 85.2 1081 2 46 85.2 1180 2	46 85.2 1205 2 46 85.2 1212 2 46 86.2 1212 2	46 85.2 1506 2 46 85.2 1668 2	46 85.2 1891 2 46 85.2 2639 2 45 81 1 451 2	45 83.3 2175 1 44 81.5 377 2	44 81.5 470 2 43 79.6 171 2	43 79.6 296 2 43 79.6 337 2 43 79.6 361 1	43 79.6 392 2 43 79.6 405 2	43 79.6 448 2 43 79.6 604 2 43 79.6 606 2	43 79.6 640 2	43 79.6 748 2 43 79.6 832 2	43 79.6 833 2 43 79.6 880 2	43 79.6 1166 2	43 79.6 2715 2 43 79.6 2957 2	43 79.6 4845 2	42 77.8 40 2	42 77.8 85 1	42 77.8 91 2 42 77.8 97 2	42 77.8 172 2 42 77.8 219 2	42 77.8 231 2	42 77.8 306 1 42 77.8 311 2	42 77.8 317 1	42 77.8 328 2 42 77.8 376 2	42 77.8 425 1	42 77.8 509 2
5.1.9 Biocceleration Ltd.	1; Search time 14.8101 Seconds (without alignments) 84.457 Million cell updates/sec				283416						by chance to have a he result being printed, distribution.		Description	4	2 auto ger pr	SH3 domains-contai abdominal segment	remale sterile nom hypothetical prote	ribosomal protein probable MASH-2 pr	achaete scute prot	homeoric protein H	paired type homeob	homeotic protein H zinc-finger protei	homeotic protein E	gene NXx6.1 protei	probable homeobox probable homeobox	basic helix-loop-h	engralled homeodom homeotic protein H	bZIP DNA-binding p	omeotic inc-fing asic hel
GenCore version 5.1.9 (c) 1993 - 2006 Biocceler using sw model	2006, 22:48:41 ; Search (without al 84.457 Mill	-10-617-568-4 Aafaaaaaaaa 13	Gapext 0.5	96216763 residues	satisfying chosen parameters:	0 2000000000	Match 0% Match 100% first 100 summaries			;	the number of results predicted by than or equal to the score of the db by analysis of the total score di	SUMMARIES	Length DB ID	10	0 0	00	7 7	0 0	100	9 07 0	0	0 0	00	10	0 0	000	0 0	٦ ٦	475 2 A43915 477 2 A47236 482 2 JC7583

ALIGNMENTS

- human

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C;Species: Drosophila melanogaster
C;Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: A46221; S22026
R;Barker. D.D.; Wang, C.:, Moore, J.; Dickinson, L.K.; Lehmann, R.
Genes Dev. 6, 2312-2226, 1992
A;Title: Pumilio is essential for function but not for distribution of the Drosophila ak
A;Reference number: A46221; MUID:93093466; PMID:1459455
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A; Reference number: $22026
A; Status: preliminary
A; Molecule type: mRNA
A; Reaidues: 1-361, A, 363-1102, R', 1104-1405, 'KN', 1408-1495,'V', 1497-1518,'S', 1520-1533
A; Cross_references: UNIPARC:UPI00001329FD; EMBL: X62589; NID: 98393; PID: 98394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL: AF030131; NID: 93002587;
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C.Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
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                                                                  Length 577;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
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R;Tapon, N.; Nagata, K.; Lamarche, N.; Hall, A.
EMBO J. 17, 1395-1404, 1998
A;Reference number: Z16552; MUID:98151363; PMID:9482736
A;Accession: T09071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-892 <TAP>
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Pred. No. 26;
0; Mismatches
                                                              Score 47; DB 2;
Pred. No. 18;
); Mismatches
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0; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SH3 domains-containing protein POSH - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Keywords: signal transduction F; 8-58/Domain: RING finger homology <RRN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Gene: FlyBase:pum
A,Cross-references: FlyBase:FBgn0003165
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nilarity 92.3%;
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Local Similarity 92.3%;
Hes 12; Conservative
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| AAVAAAAAAAAA 431
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Matches 12; Conserv
C; Keywords: zinc finger
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A,Status: preliminary
A,Molecule type: mRNA
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C. Species: Drosophila melanogaster
C. Date: 04-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C. Accession: S7223, Mang, L.; Coulter, D.E.
Genetics 144, 171-182, 1996
A.Title: Comparison of the structure and expression of odd-skipped and two related genes A.Accession: S7227, MuID:97032935; PMID:8878683
A.Accession: S7227
A.Status: Preliminary
A.Molecule type: mRNA
A.Molecu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q16676; UNIPARC:UP1000012ADC8; EMBL:U59832; NID:g1399238; PI
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C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 05-Nov-1999
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 05-Nov-1999
C;Accession: I3858
R;Ge, O; Nilasena, D.S.; O'Brien, C.A.; Frank, M.B.; Targoff, I.N.
J. Clin. Invest. 96, 1730-1737, 1995
A;Title: Molecular analysis of a major antigenic region of the 240-kD protein of Mi-2 A;Reference number: 138558; MUID:96013633; PMID:7560064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: I38558
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-530 «RES»
A;Cross-references: UNIPARC:UP1000016A09A; EMBL:U08379; NID:G761717; PIDN:AAC50228.1;
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C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Oct-2004
C;Accession: G02738
R;Enerback, S.
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Pred. No. 17;
0; Mismatches 1; Indels
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1; Indels

Score 49; DB 2; Pred. No. 8.4; 0; Mismatches

y Match Local Similarity 92.3%; hes 12; Conservative

Query Match Best Local \$ Matches 290 ALFAAAAAAAA 302

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1 AAFAAAAAAAA 13

138558 Mi-2 autoantigen 240 kDa protein - human (fragment)

Query Match 87.0%; Best Local Similarity 92.3%; Matches 12; Conservative

1 AAFAAAAAAAA 13

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C,Genetics: A,Gene: FREAC-4 F,125-216/Domain: fork head DNA-binding domain homology <FHD>

submitted to the EMBL Data Library, June 1996
A;Reference number: H01646
A;Recession: G02738
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-465 < ENE>

Gaps

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Matches

A;Cross-references: FlyBase:FBgn0004892

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C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #text_change 02-Sep-2000
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Sep-2000
C;Accession: JG5954
R;Tanaka, M.; Tanaka, T.; Harata, M.; Suzuki, T.; Mitsui, Y.
Biochem. Biophys. Res. Commun. 243, 531-537, 1998
A;Title: Triplet repeat-containing ribosomal protein L14 gene in immortalized human endth A;Reference number: JG5954; MUID:98153799; PMID:9480843
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable MASH-2 protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S11563
R;Johnson, J.E.; Birren, S.J.; Anderson, D.J.
Nature 346, 858-861, 1990
A;Title: Two rat homologues of Drosophila achaete-scute specifically expressed in neuror A;Reference number: S11562; MUID:90363294; PMID:2392153
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*Residues: 1-23 a.COH>
A;Cross-references: UNIPROT:P19359; UNIPARC:UPI0000047567; EMBL:X53725; NID:956630; PIDN
C;Keywords: DNA binding
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C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
C;Accession: A48279
Broc. Natl. Azzoli, C.G.; Baylin, S.B.; Chi, D.; Dou, S.; Donis-Keller, H.; Cumaraswan Proc. Natl. Azad. Sci. U.S.A. 90, 5648-5652, 1993
A;Title: Identification of a human achaete-scute homolog highly expressed in neuroendocz A;Reference number: A48279; MUID:93296195; PMID:8330674
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                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPARC:UPI000004E622; DDBJ:D87735; NID:g1620021; PIDN:BAA13443.1;
C;Superfamily: rat ribosomal protein L14
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A;Molecule type: mRNA
A;Residues: 1-238 <RES>
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Pred. No. 12;
0; Mismatches
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Pred. No. 11;
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Pred. No. 12;
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Best Local Similarity 92.35,
Best Local 2, Conservative
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150 AAAAAAAAAAA 162
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                             ribosomal protein L14 - human
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Matches 12; Conserv
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Matches 12; Conserv
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A;Molecule type: mRNA
A;Residues: 1-2038 <HAY>
A;Cross-references: UNIPROT:P13709; UNIPARC:UPI000012AC6C; EMBL:M23221; NID:g157452; PID
                                                                                                                                                                                                                                                                                                                                                                                        mer
                                                                                                                                                                    female sterile homeotic protein, 205K - fruit fly (Drosophila melanogaster)
N;Alternate names: membrane protein fsh, 205K
N;Contains: female sterile homeotic protein, 110K
C;Species: Drosophila melanogaster
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 31-Dec-2004
C;Accession: A43742; B43742
E;Haynes, S.R.; Mozer, B.A.; Bhatia-Dey, N.; Dawid, I.B.
Dev. Biol. 134, 246-257, 1989
A;Title: The Drosophila fsh locus, a maternal effect homeotic gene, encodes apparent a seference number: A43742; MUID:89276730; PMID:2567251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Keywords: alternative splicing; transmembrane protein
F;1-2038/Product: female sterile homeotic protein, 205K #status predicted <MA2>
F;1-1106/Product: female sterile homeotic protein, 110K #status predicted <MAT>
F;59-116/Domain: bromodomain homology <BRO1>
F;503-560/Domain: bromodomain homology <BRO2>
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C;Species: Homo sapiens (man)
C;Date: 23-Jul-1999 #text_change 09-Jul-2004
C;Accession: T12547
R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, June 1999
A;Accession: T12547
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Pred. No. 50;
0; Mismatches 1; Indels
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A;Residues: 1-1106 <HA2>
A;Cross-references: UNIPARC:UPI000017A10F; EMBL:M23222
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Pred. No. 8.4;
0; Mismatches
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92.3%;
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92.3%;
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1050 AAVAAAAAAAAA 1062
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Best Local Similarity 92.3
Matches 12; Conservative
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A.Molecule type: mRNA
A.Residues: 1-150 <OTT>
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A; Status: preliminary
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A, Residues: 1-305 <RES>
A, Cross-references: UNIPARC:UPI000024E69; GB:S79041; NID:g1042008; PIDN:AAB34947.1; PID C, Genetics: G, Genetics: A, Genetics: C, Keywords: DNA binding; homeobox, nucleus; transcription regulation F;204-260/Domain: homeobox homology <HOX>
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R;Yokoyama, M.; Nishi, Y.; Yoshii, J.; Okubo, K.; Matsubara, K.

R;Yokoyama, M.; Nishi, Y.; Yoshii, J.; Okubo, K.; Matsubara, K.

R;Yokoyama, M.; Nishi, Y.; Yoshii, J.; Okubo, K.; Matsubara, K.

A;Title: Identification and cloning of neuroblastoma-specific and nerve tissue-specific A;Reference number: JC5272; MUID:97191543; PMID:9039501

A;Contents: neuroblastma cell
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A,Residues: 1-314 < YOK>
A,Residues: 1-314 < YOK>
A,Residues: 1-314 < YOK>
C,Croment: This protein is a transcriptional repressor involved in regulating gene expre C,Comment: This protein is a transcriptional repressor involved in regulating gene expre C,Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;99-155/Domain: homeobox homology < HOX>
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A;Molecule type: DNA
A;Residues: 1-323 <IZP>
A;Cross-references: UNIPROT:P23813; UNIPARC:UPI0000029F10; EMBL:X60761; NID:g51420; PID:
B;Gerard, M.; Duboule, D.; Zakany, J.
EMBO J. 12, 3539-3550, 1993
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Nyalternate names: homeotic protein Hoxd-11
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Oct-2004
C;Accession: S16118; S40403; S57443
C;Accession: S16118; S40403; S57443
A;Izblaua-Belmonte, J.C.; Falkenstein, H.; Dolle, P.; Renucci, A.; Duboule, D.
BMBO J. 10, 2279-2289, 1991
A;Title: Murine genes related to the Drosophila AbdB homeotic gene are sequentially A;Reference number: S16317; MUID: 91293104; PMID: 1676674
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C;Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 05-Oct-2004
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Pred. No. 15;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                Score 46; DB 2
Pred. No. 15;
0; Mismatches
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Best Local Similarity 92.3%;
Matches 12; Conservative
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A,Status: translation not shown
A,Molecule type: DNA
A,Residues: 1-323 <GER>
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241 AAAAAAAAAAA 253
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Matches 12, Conservative
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homeotic protein Hox D8 - mouse
NyAlternate names: homeotic protein Hox 4.3
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
C;Accession: A43562
R;Izpisua-Belmonte, J.C.; Dolle, P.; Renucci, A.; Zappavigna, V.; Falkenstein, H.; Dubou R;Izpisua-Belmonte, J.C.; Dolle, P.; Renucci, A.; Zappavigna, V.; Falkenstein, H.; Dubou A;Itelerence number: A43562; MUID:91209232; PMID:1982431
A;Accession: A43562
A;Status: pre-liminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-289 <1ZP>
A;Cross-references: UNIPROT:P23463; UNIPARC:UPI0000177DA6
C;Superfamily: homeotic protein Hox A7; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;196-252/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                 C;Species: Drosophila sp.
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 15-Mar-2004
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 15-Mar-2004
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 15-Mar-2004
R;Zhu, T.H. Bodem, J.; Keppel, E.; Paro, R.; Royer-Pokora, B.
Oncogene 11, 1283-1290, 1995
A;Tille: A single ancestral gene of the human LIM domain oncogene family LMO in Drosophi A;Tille: A single ancestral gene of the human LIM domain oncogene family LMO in Drosophi A;Accession: 861522, MUID:96017802; PMID:7478548
A;Accession: 861522
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross_references: UNIPARC:UP10000083F4F; GB:X83012; NID:g1854500; PIDN:CAA58141.1; PID F;45-98/Domain: LIM metal-binding repeat homology <LIM1>F;109-162/Domain: LIM metal-binding repeat homology <LIM2>
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14;
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A;Molecule type: mRNA
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Pred. No.
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Best Local Similarity 92.3%;
Matches 12; Conservative
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                                                             AAAAAAAAAAAA 47
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ses 11; Conserva
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Best Local S
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-334 <KUR>
A;Residues: UNIPARC:UPI000016A2D0; EMBL:U48250; NID:91199656; PIDN:AAC72247.1;
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A,Molecule type: mRNA
A,Residues: 1-364 «FBS»
A,Cross-references: UNIPROT:Q60554; UNIPARC:UPI00001301FA; EMBL:X81409; NID:g587466; PII
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Blant J. 7, 927-938, 1995
A;Title: Alternative RNA products from a rice homeobox gene.
A;Reference number: Z15126; MuID:95322999; PMID:7599652
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A;Cross-references: UNIPROT:P93423; UNIPARC:UPI0000AB610; EMBL:D49704; NID:g1805615;
A;Experimental source: cv. Nipponbare
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C;Species: Mesocricetus auratus (golden hamster)
C;Daccession: 149188
B;Rudnick, A.; Ling, T.Y.; Odagiri, H.; Rutter, W.J.; German, M.S.
Proc. Natl. Acad. Sci. U.S.A. 91, 12203-12207, 1994
A;Title: Pancreatic beta cells express a diverse set of homeobox genes.
A;Reference number: 148185; MUID:95083670; PMID:7991607
                                                                                                                                                                        Species: Homo sapiens (man)
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C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-Oct-2004
C;Accession: T03875
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A;Reference number: H01212
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 46; DB 2; Length 334;
Pred. No. 16;
0; Mismatches 1; Indels
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Pred. No. 17;
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Best Local Similarity 92.3%;
Matches 12; Conservative
                               213 AASAAAAAAAA 225
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Best Local Similarity 92.3
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            zinc-finger protein Pur-1 - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 05-Apr-1995
C;Accession: B47236
R;Kennedy, G.C.; Rutter, W.J.
Proc. Natl. Acad. Sci. U.S.A. 89, 11498-11502, 1992
A;Title: Pur-1, a zinc-finger protein that binds to purine-rich sequences, transactivate
A;Reference number: A47236; MUID:93087555; PMID:1454839
                                                                             펍
RiD'Esposito, M.; Morelli, F.; Acampora, D.; Migliaccio, E.; Simeone, A.; Boncinelli, Genomics 10, 43-50, 1991
A;Title: BVX2, a human homeobox gene homologous to the even-skipped segmentation gene, A;Reference number: A39065; MUID:91257849; PMID:1675198
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homeotic protein EVX2 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 31-Dec-2004
C;Accession: A39065
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C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;46-102/Domain: homeobox homology <HOX>
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Pred. No. 16;
0; Mismatches 1; Indels
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Pred. No. 15;
0; Mismatches 1; Indels
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16;
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A;Experimental source: insulinoma cell line T
A;Note: sequence extracted from NCBI backbone (NCBIP:119832)
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Pred. No. 16;
0; Mismatches
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92.3%;
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92.3%;
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                                                                                                                                                                                                                                                                                    12; Conservative
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Best Local Similarity 92.3
Matches 12; Conservative
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Best Local Similarity
Matches 12; Conserv
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Best Local Similarity
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B47236
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Gaps

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Indels

Length 378;

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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004
C;Accession: A48423; S13009; A26629; A24778
E;Logan, C.; Hanks, M.C.; Noble-Topham, S.; Nallainathan, D.; Provart, N.J.; Joyner, A.L Dev. Genet. 13, 345-358, 1992
A;Title: Cloning and sequence comparison of the mouse, human, and chicken engrailed gene A;Reference number: A48423; MUID:93185339; PMID:1363401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; not compared with conceptual translation
A;Status: preliminary; not compared with conceptual translation
A;Residues: 1-401 <LOG2
A;Residues: 1-401 <LOG2
A;Residues: 1-401 <LOG2
A;Residues: 1-401 <LOG3
A;Resperimental source: CD-1, embryo
A;Experimental source: CD-1, embryo
A;Experimental source: CD-1, embryo
A;Note: sequence extracted from NCBI backbone (NCBIP:126620)
B;Holland, P-W+1, Williams, N-A.
B;
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A;Nolecule type: nucleic acid
A;Residues: 321-380 c400.
A;Residues: 4.21-380 c400.
A;Crowner, A.L.; Martin, G.R.
Genes Dev. 1, 29-38, 1987
A;Title: En-1 and En-2, two mouse genes with sequence homology to the Drosophila engrail
A;Reference number: A91620; MuID:88112776; PMID:2892757
A;Reference number: A91620; MuID:88112776; PMID:2892757
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A;Residues: 278-401 <10V>
A;Cross-references: UNIPARC:UPI000016CA7C; GB:Y00201; GB:M11987; NID:g49587; PIDN:CAA68:
R;JOYDEY, A.L.; Kornberg, T.; Coleman, K.G.; Cox, D.R.; Martin, G.R.
Cell 43, 29-37, 1985
A;Title: Expression during embryogenesis of a mouse gene with sequence homology to the I
A;Reference number: A24778; MUID:86079501; PMID:2416459
sequence extracted from NCBI backbone (NCBIN:102964, NCBIP:102966)
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C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;313-369/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   engrailed homeodomain-containing protein En-1 - mouse
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Pred. No. 18;
0; Mismatches
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A;Cross-references: UNIPARC:UPI000017A2B0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N;Alternate names: homeotic protein En-1
                                                                                                                                                            A; Cross-references: FlyBase: FBgn0013115
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Best Local Similarity
Matches 12; Conserv
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Best Local Similarity
                                                                                                                        A;Gene: FlyBase:Dvir/h
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                              A;Note: sec
C;Genetics
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A; Cross-references: UNIPARC:UDI00016DEBB; EMBL:D49704; NID:g1805615; PIDN:BAA08554.1; F
A; Cross-references: Cv. Nipponbare; splice form OSH45.
C; Genetics: A; Gene: H45
A; Introns: 174/3; 215/1; 277/3; 321/3; 367/2
C; Keywords: alternative initiators; alternative splicing; DNA binding; homeobox; nucleus F; 1-375/Product: probable homeobox protein OSH45, splice form OSH44 #status predicted <P: 197-367/Product: probable homeobox protein OSH45, splice form OSH44 #status predicted <P: 197-367/Product: probable homeobox protein OSH45, splice form OSH44 #status predicted <P: 197-367/Product: probable homeobox protein OSH45, splice form OSH44 #status predicted <P: 197-367/Product: probable homeobox protein OSH45, splice form OSH42 #status predicted <P: 197-367/Product: probable homeobox protein OSH45, splice form OSH42 #status predicted <P: 197-367/Product: probable homeobox protein OSH45, splice form OSH45 #status predicted <P: 197-367/Product: probable homeobox protein OSH45, splice form OSH45 #status predicted <P: 197-367/Product: probable homeobox protein OSH45, splice form OSH45 #status predicted <P: 197-367/Product: probable homeobox protein OSH45, splice form OSH45 #status predicted <P: 197-367/Product: probable homeobox protein OSH45, splice form OSH45 #status predicted <P: 197-367/Product: probable homeobox protein OSH45, splice form OSH45, splice form OSH45, splice form OSH45, splice dorm OSH45, splice 
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N;Contains: probable homeobox protein OSH45, splice form OSH42
C;Species: Oryza sativa (rice)
C;Species: Oryza sativa (rice)
C;Species: Oryza sativa (rice)
C;Date: 23.Apr-1999 #sequence_revision 23.Apr-1999 #text_change 05-Oct-2004
C;Accession: T03874; T03876
R;Tamaoki, M.; Tsugawa, H.; Minami, E.; Kayano, T.; Yamamoto, N.; Kano-Murakami, Y.; Mat Plant J. 7, 927-938, 1995
A;Title: Alternative RNA products from a rice homeobox gene.
A;Reference number: Z19126; MUD:95322999; PMID:7599652
A;Accession: T03874
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basic helix-loop-helix transcription repressor H - fruit fly (Drosophila virilis)

basic helix-loop-helix transcription repressor H - fruit fly (Drosophila virilis)

C;Species: Do-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 02-Jul-1998

C;Accession: A44443

Rol: Cell: Biol. 12, 2475-2483, 1992

A;Title: Point mutations in the Drosophila hairy gene demonstrate in vivo requirements fly Reference number: A44443; MUID:92269819; PMID:1588951

A;Accession: A44443

A;Status: preliminary

A;Accession: B44443

A;Residues: I-378 «MAI>
                                                                                                                                                                      A;Introns: 174/3; 215/1; 277/3; 321/3; 367/2
C;Keywords: alternative initiators; alternative splicing; DNA binding; homeobox; nucleus
F;291-352/Domain: homeobox homology <HOX>
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Pred. No. 17;
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                              C:Comment: For alternative splice forms, see PIR:T03874.
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A;Molecule type: DNA
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Pred. No.
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Best Local Similarity 92.3%;
Matches 12; Conservative
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92.3%;
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Best Local Similarity 92.3
Matches 12; Conservative
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Length 401
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Score 46; DB 2;
Pred. No. 18;
                 0; Mismatches
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A,Molecule type: DNA
A,Residues: 1-443 <STE1>
A,Cross-references: UNIPROT:P41225; UNIPARC:UPI000003F546; EMBL:X71135; NID:g468790; PI
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Dev. Biol. 151, 273-287, 1992
A;Title: Analysis of mouse Evx genes: Evx-1 displays graded expression in the primitive
A;Reference number: A43915; MUID:92249649; PMID:1349539
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A;Cross-references: UNIPROT:P49749; UNIPARC:UPI000020BC6; GB:S34322; NID:g249137; PIDN
A;Cross-references: UNIPROT:P49749; UNIPARC:UPI000020BC6; GB:S34322; NID:g249137; PIDN
A;Note: sequence extracted from NCBI backbone (NCBIN:100478, NCBIN:100480
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Proc. Natl. Acad. Sci. U.S.A. 89, 11498-11502, 1992
A;Title: Pur-1, a zinc-finger protein that binds to purine-rich sequences, transactivat. A;Reference number: A47236; MUID:93087555; PMID:1454839
A;Accession: A47236
                                                         A;Accession: I38242
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residus: 143-128,'P',160-218 <STE2>
A;Residus: 143-128,'P',160-218 <STE2>
A;Cross-references: UNIPARC:UP10000071C8C; EMBL:X71137; NID:g468793; PIDN:CAA50467.1;
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C;Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004
C;Accession: A43915
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C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 05-Apr-1995
C;Accession: A47236
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homeotic protein even-skipped homolog Evx-2 - mouse
N/Alternate names: mesodermal cell dorsoventral fates determinator Evx-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 46; DB 2; Length 475;
Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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A;Experimental source: islet cell line beta TC3
A;Note: sequence extracted from NCBI backbone (NCBIP:119831)
                                                                                                                                                                                                                                                                   A,Gene: GDB:SOX3; SOX-3; SOXB
A;Cross-references: GDB:250376; OMIM:313430
A;Map position: XG2-Kq27
C;Superfamily: human SOX3 protein; HMG box homology
F;136-211/Domain: HMG box homology <HMG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 46; DB 1
Pred. No. 20;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 85.2%; 11 Similarity 92.3%; 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                359 AASAAAAAAAAA 371
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Best Local Similarity 92.3'
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: A43915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DZIP DNA-binding protein - parsley
C;Species: Petroselinum crispum (parsley)
C;Species: Petroselinum crispum (parsley)
C;Species: Petroselinum crispum (parsley)
C;Dacession: T14911
R;Kircher, S.; Ledger, S.; Hayashi, H.; Weisshaar, B.; Schafer, E.; Frohnmeyer, H.
R;Kircher, S.; Ledger, S.; Hayashi, H.; Weisshaar, B.; Schafer, E.; Frohnmeyer, H.
Mol. Gene. 257, 555-605, 1998
A;Richer, CPRF4a, a novel plant bZIP protein of the CPRF family: comparative analysis of A;Accession: T14911
A;Reference number: Z18261; MUID:98265918; PMID:9604882
A;Accession: T14911
A;Accession: T14911
A;Accession: T420 «KIR»
A;Residues: 1-420 «KIR»
A;Residues: 1-420 «KIR»
A;Cross-references: UNIPROT:082037; UNIPARC:UPI00000A12C8; EMBL:Y10810; NID:g3336904; PI
                                            C;Species: Homo sapies (man)
C;Species: Homo sapies (man)
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 31-Dec-2004
C;Accession: A53662
R;Harrison, K.A.; Druey, K.M.; Deguchi, Y.; Tuscano, J.M.; Kehrl, J.H.
J. Biol. Chem. 269, 19968-19975, 1994
A;Title: A novel human homeobox gene distantly related to proboscipedia is expressed in A;Reference number: A53662; MUID:94327547; PMID:7914194
                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-403 <HAR>
A;Cross-references: UNIPARC:UPI000017A29E; GB:U07663
A;Note: the nucleotide sequence and conceptual translation as given are self-consistent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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A;Note: CPRF4b
C;Superfamily: BZIP G-box-binding protein; fos/jun DNA-binding domain homology
C;Keywords: DNA binding; leucine zipper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transcription factor SOX3 - human
NyAlternate names: SRY (sex determining region Y)-box 3
NyAlternate names: SRY (sex determining region Y)-box 3
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: 138239; 138242; $67816
R;Stevanovic, M:, Lovell-Badge, R.; Collignon, J.; Goodfellow, P.N.
Hum. Mol. Genet. 2, 2013-2018, 1993
A;Title: SOX3 is an X-linked gene related to SRY.
A;Reference number: 138239; MUID:94154672; PMID:8111369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 1q41-1q42.1
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;244-300/Domain: homeobox homology <HOX>
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                                                                                                                                                                                                                                                                                      A;Status: preliminary; not compared with conceptual translation A;Molecule type: DNA
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llarity 92.3%; Pred. No. 19;
Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GDB:136411; OMIM:142994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 AAAAAAAAAAA 133
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les 12; Conserv
                            homeotic protein HB9
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A;Gene: GDB:HLXB9
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0; Mismatches

85.2%;

Query Match Best Local Similarity

JC7583 basic helix-loop-helix protein, DEC2 - human

96 ададададада 108

셤

1 AAFAAAAAAAA 13

12; Conservative

Matches

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R; Pyrc, J.J.; Moberg, K.H.; Hall, D.J.
Biochemistry 31, 4102-4110, 1992
A; Title: Isolation of a novel cDNA encoding a zinc-finger protein that binds to two site A; Reference number: A42170; MUID:92232709; PMID:1567856
A; Accession: A42170
                                                                                                                                                                                                                                                                                                                                                                                                                            A.Cross-references: UNIPROT: P56270; UNIPARC:UP1000017C427; GB:J05371
A;NOte: it is uncertain whether Met-18 is the initiator or whether translation is initial R;Bossone, S.A.; Asselin, C.; Patel, A.J.; Marcu, K.B.
Proc. Natl. Acad. Sci. U.S.A. 89, 7452-7456, 1992
A;Title: MAZ, a zinc finger protein, binds to c-MYC and C2 gene sequences regulating tra A;Reference number: A46153; MUID:92366479; PMID:1502157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:P31361; UNIPARC:UP10000029AAF; EMBL:M88299; NID:g200444; PII C;Superfamily: transcription factor Brn-1; homeobox homology; POU domain homology C;Keywords: DNA binding; homeobox; nucleus; transcription regulation F;27-49/Region: glycine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R,Hara, Y.; Rovescalli, A.C.; Kim, Y.; Nirenberg, M. Proc. Natl. Acad. Sci. U.S.A. 89, 3280-3284, 1992
A,Title: Structure and evolution of four POU domain genes expressed in mouse brain. A,Reference number: S31223; MUID:92228768; PMID:1565620
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C;Date: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S31223
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 18-417,'L',419-494 <BOS>
A;Cross-references: UNIPARC:UPI000012ECF8; GB:M94046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 46; DB 2;
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                    A;Status: not compared with conceptual translation
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0; Mismatches
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Pred. No.
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F;267-291/Region: histidine/proline-rich
F;316-383/Domain: POU domain homology <POU>
F;402-458/Domain: homeobox homology <HOX>
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F;162-180/Region: histidine/proline-rich
F;186-201/Region: alanine-rich
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Local Similarity 92.3%;
les 12; Conservative
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F:207-230/Region: zinc finger
F:256-318/Region: zinc finger
F:324-346/Region: zinc finger
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F,409-430/Region: zinc finger
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A; Residues: 1-495 < HAR>
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-494 < PYR>
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A; Status: preliminary
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TOPO84
phosphatidylinositol 3-kinase - Chlamydomonas reinhardtii (fragment)
CiSpecies: Chlamydomonas reinhardtii
CiSpecies: Chlamydomonas reinhardtii
CiSpecies: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
CiAccession: T09084
Rimolendiik, A.J.; Irvine, R.F.
Rimolendiik, A.J.; Irvine, R.F.
Rimolendiik, A.J.; Irvine, R.F.
A;Reference number: Z16411; MUID:98281574; PMID:9620264
A;Accession: T09084
A;Accession: T09084
A;Accession: Topo84
A;Accession: To
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JC7583
R;Fujimoto, K.; Shan, M.; Noshiro, M.; Matsubara, K.; Shingu, S.; Honda, K.; Yoshida, E. Biophys. Res. Commun. 280, 164-171, 2001
Biochem. Biophys. Res. Commun. 280, 164-171, 2001
A;Title: Molecular cloning and characterization of DEC2, a new member of basic helix-lod A;Reference number: JC7583; MUID:21092582; PMID:11162494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: UNIPROT:004270; UNIPARC:UPI00009C6FA; EMBL:U97663; NID:g2109290; PI
A,Experimental source: strain cw-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           zinc finger protein MAZ – human (fragment)
N;Alternate names: MYC-associated zinc finger protein MAZ; zinc finger protein ZF87
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                    Score 46; DB 2; Length 477;
Pred. No. 21;
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F;130-173/Domain: Orange #status predicted <ORA>
F;286-411/Region: alanine and glycine-rich #status predicted
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Query Match
Best Local Similarity 92.3%;
Matches 12; Conservative

396 AAAAAAAAAAA 408

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1 AAFAAAAAAAA 13

C; Keywords: transcription factor

A;Gene: dec2 A;Map position: 12p11.23-p12.1

Pred. No. 22; 0; Mismatches

115 AATAAAAAAAA 127

RESULT 31 A42170

1 AAFAAAAAAAA 13

12, Conservative

Query Match Best Local Similarity

A;Introns: 265/3; 331/3; 370/3; 455/1; 481/3

A; Residues: 1-490 < MOL>

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NyAlternate names: specific body pattern development protein.
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Accession: A90862; A93354; A03321; A03563; A55682; S03667
R;Poole, S.J.; Kauvar, L.M.; Drees, B.; Kornberg, T.
A;Title: The engrailed locus of Drosophila: structural analysis of an embryonic transcr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:P02836; UNIPARC:UPI000012CA13; GB:M10017; NID:g157363; PIDN R;Fjose, A.; McGinnis, W.J.; Gehring, W.J.
Rature 313, 284-289, 1985
A;Title: Isolation of a homoeo box-containing gene from the engrailed region of Drosoph A;Reference number: A93354; MUID:90114393; PMID:2481829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 447-485, 'E',487-518,'WH' <FJO>
A;Cross-references: UNIPARC:UP100001145BF; GB:X01765; GB:K03059; NID:g8084; PIDN:CAA259
A;Note: the translation of the nucleotide sequence from Fig. 5 is shown, not the transl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBO J. 5, 3583-3589, 1986

A, Title: Sequence conservation in the protein coding and intron regions of the engraile A, Reference number: A91059; MUID:87161768; PMID:2881781

A, Contents: annotation; intron locations and sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R,Gay, N.J.; Poole, S.J.; Kornberg, T.B.

Nucleic Acids Res. 16, 6637-6647, 1988

A;Title: The Drosophila engrailed protein is phosphorylated by a serine-specific protein the Drosophila engrailed protein; PMID:2899884

A;Reference number: 803667; MUID:88289425; PMID:2899884

A;Contents: annotation; potential phosphorylation sites; homeobox domain

C;Comment: This protein specifies the body segmentation pattern.
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C;Keywords: DNA binding; embryo; homeobox; nucleus; segmentation; transcription regulat
F;26-53/Region: glutamine-rich
F;232-240/Region: alanine-rich
F;320-368/Region: serine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable YME1 ATP-dependant proteinase [imported] - Arabidopsis thaliana NyAlternate names: YTA1 protein homolog T19L18.5 C;Species Arabidopsis thaliana (mouse-ear cress) C;Species Arabidopsis thaliana (mouse-ear cress) C;Date: 24-Mar-1999 #text_change 31-Dec-2004 C;Accession: T02610; H84656 Erevision 24-Mar-1999 #text_change 31-Dec-2004 S;Accession: Tozelo; Kaul, S; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, August 1998 A;Description: Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence.
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     fruit fly (Drosophila melanogaster)
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R; Kassis, J.A.; Poole, S.J.; Wright, D.K.; O'Farrell, P.H.
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Pred. No. 24;
0; Mismatches
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A,Map position: 2R,62.0 (48A1-4)
A,Introns: 438/1; 470/3
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A,Status: translated from GB/EMBL/DDBJ
A,Rolecule type: DNA
A,Residues: 1-627 <ROU>
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92.3%;
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Best Local Similarity 92.3
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Accession: A90862
A, Molecule type: mRNA
A, Residues: 1-552 < POO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: A93354
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N; Alternate names: MAZ protein
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 05-Nov-1999
C; Accession: JC5076
R; TSUGUSUI, H; Sakatame, O.; Itakura, K; Yokoyama, K.K.
Biochem. Biophys. Res. Commun. 226, 801-809, 1996
A; Title: Members of the MAZ family: A novel cDNA clone for MAZ from human pancreatic isl
A; Reference number: JC5076; MUID:96428591; PMID:8831693
A; Accession: JC5076
A; Molecule type: mRNA
A; Residues: 1-497 cTRN
A; Residues: 1-497 cTRN
A; Residues: UNIPARC:UPI0000163B39; DDBJ:DBS131; NID:g1752741; PIDN:BAA12728.1; F
A; Experimental source: pancreatic islet
C; Comment: This protein plays a role in the control of transcriptional initiation of gen and between the introns of the mouse gene for immunoglobulin M-D.
C; Keywords: phosphoprotein; zinc finger
F; 146, 204, 480/Binding site: phosphate (Ser) (covalent) #status predicted
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A48233

Polyomavirus enhancer-binding protein 2 alpha chain type 1 - mouse

Nolyomavirus enhancer-binding protein 2 alpha chain type 1 - mouse

Nolyomavirus enhancer-binding protein 2 alpha chain type 2; PEBP2 alpha chain type 2; Species: Mus musculus (house mouse)

C;Species: Mus musculus (house mouse)

C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004

C;Accession: M48233 B4223

R;Ogawa, E.; Maruyama, M.; Kagoshima, H.; Inuzuka, M.; Lu, J.; Satake, M.; Shigesada, K.

Proc. Natl. Acad. Sci. U.S.A. 90, 6859-6863, 1993

A;Reference number: A48233

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A/SCALUS: preliminary
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Pred. No. 22;
0; Mismatches
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Best Local Similarity 92.3%;
Matches 12; Conservative
                                                                                                      186 AAAAAAAAAAA 198
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122 AAAAAAAAAAA 134
1 AAFAAAAAAAA 13
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Gaps

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R;Rampazzo, A.; Pivotto, F.; Occhi, G.; Tiso, N.; Bortoluzzi, S.; Rowen, L.; Hood, L.; N
Biochem. Biophys. Res. Commun. 278, 766-774, 2000
A;Title: Characterization of C14orf4, a novel intronless human gene containing a polyglu
A;Reference number: JC7555, MUID: 20549026; PMID:11095982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q9H1B7; UNIPARC:UPI00000738BA; GB:AJ277365
C;Comment: This protein, a proline-rich nuclear protein, functions as a transcriptional
s and undergoes rapid degradation.
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C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T49385
R;Schulte, U:, Aign, V:, Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000
A;Reference number: 225022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: DNA
*Kesiduse: 1-805 <SCH3-
A;Cross-references: UNIPROT:Q9P682; UNIPARC:UPI000017B46C; EMBL:AL355927; GSPDB:GN00116.
A;Experimental source: BAC clone B1D1; strain OR74A
A,Gene: FlyBase:srp
A,Cross-references: FlyBase:FBgn0003507
C;Superfamily: box A-binding factor, GATA-type zinc finger homology
C;Keywords: DNA binding; nucleus; transcription factor; transcription regulation; zinc C;Keywords: DNA binding; nucleus; transcription factor; transcription regulation; Zinc F;316-369/Domain: GATA-type zinc finger homology <GZF>
F;316-343/Region: zinc finger GATA motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Homo sapiens (man)
Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
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Pred. No. 32;
0; Mismatches
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Pred. No. 31;
0; Mismatches
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Pred. No.
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92.3%;
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Best Local Similarity 92.3%;
Matches 12; Conservative
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Matches 12; Conservative
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Best Local Similarity 92.3
Matches 12; Conservative
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A;Map position: 6
A;Introns: 54/3; 212/3
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C;Date: 30-Jun-2001
C;Accession: JC7555
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NyAlternate names: ABF; transcription factor dGATAb
CiSpecies: Drosophila melanogaster
CiDate: 13-dan-1995 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
CiDate: 13-dan-1995 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
CiDate: 13-dan-1995 #squence_revision 06-Sep-1996 #text_change 09-Jul-2004
CiDate: 10-Sep-1996 #text_change 09-Jul-2004
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CiDate: ABE-Sep-1996
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                                            Riin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, b.; Tallon, L. Neure 402, Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A,Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A,Reference number: A4420; MUD:20083487; PMID:10617197
A,Scatus: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: UNIPARC: UPI000017885F; GB: AE002093; NID: 93413700; PIDN: AAC31223.1;
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S39356
Liange Entroit of a control of control cont
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A;Introns: 40/1; 119/1; 160/3; 319/3
C;Superfamily: FtsH/SEC18/CDC48-type ATP-binding domain homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 85.2%; Score 46; DB 2; Length 627; 1 Similarity 92.3%; Pred. No. 26; 12; Conservative 0; Mismatches 1; Indels
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Pred. No. 27;
0; Mismatches 1; Indels
                      A; Experimental source: cultivar Columbia
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A;Introns: 245/2
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Best Local Similarity 92.3
Matches 12; Conservative
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A; Residues: 1-627 <STO>
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03UQW8_MOUSE

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04PE18_USTWA

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QBBKB9_MOUSE
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QSVTV0_HUMAN
Q6GLG1_XENTR
Q6GLC3_HUMAN
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Gapop 10.0 , Gapext 0.5
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ALIGNMENTS

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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22767835; PubMed=12885558; DOI=10.1016/S0012-1606(03)00217-3; Prpic N.M., Tautz D.; Prpic n.M., Tautz 
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01-JUN-2001, sequence version 1.
21-FEB-2006, entry version 1.
CSJNBa-2006, entry version 1.
OSJNBa0004G10.7 protein (Hypothetical protein B1008C01.41).
Name=OSJNBa0004G10.7, Synonyms=B1008C01.41;
Oryza sativa (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22337376; PubMed=12447438; DOI=10.1038/nature01184; Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y. Wu J., Nlimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H., Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M., Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C., Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR01256; Homeodox.
InterPro; IPR012287; Homeodomain-rel.
                                                                                                                                                                                                                                                                   Glomeris marginata.
Eukaryota, Metazoa, Arthropoda, Myriapoda, Diplopoda, Pentazonia,
Glomerida, Glomeridae, Glomeris.
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                                                                                     01-OCT-2003, integrated into UniProtKB/TrEMBL
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Q9ARRT;
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PROSITE; PS50071; HOMEOBOX 2; 1.
DNA-binding; Homeobox; Nuclear protein.
                                                                                                                                   01-OCT-2003, sequence version 1. 07-FEB-2006, entry version 11.
                                                                                                                                                                                                   Distal-less protein (Fragment).
Name=dll;
                        PRELIMINARY;
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Dev. Biol. 260:97-1
                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=62006;
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                            Q7YTA3_9MYRI
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RA MADIANE-20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; RD LOIDECTIDE SEQUENCE.

RA Admanatides P.G., Scherer S.E., Lip P.W., Hoskins R.A., Galle R.F., Adams M.D., Celniker S.E., Lip P.W., Hoskins R.A., Galle R.F., Adams M.D., Lewis S.E., Lip P.W., Hoskins R.A., Galle R.F., Addens M.C., Lewis S.E., Lip P.W., Hoskins R.M., Hoskins R.N., Bardell M.D., Zhang Q., Chen L.X., Andrews P.C., Rayder Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Baradon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Ballew R.M., Basu A., Baxendale J., Andrews-Pfannkoch C., Baldwin D., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Abril J.F., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Berman B.P., Bhandari D., Bolshakov S., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Cahler A., Deng Z., Mays A.D., Dewi I., Dietz S.M., de Pablos B., Delcher A., Deng Z., Mays A.D., Dewi I., Dietz S.M., Adelode N., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Gabley F., Gorrell J.H., Gu Z., Guan P., Harris M., Haiman T.J., Hermandez J.R., Houston K.A., Howland T.J., Hermandez J.R., Houston K.A., Howland T.J., Heiman T.J., Herman S., Florey M. Howley D., Howland G.H., Ke Z., Kennison J.A., Ketchum K.A., Jalali M., Kalush F., Kaipen G.H., Kazvitz S., Kalup D., Lai Z., Hastin M., Mattei B., McIntosh T.C., McLeod M.P., Morberson D., Morkei B., Morkei B
                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
Ikeno M., Ito S., Ito T., Ito Y., Ito Y., Iwabuchi A., Kamiya K., Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I., Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y., Magasaki H., Makashima M., Nakama Y., Makami Y., Nakamura M., Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M., Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K., Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K., Yano M., Jiang J., Gojobori T. Ito H., Hahn J.H., Kim H.-I., Eun M.-Y., The genome sequence and structure of rice chromosome 1.";
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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.6%; Score 50; DB 2; Length 269; 100.0%; Pred. No. 39; o; Indels ive 0; Mismatches 0; Indels
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PRINTS; PR01852; SIBAPROTEIN.
Hypothetical protein.
SEQUENCE 269 AA; 27747 MW; 861429FCDB1141DF CRC64;
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EMBL; AP003196; BAB93147.1; -; Genomic_DNA.
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07-FEB-2006, entry version 14.
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271 AAFAAAAAAALAA 283

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Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
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Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                          Celliker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstrock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M., Frishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22426669; PubMed=12537572; Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.
Yu C., Rubin G.;
"Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Annotation of the Drosophila melanogaster euchromatic genome: a systematic review.";
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Local Similarity 92.3%; Pred. No. 59;
les 12; Conservative 0; Mismatches 1. T-dele
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FlyBase; FBgn0051422; CG31422.
SEQUENCE 305 AA; 32565 MW; 472F8AA40CFF9953 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a genomics perspective.";
Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002)
                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
MEDLINE=22426065; PubMed=12537568;
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                                                                                                                                                                                                                Labbe M., Pery P.;
"Characterization of ribosomal phosphoprotein P0 of Eimeria tenella.";
"Characted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Ribosomal protein P0 is the functional equivalent of
E.coli protein L10.
-!- SUBUNIT: P0 forms a pentameric complex by interaction with dimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Galagan J.E., Calvo S.E., Cuomo C., Ma L.-J., Wortman J.R.,
Batzoglou S., Lee S.-I., Bastuerkmen M., Spevak C.C., Clutterbuck J.,
Kapitonov V., Jurka J., Scazzocchio C., Farman M., Butler J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
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                                                                                                                                                                                                                                                                                                                                  -1- PTM: Phosphorylated (By similarity).
-!- SIMILARITY: Belongs to the ribosomal protein L10P family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60S acidic ribosomal protein PO. /FTId=PRO 0000154770. 13214EFI694BDAC6 CRC64;
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Eurotiales; Trichocomaceae; Emericella.
NCBI_TaxID=227321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.7%; Score 49; DB 1; Length 314; 92.3%; Pred. No. 60; 1; Indels tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00428; Ribosomal 608; I.
Pfam; PF00466; Ribosomal L10; 1.
PRINTS; PR00456; RIBOSOMĀLP2.
Phosphorylation; Ribonucleoprotein; Ribosomal protein.
                             20-JUN-2002, integrated into UniProtKB/Swiss-Prot. 01-DEC-2001, sequence version 1.
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 314 AA.
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PubMed=16372000; DOI=10.1038/nature04341;
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF353516; AAK38887.1; -; mRNA.
InterPro; IPR001813; Ribosomal 60S.
InterPro; IPR001790; Ribosomal LiO.
InterPro; IPR001859; Ribosomal P2.
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 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-APR-2005, sequence version 1.
O-YMA-2006, entry version 5.
Hypothetical protein.
ORFNames=ANS13.2;
                                                               07-FEB-2006, entry version 21.
60S acidic ribosomal protein P0.
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QSB2U7;
                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [MRNA].
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                                                                                                                                                NCBI_TaxID=5802;
                                                                                                   Eimeria tenella
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RLAO EIMTE 0967\overline{Y}7;
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Gaps

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Query Match

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Query Match
       MRDDLINE=20196006; FUDNEd=10731132; DOL=10.1126/SCIENCE.287.5461.2185; Adama N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Holt R.A., Evans C.A., Galle R.P., Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., R.A standon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., R.A han K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G., R.Abrill J.F., Agdayani A., Ah H.-J., Andrews-Pfannkoch C., Baldwin D., R.A Ballew R.M., Basu A., Baxendale J., Barkstaroglu L., Beasley E.M., Ballew R.M., Basu A., Baxendale J., Barkstaroglu L., Beasley E.M., Ballew R.M., Basu A., Baxendale J., Barkstaroglu L., Beasley E.M., Ballew R.M., Butler H., Cadieu E., Center A., Chandra I., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Burtis K.C., Busam D.A., Butler H., Cadieu E., Davies P., Buttis K.C., Busam D.A., Daw I., Davies P., Burtis K.C., Busam D.A., Dang Z., Mays A.D., Dew I., Davies P., Acherry J.M., Cavley S., Dahlke C., Perrac C., Ferriera S., Fleischmann W., Brobin K.J., Evangeliste C., Ferrac C., Ferriera S., Fleischmann W., Glodek A., Gong F., Gorg N., Guran P., Harris M. C., Harvey D.A., Heiman T.J., Wei M.-H., I. Degwan C., Katchum K.A., Hostin D., Houston K.A., Heiman T.J., Wei M.-H., I. Degwan C., Katchum K.A., Jasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Atland B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., Marketei B., Morincesh T.C., Mortis J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Moshrefi J., Moshrefi J., Melson D.R., RA Nelson D.R., RA Nelson D.R., Pacier D.R., Nelson D.R., Pacier D.R., Nelson D.R., Pacier D.R., Nelson D.R., Pacier D.R., Nelson D.R., Rak Nelson D.R., Rak Nelson D.R., Rak Nelson D.R., Rak Nelson D.R., Nelson 
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                                                                                                                                                                                                                                                                                                                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
Purcell S., Harris S., Braus G.H., Draht O., Busch S., D'Enfert C., Bouchier C., Goldman G.H., Bell-Pedersen D., Griffiths-Jones S., Doonan J.H., Yu J., Vienken K., Pain A., Freitag M., Selker B.U., Archer D.B., Penalva M.A., Oakley B.R., Momany M., Tanaka T., Kumagai T., Asai K., Machida M., Nierman W.C., Denning D.W., Caddick M., Hynes M., Paoletti M., Fischer R., Miller B.L., Dyer P.S., Sachs M.S., Osmani S.A., Birren B.W.;
"Sequencing of Appergillus nidulans and comparative analysis with A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                    -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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01-MAY-2000, sequence version 1.
07-FEB-2006, entry version 20.
061-FEB-2006, e
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Pred. No. 72;
0; Mismatches 1; Indels
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SEQUENCE 399 AA; 43735 MW; 8D25BD74EFA8AD24 CRC64;
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                                                                                                                                                                                                                          fumigatus and A. oryzae.";
Nature 438:1105-1115(2005).
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les 12; Conservative
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Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Wariskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhou K., Zhu S., Zhu S., Zhu S., Rubin H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster.";
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MEDINE=22426055; PubMed=12537568;

MEDINE=22426055; PubMed=12537568;

MEDINE=22426055; PubMed=12537568;

MEDINE=22426055; PubMed=12537568;

Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,

Racial J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,

Patel J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,

Patel J.M., Park S., Myers E.W., Gibbs R.A., Rubin G.M.,

Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,

"Finishing a whole-genome shotgun: release 3 of the Drosophila
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MEDILNE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
Raminker J.S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
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MEDLINE=22426065; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Misra S., Crosby M.A., Mungall C.J., Millburn G.H., Prochnik S.E.,
Fradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.
Yu C., Rubin G.;
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
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Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
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Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
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Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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EMBL; BT022700; AAY55116.1; -; mRNA.
FlyBase; FBgn0029746; CG15465.
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90.7%; Score 49; DB 2; Length 422;

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                                                                                                                                                                                                                                                                                                                       07-FEB-2006, entry version 39.
Forkhead box protein D1 (Forkhead-related protein FKHL8) (Forkhead-related transcription factor 4) (FEBAC-4) (Brain factor-2) (HFH-BF-2) Name=Foxdl; Synonyms=Fkhl8, Freac4, Hfhbf2;
                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          developing vertebrate.

DEVELOPMENTAL STAGE: At B9.5 embryos, expressed in a limited region of the neuroepithelium and also in the temporal half of the primary optic cup and the optic stalk. At E10.5, seen in the hypothalamus, temporal half of the optic stalk, and temporal half of the optic stalk, and temporal regions of condensed mesenchyme of the head, and as neuroepithelial cells begin to differentiate and migrate outward
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the ventrotemporal area of the retina and aberrant morphogenesis of the optic chiasm. Their kidneys remain fused, have a disorganised ureteric tree and fail to ascend to a lumbar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=BALB/c; TISSUE=Embryo; MEDLINE=95114592; PubMed=7815060; MALIANE=95114592; PubMed=7815060; Mathin V., Tao M., Lai E.; Expression of winged helix genes, BF-1 and BF-2, define adjacent domains within the developing forebrain and retina."; J. Neurobiol. 25:1293-1309(1994).
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Herrera E., Marcus R., Li S., Williams S.E., Erskine L., Lai
Mason C.;
                            Indels
                                                                                                                                                                                                                                                                             15-JUL-1998, integrated into UniProtKB/Swiss-Prot
                                                                                                                                                                                                                                  456 AA.
    ed. No. 75;
Mismatches
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    Pred.
                                                                                                                                                                                                                                                                                                       sequence version 1.
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NCBI_TaxID=10090;
    92.3%;
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                                                                      1 AAFAAAAAAAA 13
                                                                                                                 AQFAAAAAAAA 77
                         12, Conservative
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Best Local Similarity
Matches 12, Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                 PROSITE; PS00657, FORK HEAD 1; 1.
PROSITE; PS00659; FORK HEAD 2; 1.
PROSITE; PS0039; FORK HEAD 3; 1.
Developmental protein; DNA-binding; Nuclear protein; Transcription; Transcription;
                                                                         R HSSP 063451 24DC.

R RANSFAC 13451 129-25.

R TRANSFAC 102293 - .

R Ensembl; ENSMTGG0000050789; Mus musculus.

R MG1; MG1:1347463; Foxdl.

R G5; G0:0003677; F:DNA binding; IDA.

G0; G0:0007411; P:axon guidance; IMP.

G0; G0:000357; P:regulation of transcription from RNA polyme. . .;

R InterPro; IPR011991; Wing_hlx_bNa_bd.

R InterPro; PR00156; FF Pcrk head; 1.

R PRINTS; PR00053; FOXEKHEAD.

R PRODOM; P0000425; FF Fork_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-OCT-2005, integrated into UniProtKB/TrEMBL.
11-OCT-2005, sequence version 1.
07-FEB-2006, entry version 6.
12 days embryo eyeball cDNA, RIKEN full-length enriched library, clone:D23000910 product:forkhead box D1, full insert sequence (16 days embryo head cDNA, RIKEN full-length enriched library, clone:4122401E09 product:forkhead box D1, full insert sequence).
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Fork-head.
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0; Mismatches
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Poly-Gly.
Poly-Arg.
Poly-Asp.
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Poly-Ala.
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                                                EMBL; L38607; AAC42042.1; -; mRNA.
HSSP; Q63245; 2HDC.
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NUCLEOTIDE SEQUENCE
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Q3UQW87
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[2] NUCLEOTIDE SEQUENCE.

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Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License NUCLEOTIDE SEQUENCE.

STRAIN=C57BL/6J; TISSUE=Eyeball, and Head;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Xonno H., Ishii Y., Nakamura S., Hazama M., Nishine T., Kashiwagi K., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Aokazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; STRAIN=C57BEL/63; TISSUE=Eyeball, and Head; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Nuramatsu M., Hayashizaki Y.; Nuramatsu M., Hayashizaki Y.; Shibata to brepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000). Birney E., Hayashizaki Y.; "Analysis of tunctional annotation of "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002). ATRAIN-CSTBL/6J; TISSUE-Eyeball, and Head;
Arakawa T. Carninci P., Fukuda S., Hashizume W., Hayashida K.,
Hori P., Idad J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
Shibata K., Shiraki T., Tagami M., Fagami Y., Waki K., Watahiki A.,
Muramatsu M., Hayashizaki Y.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
-:- SUBCELLULAR LOCATION: Nuclear (By similarity). "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001). Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander B.S., Rogers J., Sato Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., STRAIN=CS7BL/67; TISSUE=Eyeball, and Head; MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500; EMBL; AK142034; BAE24920.1; -; mRNA. EMBL; AK132390; BAE21140.1; -; mRNA. NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE. [5] NUCLEOTIDE SEQUENCE Hayashizaki Y.; 

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GO; GO:0003677; F:DNA binding; IDA.
GO; GO:0007411; P:axon guidance; IMP.
GO; GO:0005357; P:regulation of transcription from RNA polyme. . .; IDA.
GO; GO:0006357; P:regulation of transcription from RNA polyme. . .; IDA.
InterPro; IPR00176; TF Fork head.
InterPro; IPR00201; Tubulin.
Pfam; PF00256; Fork head; 1.
PRINTS; PR00563; FORK head; 1.
PRODOM; PD000425; TF Fork head; 1.
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                                                                                                   SWART; SW00339; FH; 1.
PROSITE; PS00657; FORK HEAD 1; 1.
PROSITE; PS00658; FORK_HEAD_2; 1.
PROSITE; PS50039; FORK HEAD_3; 1.
PROSITE; PS00227; TUBULIN; UNKNOWN 1.
DNA-binding; Nuclear protein; Transcription regulation.
SECUENCE 456 AA; 45371 MW; 3153172991DC99A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-55045392; PubMed-1957066;
Pierrou S., Hellqvist M., Samuelsson L., Enerbaeck S., Carlsson P.;
"Cloning and characterization of seven human forkhead proteins:
binding site specificity and DNA bending.";
-1. FUNCTION: Transcription factor required for formation of
positional identity in the developing retina, regionalization of
the optic chiasm and morphogenesis of the kidney (By similarity).
-1. SUBCELLULAR LOCATION: Nucleus.
-1. SIMILARITY: Contains 1 fork-head DNA-binding domain.
                                                                                                                                                                                                                                                                                                                                               FOXD1 HUMAN STANDARD, PRT, 465 AA. 016676; Q12949; OLNOV-1997, integrated into UniProtXB/Swiss-Prot. 01-NOV-1997, sequence version 1. 01-NOV-1997, sequence version 1. 00-FBB-2006, entry version 3. Forkhead box protein D1 (Forkhead-related protein FKHL8) (Forkhead-related transcription factor 4) (FRBAC-4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLECTIDE SEQUENCE [GENOMIC DNA / MENA].
MEDLINE=96355467; PubMed=8702877; DOI=10.1074/jbc.271.35.21094;
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                                                                                                                                                                                                          DB 2; Length 456;
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EMBL; U59832; AAC50661.1; -; mRNA.
EMBL; U13222; AAA92039.1; -; mRNA.
PIR; G02738; G02738.
PIR; S51627; S51627.
HSSP; Q63248; 21627.
HSSP; Q63646; 124-220.
TRANSFAC; T02472; -.
                                                                                                                                                                                                               92.3%; Preq. w...
                                                                                                                                                                                                         90.7%; Score 49; 92.3%; Pred. No. 8
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                                                                                                                                                                                                                                                                                     290 ALFAAAAAAAA 302
                                                                                                                                                                                            Query Match
Best Local Similarity 92.3.
Best Local 2, Conservative
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HGNC; HGNC:3802; FOXD1
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MIM; 601091; gene.

GO: GO: 0003700; F: transcription factor activity; TAS.

InterPro; IPROU166; TF Pork head.
InterPro; IPRO11991; Wing hlx_DNA_bd.
Pfam; PF00250; Fork head; 1.
PRINTS; PR00653; FORKHEAD.
ProDom; PD000425; TF Fork head; 1.
SMART; SM00339; FORK HEAD 1; 1.
PROSITE; PS00657; FORK HEAD 1; 1.
PROSITE; PS00659; FORK HEAD 2; 1.
PROSITE; PS00659; FORK HEAD 3; 1.
PROSITE; PS00039; FORK HEAD 3; 1.
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Bukarych; Viridiplantea; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
Enrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jy-Ala.
D3E7854909CCBFAE CRC64;
                                                                                                                                                                                                                           Forkhead box protein D1.
/FTId=PRO 0000091811.
Fork-head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 49; DB 1;
Pred. No. 81;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004, integrated into UniProtKB/TrEMBL.
05-JUL-2004, sequence version 1.
07-FBB-2006, entry version 14.
Zinc finger protein family-like.
Name=P0606H11.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AP004762; BAD10011.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                       Poly-Gly.
Poly-Arg.
Poly-Glu.
Poly-Asp.
Poly-Asp.
Poly-Gly.
Poly-Ala.
Poly-Ala.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Poly-Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QGZ8T9 ORYSA PRELIMINARY; PRT;
Q6Z8T9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46140 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290 ALFAAAAAAAA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AAFAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12; Conservative
                                                                                                                                                                                                                                                                    215
34
43
43
72
76
1113
234
256
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26
26
39
52
69
73
73
73
252
253
259
309
315
465 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=39947;
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SERBERRE

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Submitted
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RATAIN-221;

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Ustilaginomycetidae, Ustilaginales, Ustilaginaceae, Ustilago
                                                                                                                                                                                                                                 Score 48; DB 2; Length 167;
Pred. No. 50;
0; Mismatches 1; Indels
InterPro; IPR011016; RINGv.
InterPro; IPR001841; Znf RING.
Pfam; PF00097; Talf4; Znf4; 1.
SMART; SM00184; RING; 1.
SMART; SM00744; RINGv; 1.
PROSITE; PS50089; Ze RING2; 1.
Metal-binding; Nuclear protein; Zinc; Zinc-finger.
SEQUENCE 167 AA; 17664 MW; 4729ACE00A901AE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUL-2005, integrated into UniProtKB/TrEMBL.
19-JUL-2005, sequence version 1.
07-FEB-2006, entry version 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q4PE18 USTWA PRELIMINARY; PRT; 361 AA.
Q4PE18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zimmer A., Zody M., Lander E.S.;
"The genome sequence of Ustilago maydis.";
                                                                                                                                                                                                                                      88.9%;
                                                                                                                                                                                                                                                                                                                                           1 AAFAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                           S6 AAIAAAAAAAA 68
                                                                                                                                                                                                                                                                 Local Similarity 92.3
nes 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
ORFNames=UM01475.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ustilago maydis 521
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                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                         Matches
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O40 PELS UST

10 040 PELS

O40 PELS

O40 PELS

O50 CONTROL

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                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae, Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
nitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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--- FUNCTION: May be involved in transcriptional regulation.
--- SUBCELLIULAR LOCATION: NUCleus (Potential).
--- SIMILARITY: Contains 1 BTB (POZ) domain.
--- SIMILARITY: Contains 2 C2H2-type zinc fingers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 48; DB 2; Length 361;
Pred. No. 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AACP01000053; EAK82242.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 361 AA; 39615 MW; 038F774408202041 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-APR-2004, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-MAR-2006, entry version 22.
Zinc finger and BTB domain-containing protein 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              484 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ensembl; ENSMUSGO0000048485; Mus musculus.
MGI; MGI:2387181; Zbtb8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; BC023839; AAH23839.1; -;
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InterPro; IPR013069; BTB_POZ.
InterPro; IPR007087; Znf_C2H2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.9%;
92.3%;
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hes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                          preliminary data.
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Q8CIIO;
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Rayalw-C57BL/6J; TISSUE=Cerebellum, and Head;

Rayalw-C57BL/6J; TISSUE=Cerebellum, S., Gough J., Frith M.C., Maeda N., Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Anjer C., Baraic C., Rodzius R., Shimokawa K., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Aidinis V., Allen J.B.,

Ambesi-Impiombato R., Apweiler R., Aturaliya R.N., Bailey T.L.,

Ambesi-Impiombato R., Baisel K.W., Bersano T., Bono H., Chalk A.M.,

Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,

Crowe M.L., Dalla B., Dalrymple B.P., de Bono B., Della Gatta G.,

Al Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,

Al Bernardo D., Down T., Engstrom P., Futaki S., Gariboldi M.,

Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,

Challin D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,

Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelbo J., Kitamura H.,

Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-OCT-2005, integrated into UniProtkB/TrEMBL.
11-OCT-2005, sequence version 1.
21-FBB-2006, entry version 7.
16 days embryo head cDNA, RIKEN full-length enriched library, clone:C130068L16 product:Zinc finger and BTB domain containing 8, full insert sequence (0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C130068H07 product:Zinc finger and BTB domain containing 8, full insert sequence) (14, 17 days embryo head cDNA, RIKEN full-length enriched library, clone:3222401B20 product:Zinc finger and BTB domain finger and BTB domain containing 8, full insert sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CS7BL/6J; TISSUE=Cerebellum, and Head;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                        SMART; SM00355; 2412.
PROSITE; PS50097; BTB; 1.
PROSITE; PS500157; ZINC_FINGER_C2H2_1; 1.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.
DNA-binding; Metal-binding; Nuclear protein; Repeat; Transcription; Transcription; Zinc; Zinc-finger.
Transcription regulation; Zinc; Zinc-finger and BTB domain-containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 48; DB 1; Length 484;
Pred. No. 1.1e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                    24 92 BTB. —
331 353 C2H2-type 1.
359 342 C2H2-type 2.
132 149 Ala-rich.
484 AA; S3387 MW; B4FP082555BOCAlA CRC64;
                                                                                                                                                                                                                                                      protein 8.
/Frid=PRO_0000047722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                        ProDom; PD000003; Znf C2H2; 1.
SMART; SM00225; BTB; I.
SMART; SM00355; ZnF C2H2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                          88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 AAMAAAAAAAAA 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Conservative
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Q3US18 MOUSE
ID Q3US18_MOUSE F
AC Q3US18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                      DOMAIN
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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Muscochin I.V. Jarsan I.F. Jeasan I.F. Jeasance D. Jigovich I. V. Jarsan I.F. Jeasan I.F.
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Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Ruchl P., Lewis S., MarGuo Y., Nixaido T., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake U., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustinoich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakanco N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wanshell R., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUE=Cerebellum, and Head; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length CDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K., Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S., Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N., Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D., Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A., Muramatsu M., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K., Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K., Hori P., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N., Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D., Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A., Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Miramateu M., Inoue Y., Kira A., Hayashizaki Y.; Rikki integrated sequence analysis (RISA) system-384-format
                                                                                                                                                                                                                                                                                                                                Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).
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EMBL; AK163930; BAE37541.1; -; mRNA.
EMBL; AK132152; BAE20999.1; -; mRNA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005676; F:metal ion binding; IEA.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0008215; F:procein binding; IEA.
GO; GO:0008210; F:zinc ion binding; IEA.
INTERPRO; IPR001010; BTB.
INTERPRO; IPR013069; BTB_POZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J; TISSUE=Cerebellum;
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RAMEREZOTIDE SCUENCE.

RAM MULLINE-20196006; PubMed-10731132; DDI=10.1126/science.287.5461.2185;

RAM Annantides P.G., Scherer S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RAM Annantides P.G., Scherer S.E., it P.W., Brokkins R.A., Galle R.F.,

Ray George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.M.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RAM R.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RAM AM K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RAM AM K.H., Basu A. Baxendle J., Bayraktaroglu L., Basaley E.M.,

RADILEW R.W., Basu P.W., Barman B.P., Bhandari D., Boltahkov S.,

RA Berson K.Y., Benos P.V., Berman B.P., Bhandari D., Boltahkov S.,

RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Caaley S., Dahlke C., Davenport L.B., Davies P.,

RA Doublin K.J., Paragelista C.C., Ferraz C., Perriars P., Diet S.M.,

RA Cherry J.M., Sanagelista C.C., Ferraz C., Perriars S., Pleischmann W.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

Harris N.L., Harvey D.A., Henhan T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

Kammel B.E., Kodiret C.D., Kraft C., Kravitz S., Kallp D., Lai Z.,

Kimmel B.E., Kodiret C.D., Kraft C., Kravitz S., Kallp D., Lai Z.,

Kimmel B.E., Kodiret C.D., Kraft C., Mortis J., Moshrefi A.,

Mollson D.R., Nelson K.A., Howland T.C., Mortis J., Moshrefi A.,

RA Balazolo M., Pithman G.S., Pan M. Weiten B., Mollson D.K.,

RA Rainer K.W., Pandelling N.V., Mobarry C., Morris J., Was R., Resee M.G.,

RA Rainer K., Remington K.A., Wilson K., Bunders B., Waller K., Santh T.,

RA Rainer E., Spraddling A.C., Staplecom M., Strong K., Waller E., Shen H.,

RA Spier E., Siden-Kamer D.A., Weiter E., Wang A.H., Wang X.,

RA Mund S.M., Welson D.A., Weiter E., Wang S., Yang X., Zhan M., Zhang G., Zhan M., Zhang G., Zhan M., Zhang G., Zhan K., Zhang C., Zhan K., 
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Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa, Arthropoda, Hexapoda; Insecta; Pterygota;
Neoptera; Endoptera; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                              Probom; PP000003; Znf CZH2; 1.
SMART; SM00225; BTB; 1.
SMART; SM00355; ZnF CZH2; 2.
SMART; SS0097; BTB; 1.
PROSITE; PS00097; BTB; 1.
PROSITE; PS00028; ZINC FINGER CZH2 1; 1.
PROSITE; PS0157; ZINC FINGER CZH2 2; 2.
Metal-binding; Nuclear protein; Repeat; Zinc; Zinc-finger.
                                                                                                                                                                                                                                                                                        Length 484;
                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                       484 AA; 53414 MW; ACABID5402A2E7F4 CRC64;
                                                                                                                                                                                                                                                                                      88.9%; Score 48; DB 2; L 92.3%; Pred. No. 1.1e+02; Live 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2002, sequence version 2. 21-FEB-2006, entry version 39.
InterPro; IPR007087; Znf_C2H2.
Pfam; PF00651; BTB; 1.
Pfam; PF00096; zf-C2H2; 2.
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                                                                  MEDLINE=22426065; PubMed=12537568; Calliker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise B., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinishing a Whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence.";
                                                                                                                                                                                                                                          MEDLINE=22426070; PubMed=12537573; Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Calniker S.E.;

"The transposable elements of the Drosophila melanogaster euchromatin: a genomics perspective.",
Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
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MEDLINE=224456069; PubMed=12537572;
MEDLINE=224456069; PubMed=12537572;
MISTAR S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pacleb J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stapleton M., Carlson J., Chavez C., Frise E., George R., Park S., Wan K., Yu C., Celniker S.; Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases. -! SUBCELLULAR LOCATION: Nuclear (By similarity). -!- SIMILARITY: Contains 2 LIM zinc-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
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EMBL; BT003467; AAO39470.1; -; mRNA.
HSSP; P50480; 1BW5.
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InterPro; IPR012287; Homeodomain-rel.
InterPro; IPR017107; LIM_homeo.
InterPro; IPR001781; LIM_Zn bd.
InterPro; IPR001781; LIM_Zn bd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hordeum vulgare var. distichum (Two-rowed barley).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP clade,
Pooideae, Triticeae, Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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GO; GO:0008883; F:glutamyl-tRNA reductase activity; IEA.
GO; GO:00046883; F:glutamyl-tRNA reductase activity; IEA.
GO; GO:000464; F:shikimate 5-dehydrogenase activity; IEA.
GO; GO:0006779; P:porphyrin biosynthesis; IEA.
InterPro; IPR001343; GlutR.
InterPro; IPR00151; Shikimate_DH.
Pfam; PF05201; GlutR N; 1.
Pfam; PF05201; GlutR N; 1.
Pfam; PF05201; GlutR N; 1.
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R Pfam; PF00412; LIM; 2.

R PRINTS; PR00024; HOMBOBOX; 1.

R PCDOOM; PD000014; LIM; 2.

R SWART; SM00139; HOX; 1.

R SWART; SM00139; HOX; 1.

R PROSITE; PS00027; HOMEOBOX_1; 1.

R PROSITE; PS00071; HOMEOBOX_2; 1.

R PROSITE; PS00478; LIM_DOMAIN_1; 2.

R PROSITE; PS01359; ZF_PHD 1; UNKNOWN 1.

R PROSITE; PS01359; ZF_PHD 1; UNKNOWN 1.

R PROSITE; PS01359; ZF_PHD 1; UNKNOWN 1.

R PROSITE; PS01359; ZF_PHD 1; TRANSCIPLION; LIM domain; Metal-binding; Nouclear protein; Homeobox; LIM domain; Metal-binding; Nouclear protein; Hanscription; Metal-binding; Nouclear protein; Transcription; Zinc; Transcription; Days 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                88.9%; Score 48; DB 2; Length 640.
92.3%; Pred. No. 1.46+02;
                                                                                                                                                                                                                                                                                                                                                                                            67760 MW; A1A10F826018C98E CRC64;
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01-MAR-2001, sequence version 1.
01-FEB-2006, entry version 17.
Glutamyl-tRNA reductase (Fragment).
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HSSP; Q9UXR8; 1GPJ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.

Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,

Nakajima Y., Mizuno T., Morinaga M., Ota T., Suzuki Y., Obayashi M.,

Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.,

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia; Butheria, Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea, Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      378 AA; 42533 MW; 1E7E5C741ACF6BA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AK000115; BAA91078.1; -; mRNA.
Ensembl; ENGG0000091542; Homo sapiens.
GO; GO:0005506; F:iron ion binding; IEA.
GO:0016491; F:oxidoreductase activity; IEA.
InterPro; IPR065123; 20G-FeII_Oase.
Pfam; PF03171; 20G-FeII_Oxy; I.
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                                                                                                                                                                                                                                       01-CCT-2000, integrated into UniProtKB/TrEMBL. 01-OCT-2000, sequence version 1. 07-FRB-2006, entry version 18. Hypothetical protein FLJ20308. Homo sapiens (Human).
                                                                                                                                                                         378 AA.
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                                                                                                                                                                    Q9NXD6_HUMAN PRELIMINARY;
Q9NXD6;
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12; Conservative
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080050 MOUSE

080050 MOUSE

DT 01-JUN-20

MARTIN-11

RP MARTIN-12

RA NUCLEOTIT

RA ALTSCHUL

RA REMARS S.P.

RA BOGAR S.P.

RA BOGAR S.P.

RA BOGAR S.P.

RA RICHARGA

RA HICHARGA

RA HICHARGA
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Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Musinae; Mus.
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01-MAR-2003, sequence version 1.
01-MAR-2003, sequence version 1.
01-FBR-2006, entry version 2.
0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone: B130207K11 product: hypothetical Alanine-rich region/Type I antifreeze protein/20G-Fe(II) oxygenase superfamily containing protein, full insert sequence (2 cells egg cDNA, RIKEN full-length enriched library, clone: B202011005 product: Hypothetical alanine-rich region/type I antifreeze protein/20G-Fe, full insert sequence) (Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; TISSUE-Egg, and Eyeball;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Aldinis V., Allen J.E., Ambesi-Impiombato A., Apweller R., Aturaliya R.N., Bailey T.L., Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; BC052076; AAH52076.1; -; mRNA.
Ensembl; ENSMUSG0000042650; Mus musculus.
MG1:2144489; AW050020.
GO; GO:000560; Firon ion binding; IEA.
GO; GO:0016491; Ficxidoreductase activity; IEA.
InterPro; IRR065123; 20G-FeII Oase.
Pfam; PP03171; 20G-FeII Oay; I.
Hypothetical protein; Iron; Oxidoreductase.
SEQUENCE 395 AA; 44410 MW; 4CE25B4FB5B04DEB CRC64;
                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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PubMed=16141072; DOI=10.1126/science.1112014;
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"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QBEKCI MOUSE PRELIMINARY; PRT;
QBEKCI;
                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6; TISSUE=Mouse;
NIH MGC Project;
                                                                                                                                                                                                                                          and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AAFAAAAAAAA 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12; Conservative
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ture 420:563-573(2002).

RC STRAING-CSTBL/64; TISSUE-Egg, and Eyeball;

RC STRAING-CSTBL/64; TISSUE-Egg, and Eyeball;

RA MAZAXI Y. FULUND M. Kasukawa T., Adachi J., Bono H.; Kondo S.,

RA ALAZAXI Y., FULUND M., Kasukawa T., Adachi J., Bono H.; Kondo S.,

RA Mikaido I., Obato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Jadarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Schriml L.M., Kanapin A., Matcuda H., Batallov S., Beisel K.W.,

Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

RA Balla E., Dragani T.A., Fletcher C.F., Forrest A., Gough J.,

RA Gasterland T.A., Fletcher C.F., Forrest A., Gough J.,

RA Malla E., Nawaji H., Kawasawa Y., Kadiirerki R.A., Gough J.,

RA Majott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Magsahima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RA RASASHA T., Numata R., Pontiu J.U., Di D., Reid J., Rimg B.Z., Rimgwald M.,

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Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Rimgwald M.,

Randelin A., Schneider C., Semple C.A., Serou M., Shimada K.,

Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D. Tomita M.

RA Wilming L.G., Wymahaw-Borris A., Yanaqisawa M., Yang I., Yang L.,

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RT Go, 770 full-length cDNAs."; Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,

Growe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,

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RA Jakt M., Kanapin A., Katch M., Kawasawa Y., Kalso J., Kitamura H.,

RA Jakt M., Kanapin A., Katch M., Kawasawa Y., Kalso J., Kitamura H.,

RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,

RA Kitano H., Molliam S., Madan Babu M., Madera M., Marchionni L.,

RA Mottagui-Tabar S., Wilder N., Nakano N., Nakauchi H., Ng P.,

RA Mottagui-Tabar S., Wulder N., Nakano N., Nakauchi H., Ng P.,

RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,

RA Rost B., Kuan Y., Salzberg S.L., Sandelin A., Schneider C.,

RA Schonbach C., Sekiguchi K., Sandelin A., Schneider C.,

RA Schonbach C., Sekiguchi K., Sandelin A., Schneider C.,

RA Schonbach C., Sekiguchi K., Sugmile C.A., Seno S., Sessa L., Taknaka Y.,

RA Schonbach C., Sekiguchi K., Sugmile C.A., Seno S., Sessa L.,

Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,

RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,

RA Tammoja K., Tasasdale R.D., Liuu E.T., Pagner J., Teichmann S.A.,

RA Tammoid S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,

RA Mahlestedt C., Mattick Y. Suzuki M., Aoki J., Arakawa T.,

RA Manishima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,

RA Rawashima T., Kojima M., Plessy C., Shibata K., Shiraki T., Suzuki S.,

RA Havashizaki Y.,

Ra Ha STRAIN=CS7BL/63; TISSUB=Egg, and Byeball;
PubMed=16141073; DOI=10.1126/science.1112009;
RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;
"Antisense Transcription in the Mammalian Transcriptome."; "The transcriptional landscape of the mammalian genome."; Science 309:1559-1563(2005). Science 309:1564-1566(2005). NUCLEOTIDE SEQUENCE NUCLEOTIDE SEQUENCE Tagami M., Waki Hayashizaki Y.; 

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Carboline Section 10 (1987) and Eyeball;

KRAIN=CSTRL/65, TISSUE=Egg, and Eyeball;

KRAIN=CSTRL/65, Shibada R., Shibata K., Yoshino M., Itoh M., Ishii Y.,

KRAWAI J., Shinagawa A., Shibata K., Xohino M., Adachi J., Fukuda S.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

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Kadota K., Matsuda H.A., Ashburnar M., Batalov S., Casivan T.,

Radota K., Matsuda H.A., Ashburnar M., Eatalov S., Casavant T.,

Richl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

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Bronstein M.J., Bult C., Fletcher C., Fulita M., Mombaerts P.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Lyons P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Wanshaw-Bonis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

M. Wynshaw-Bonis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
STRAIN=CSTBL/GG; TISSUE=Egg, and Eyeball;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Whomalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA ibraries for rapid discovery of new genes:"; Genome Res. 10:1617-1630(2000).
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STRAIN=C57BL/6J; TISSUB=Egg;
Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
Arakawa T., Carninci P., Fukuda S., Hashizume W., Kanagawa S.,
Hori F., Iida J., Imamura K., Imotani K., Itch M., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
Muramatsu M., Hayashizaki Y.,
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M., Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Rashiwagi K., Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa K., Tanaka T., Ohara E., Watshiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rike integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             annotation of a full-length mouse cDNA collection.";
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STRAIN=C57BL/6J; TISSUE=Eyeball;
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                                                NUCLEOTIDE SEQUENCE
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NATIONAL SEQUENTS:

NATIONAL SEQUENTS:

CARTINGT P., Kasukawa T., Katayama S., Goudh J., Frith M.C., Maeda N., Carningi P., Kasukawa T., Katayama S., Goudh J., Frith M.C., Maeda N., Carningi P., Kasukawa T., Katayama S., Goudh J., Frith M.C., Maeda N., Bajic V.B., Brenner S.B., Batalov S., Forrest A.R., Zavolan M., Bajic V.B., Brenner S.B., Aldinis V., Allen J.E., Davis M.J., Wilming L.G., Aidinis V., Allen J.E., Bono H., Chalk A.M., Ambesi-Impiombato A., Apweller R., Aturaliya R.N., Banisy M., Barter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., Ambesi-Impiombato A., Apweller R., Aturaliya R.D., Della Gatta G., Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R., Chou K.P., Dalla B., Dallarymple B.P., de Bono B., Della Gatta G., A. Hiller C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M., Retcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M., Goorgil-Hemming P., Gligeras T.R., Hensch T.K., Hirokawa T., Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T., Jak M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Althan S.P., Kruger A., Kummerfeld S., Krishnan S.P., Kruger A., Kummerfeld S., Kutochkin I.W., Lareau L.F., Lazarevic D., Lipovich L., Liu J., S., McWilliam S., Madan Babu M., Madera M., Marchlonni L.,
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                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CS7BL/6J; TISSUE=In vitro fertilized eggs;
MEDLINE=99279253; Pubmed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-0CT-2005, integrated into UniProtKB/TYEMBL.
11-0CT-2005, sequence version 1.
07-MAR-2006, entry version 6.
In vitro fertilized eggs CDNA, RIKEN full-length enriched library, clone: 7420402E17 product: Hypothetical alanine-rich region/type I antifreeze_protein/20G-Fe, full insert sequence.
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                                                                                                                                                                                                                                                                                         87.0%; Score 47; DB 2; Length 395; 92.3%; Pred. No. 1.3e+02; ive 0; Mismatches 1; Indels
                               Tracey A.;
Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                     GO; GO:0015566; Filton ion binding; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
InterPro; IPR005121; 20G-FeII Oase.
Ppfam; PF03171; 20G-FeII Oay; I.
Hypothetical protein; Iron; Oxidoreductase.
SEQUENCE 395 AA; 44411 MW; 2822BF4BFFFEETEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carninci P., Hayashizaki Y.,
"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
                                                                                                             EMBL; AKO53695; BAC35478.1; -; mRNA.
EMBL; AK163294; BAB37281.1; -; mRNA.
EMBL; AL596386; CA135332.1; -; Genomic_DNA.
Ensembl; ENSMUSG00000042650; Mus musculus.
MGI; MGI:2144489; AM050020
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Matches 12, Conservative
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Q3TSG4_MOU
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Merenda H., Merenda N., Wishikano N. Makachi H. Mayabe S., Morris K.,
Milason R. Mishigano B. Mishikano N. Makachi H. Mayabe S., Morris K.,
Milason R. Mishigano B. Mishikano N. Makachi H. Marenda M. Milason R. Mishikano B. Maris C. Detaro O.,
Osaaaki Y., Orlando V., Fange S. C., Pavasa W.J., Pavesi G., Pecole G.,
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Shibasi S., Mann Y., Salzberg S. L., Sandolla N., Schhedder C.,
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A. Osaaki W., Washi K., Wataliki M., Osaaki J., Sandi D., Wannishi M.,
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A. Mahlested C., Muttick J., Shumer A., Rai C., Sandi D., Shumi Y.,
A. Mahlested C., Muttick J., Shumer A., Rai C., Sandi D., Wannishi M.,
A. Mahlested C., Muttick J., Watali M., A., Osamura-Obo Y., Suruki H., Wannishi Y.,
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                 STRAIN=CS7BL/6J; TISSUE=Eyeball;
MEDLINE=99279213; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninoi P., Hayashizaki Y.;
Hidp-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
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01-MAR-2003, sequence version 1.
07-MAR-2006, entry version 24.
0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:B103101021 product:hypothetical Alanine-rich region/Type antifreeze protein/20G-Fell) oxygenase superfamily containing protein, full insert sequence.
                                                                                                                                                Mus musculus (Mouse).
                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE
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                                                                                                                             Name=AW050020;
       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6J; TISSUE=In vitro fertilized eggs;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
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Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection.";
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395 AA; 44494 MW; 1F3B93E0E71AF27D CRC64;
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GO; GO:0005506; F:iron ion binding; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
InterPro; IPR005123; 20G-FeII Oase.
Pfam; PF03171; 20G-FeII Oxy; I.
Hypotherical protein.
SEQUENCE 395 AA; 44494 MW; IF3B93E0E71AF27D
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les 12; Conserv
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STRAIN=C57BL/67; TISSUB=Eyeball; PubMed=16141073; DOI=10.1126/science.1112009; RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium; "Antisense Transcription in the Mammalian Transcriptome."; Science 309:1564-1566(2005).
                                                                                                                                                                                                                                                                                                                            transcriptional landscape of the mammalian genome.";
                                                                                                                                                                                                                                                                                                                                    Science 309:1559-1563(2005).
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NUCLEOTIDE SEQUENCE

395 AA.

PRT;

PRELIMINARY;

QBBKB9 MOUSE Q8BKB9;

MOUSE

RESULT 20 O8BKB9 N ID O8E AC O8E

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Gaps

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1, Indels

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Conservative

Matches

MEDINIE=22354683; Pubmed=1246681; DOI=10.1038/nature01266;
A Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Konosawa H.,
A Nakaido I., Osato N., Salto R., Suzuki H., Yamanaka I., Kiyosawa H.,
A Yagi K. Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
B Badarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
B Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
B Balake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
R Balake J.A., Bradt D., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
Konagaya A., Kurochkin L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pescole G.,
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Readelin A., Schneider C., Semple C.A., Serou M., Shimada K.,
Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang I.,
RA Hirozane-Kishikawa T., Kamo H., Nakamura M., Sakazume N., Sakazume N., Sakazume W., Imotani K., Itoh M., Kagawa I.,
RA Hirozane-Kishikawa T., Kama J., Aizawa K., Arakawa T., Fukuda S.,
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RT Go,770 full-length conne. Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Itoh M., Atakawa T., Hara A., Shibata K., Yoshino M., Itoh S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito K., Schoenbach J., Mondbactts P., All D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Iyons P., Marchionni L., Mashima J., Mazarcelli J., Mondbactts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Saito K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Wanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Andashizaki V., STRAIN=C57BL/6J; IISSUE=Eyeball; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000). MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishiine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Hayashizaki Y.;
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Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License NOCEDIA STATESTREEN STATESTRE STATESTREEN STRAND ST Kaestner K.H., Schuetz G., Monaghan A.P.;
"Expression of the winged helix genes fkh-4 and fkh-5 defines domains in the central nervous system.";
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Murinae; Mus. Gaps MEDLINE=97014266; PubMed=8861101; DOI=10.1016/0925-4773(96)00507-2; S., Kawai J., ö Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kaw Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000). Length 395; 1; Indels al protein. 395 AA; 44415 MW; 6D22C26B1A99EDA8 CRC64; 01-NOV-1997, integrated into UniProtKB/Swiss-Prot. 01-NOV-1997, sequence version 1. 07-FEB-2006, entry version 31. Porkhead box protein B2 (Transcription factor FKH-4) 87.0%; Score 47; DB 2; I 92.3%; Pred. No. 1.3e+02; Ensembl; ENSAUSGO0000042650; Mus musculus. MGI; MGI:2144489; AW050020. GO; GO:0005506; F:iron ion binding; IEA. GO; GO:0016491; F:oxidoreductase activity; IEA. 428 AA. 0; Mismatches EMBL; AK053700; BAC35481.1; -; mRNA. PRT; NUCLEOTIDE SEQUENCE OF 4-114. 92.3%; Forkhead box protein B2 (T) Name=Foxb2; Synonyms=Fkh4; 1 AAFAAAAAAAAA 13 36 AAVAAAAAAAA 48 12; Conservative STANDARD; Mus musculus (Mouse). NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE. Sest Local Similarity Hypothetical SEQUENCE 35 FOXB2 MOUSE Query Match MOUSE Q6473<u>3</u> Matches RESULT FOXB2 M ઠે 셤

Kaestner K.H., Lee K.H., Schloendorff J., Hiemisch H., Monaghan A.P.,

MEDLINE=93361500; PubMed=7689224;

STRAIN=129

"Six members of the mouse forkhead gene family are developmentally regulated.";

Proc. Natl. Acad. Sci. U.S.A. 90:7628-7631(1993).
-!- SUBCELLULAR LOCATION: Nucleus.
-!- DEVELOPMENTAL STAGE: Expressed during embryogenesis.

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Qeglgi_xentr
Qeglgi;
                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                        RESULT 23
Q6GLG1_XENTR
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 SERBERE
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                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                MGI: 1347468; FOXD2.
InterPro; IPR01766; TF Fork head.
InterPro; IPR011991; Wing llx_DNA_bd.
Pfam; PF001250; Fork head; 1.
PRINTS; PR00053; FORKHEAD.
ProDom; P0000425; TF Fork head; 1.
SMART; SM00339; FORK HEAD 1; 1.
PROSITE; PS00659; FORK HEAD 1; 1.
PROSITE; PS00659; FORK HEAD 2; 1.
PROSITE; PS0039; FORK HEAD 2; 1.
DRASITE; PS0039; FORK HEAD 2; 1.
CRAIN: 1 428 FORK HEAD 3; TANSCRIPTION regulation.
CHAIN: 1 428 FORK Head box protein B2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AL353637; CAH70683.1; -; Genomic_DNA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:000335; P:regulation of transcription, DNA-dependent; IEA.
GO; GO:0006355; P:transcription; IEA.
InterPro; IPR011991; Wing_hlx_DNA_bd.
InterPro; IPR011991; Wing_hlx_DNA_bd.
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0
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Pred. No. 1.4e+02;
); Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 1 fork-head DNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB8A8EFD1E94AB10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           Forkhead box protein B2./FTId=PRO_000091805.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-DEC-2004, integrated into UniProtKB/TrEMBL.
07-DEC-2004, sequence version 1.
07-FEB-2006, entry version 12.
OTTHOMRO00000021510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                432 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                  Ensembl; ENSMUSG0000056829; Mus musculus.
                                                                                        EMBL; X92591; CAA63335.1; -; mRNA.
EMBL; X71942; CAA50744.1; -; Genomic_DNA.
PIR; D47746; D47746.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Poly-His.
Poly-His.
Poly-Pro.
Poly-Ala.
Poly-Ala.
Poly-Ala.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45170 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QSVYVO HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORFNames=RP11-159H20.4-001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 92.3.,
Local 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218 AAVAAAAAAAAA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AAFAAAAAAAA 13
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153
162
172
172
231
231
330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163
217
249
249
321
396
428 AA;
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                                                                                                                                              HSSP; 063245; 2HDC.
TRANSFAC; T02442; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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Submitted (MA)
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COMPBIAS
COMPBIAS
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COMPBIAS
COMPBIAS
SEQUENCE
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QSVYVO HUM
DD QSVYVO
AC QSVYVO
AC QSVYVO
DT 07-DE
DT 07-DE
DG OTTHU
GN HOMO
OC BUKAT
OC BUKAT
OC BUKAT
OC HOMO
OC NOBI
RN HULLI
RA KIMDI
RL SUDMI
CC CC COPY
CC CC COPY
CC CC COPY
CC C COPY
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CC C C C C C C C C C C C C C C C 
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MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

A trausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A trausher R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A trachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A trachul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

B Diatchenko L., Marushia K., Farmer A.A., Rubin G.M., Hong L.,

B Lapleton M.J., Usdin T.B., Ponaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha S.S., Loquellann A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J.S., Schmutz J., Myers R.M.,

Rutterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Romerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Russers A. Schein J.E., Jones S.J.M., Marra M.A.;

Russers A. Schein J.E., Jones S.J.M., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                          ProDom; PUDUOUS, FH; I. SMART; SMR0339; FH; I. PRORK HEAD 1; 1. PROSITE; PS00659; FORK HEAD 1; 1. PROSITE; PS00658; FORK HEAD 2; UNKNOWN 1. PROSITE; PS0039; FORK HEAD 3; 1. DNA-binding; Nuclear protein; Transcription; Transcription regulation. DNA-binding; Nuclear protein; Transcription; PA32 AA; 45581 MW; 9A832ACD99765EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Ensembl; ENSXETG0000021355; Xenopus tropicalis.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR00910; HMG_12_box.
Pfam; PF00505; HMG_box; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi, Amphibia; Batrachia, Anura, Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Silurana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JUL-2004, sequence version 1.
07-FEB-2006, entry version 16.
07-FEB-2006, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1.
Name-smarcel-proy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Embryo;
Klein S., Gerhard D.S.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                     Score 47; DB 2; I
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUL-2004, integrated into UniProtKB/TrEMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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Pfam; PF00250; Fork head; 1.
PRINTS; PR00053; FORKHEAD.
ProDom; PD000425; TF_Fork_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                     87.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Conservative
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Pfam; PF00651; BTB; 1.
Pfam; PF00096; zf-C2H2; 2.
SMART; SM00225; BTB; 1.
SMART; SM00355; ZnF_C2H2; 2.
                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 |||||||||
218 AAVAAAAAAAAA 230
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                              36 AAVAAAAAAAA 48
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1 AAFAAAAAAAAA
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                                                                                                                           Q3S2W8_ACHDO
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                                                                                         RESULT 25
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ZBTB8 H
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Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buerow K.H., Scheefer C.F., Bhar N.K.,
Appkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Soares M.B., Bonaldo M.F., Gasavant T.L., Scheetz T.E.,
Rosak S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman M., Madan A., Rodrigues S., Sanchez A.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Rodriguez A.C., Grimmood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
R. Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Pred. No. 1.5e+02;
0; Mismatches 1; Indels
                                                                         Length 435;
                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH MGC Project;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51409 MW; 88ACCDA9992B5AEB CRC64;
                 PROSITE; PS50118; HMG BOX 2; 1.
SEQUENCE 435 AA; 48441 MW; 6F227A5D387A9CA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; BC062339; AAH62339.1; -; mRNA.
Ensembl; ENSG0000091542; Homo sapiens.
GO; GO:0005605; F::ron ion binding; IEA.
GO; GO:0016491; F::oxidoreductase activity; IEA.
InterPro; IPR065123; 2OG-FEII Oase.
Pfam; PF03171; 2OG-FEII Oxy; I.
Hypothetical protein; Iron; Oxidoreductase.
SEQUENCE 458 AA; 51409 MW; 88ACCDA9992B5AEB
                                                                       87.0%; Score 47; DB 2; I 92.3%; Pred. No. 1.4e+02; tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                      Q6P6C2;
05-UUL-2004, integrated into UniProtKB/TrEMBL.
05-UUL-2004, sequence version 1.
07-FEB-2006, entry version 16.
Hypothetical protein OFOXD.
                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                    QEP6C2 HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 92.3%;
Matches 12; Conservative (
                                                                                          Local Similarity 92.3%;
les 12; Conservative
                                                                                                                                                                          1 AAFAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.
   SMART; SM00398; HMG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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                                        SEQUENCE
                                                                             Query Match
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                                                                                                                  Matches
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                         Erezyilmaz D.F., Riddiford L.M., Truman J.W.;
"An ancestral role for a metamorphosis-determining factor in a direct-
                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          developing insect.";
Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PSO097; BTB; 1.
PROSITE; PSO0097; BTB; 1.
PROSITE; PSO0028; ZINC FINGER C2H2 1; 2.
PROSITE; PSO1057; ZINC FINGER C2H2 2; 2.
Metal-binding; Nuclear protein; Zinc; Zinc-finger.
SEQUENCE 506 Aa; 54175 MW; F4FCCA9BE6415EC0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QBNAP8; Q5VXR5;
C=CARR-2004, integrated into UniProtKB/Swiss-Prot. 01-0CT-2002, sequence version 1. 07-MAR-2006, entry version 25. 21nc finger and BTB domain-containing protein 8. Name-2ETB8; Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 87.0%; Score 47; DB 2; I
1 Similarity 92.3%; Pred. No. 1.6e+02;
12; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, DQ176003; ABA02190.1; -; mRNA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0008270; F:procein binding; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
InterPro; IPR001010; BTB.
InterPro; IPR001089; ZIE_C2H2.
                                                              11-OCT-2005, integrated into UniProtKB/TrEMBL
506 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIC.
TISSUB-Brain;
PubMed=14702039; DOI=10.1038/ng1285;
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      PRT;
                                                                                                                                                                                               Acheta domesticus (House cricket).
                                                                                                      11-OCT-2005, sequence version 1.
21-FEB-2006, entry version 7.
BroadZl isoform.
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Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
Rakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
Antakami K., Yasuda T., Imayangi T., Magatsuma M., Shiratori A.,
Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa E., Omura Y.,
Abe K., Kamihara K., Matanabe M., Hiraoka S., Chiba Y., Ishida S.,
Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
Antani H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
Ono Y., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
Anehori K., Takahashi-Fujii A., Hara H., Anta M., Imose N.,
Nasashino K., Yuuki H., Oshima A., Saaaki N., Anta M., Imose N.,
Nasashino K., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
Nomiyama H., Satoh N., Takami S., Terashima Y., Sarok S.,
Nakagawa S., Romiyama H., Satoh N., Takami S., Fukuzumi Y.,
Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
Amazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami Y.,
Anazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami Y.,
Ono T., Yamada K., Kumagai A., Itakura S., Fukuzumi Y.,
Anazaki M., Watanabe T., Sugiyama A., Takemoto M., Salaki M.,
Ono T., Yamada K., Ruiyama M., Tashiro H., Tanagami A., Salaki M.,
Anazaki M., Watanabe T., Sugiyama A., Takemoto S.,
Okitani R., Kawakami T., Noguchi S., Itoh T., Shigata K., Sanba T.,
Antushima-Sugano J., Satoh T., Shiza Y., Takahashi Y., Nakagawa K.,
Antushima-Sugano J., Satoh T., Shiza Y., Takahashi Y., Wasashita R.,
Nakai Y., Yada T., Nomura Y., Ohara O., Isogai T., Sugano S.,
Anakai E., Nakamura Y., Ohara O., Isogai T., Sugano S.,
Anakai E., Nakamura Y., Ohara O., Isogai T., Sugano S.,
Anakai E., Nakamura Y., Ohara O., Isogai T., Sugano S.,
Anakai E., Nakamura Y., Ohara O., Isogai T., Sugano S.,
Anakai E., Nakamura Y., Ohara O., Isogai T., Sugashi M.,
Anakai E., Satoh M., Wasuho Y., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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PROSITE; PSS0097; BTB; 1.
PROSITE; PSS00157; ZINC_FINGER_C2H2_1; 1.
PROSITE; PSS0157; ZINC_FINGER_C2H2_2; 2.
DNA-binding; Metal-binding; Nuclear protein; Repeat; Transcription; Transcription; Zinc; Zinc-finger.
Transcription regulation; Zinc; Zinc-finger and BTB domain-containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
Human chromosome 1 international sequencing consortium;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May be involved in transcriptional regulation.
-!- SUBCELLULAR LOCATION: Nucleus (Potential).
-!- SIMILARITY: Contains 1 BTB (POZ) domain.
-!- SIMILARITY: Contains 2 C2H2-type zinc fingers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BB970D200B60CC9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein 8.
/FTId=PRO_0000047721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AK092326; BAC03863.1; -; mRNA.

EMBL; AL356986; CAH73365.1; -; Genomic_DNA.

EMBL; AL033529; CAH73365.1; JOINED; Genomic_DNA.

EMBL; AL033529; CAI20022.1; -; Genomic_DNA.

EMBL; AL356986; CAI20022.1; -; Genomic_DNA.

EMBL; ENSG00000185718; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C2H2-type 1.
C2H2-type 2.
Poly-Ala.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000210; BTB.
InterPro; IPR010069; BTB. POZ.
InterPro; IPR010069; BTB. POZ.
InterPro; IPR010069; Zf_CZHZ.
Pfam; PF00065; Zf_CZHZ; 2.
ProDom; PD000003; Zf_CZHZ; 2.
SWART; SM00255; BTB; 1.
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363 C2
392 C2
153 Po
55562 MW;
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341 3
369 3
132 1
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ZN_FING
ZN_FING
COMPBIAS
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DB 1; Length 512;

Score 47;

87.08;

Query Match

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                  Gaps
                                                                                                                                                                                                                                                               Anopheles gambiae str. PEST.
Eukaryota, Matazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Culicidae,
Anophelinae, Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Anopheles gambiae Sequence Committee;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.0%; Score 47; DB 2; Length 521
92.3%; Pred. No. 1.6e+02;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                   The Anopheles gambiae Sequence Committee, "Anopheles gambiae re-annotation."; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55760 MW; 68A0C7DEA9FE24DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AAAB01008933; EAA09944.3; -; Genomic_DNA. GO; GO:0003676; F:nucleoide acid binding; IEA. GO; GO:000166; F:nucleotide binding; IEA. InterPro; IPR012677; a b_plait_nuc_bd. InterPro; IPR00532; PolyU bd. InterPro; IPR00534; RNI_IRNa_bd. InterPro; IPR003694; RNI_IRNa_bd. InterPro; IPR003954; RNM_I. POHYU_half_pint; 2.
   Pred. No. 1.6e+02; ); Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JUL-2005, integrated into UniProtKB/TrEMBL.
19-JUL-2005, sequence version 1.
07-FEB-2006, entry version 4.
ORPNames=UM05773.1;
                                                                                                                                                                                   15-DEC-2003, integrated into UniProtKB/TrEMBL
                                                                                                                                                       521 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        529 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00076; RRM 1; 3.
SMART; SM00360; RRM; 3.
SMART; SM00361; RRM 1; 1.
TIGREAMS; TIGR01645; half-pint; 1.
BROSITE; PS50102; RRM; 3.
SEQUENCE 521 AA; 55760 MW; 68A0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q4P290 USTMA PRELIMINARY; PRT;
Q4P290;
                                                                                                                                                       PRT;
                                                                                                                                                                                                 07-DEC-2004, sequence version 2. 07-FEB-2006, entry version 16. ENSANGP0000016235.
                 ;
                                                                                                                                                                                                                                             ORFNames=ENSANGG00000013746;
 92.3%;
                                                                                                                                                       Q7PPS0_ANOGA PRELIMINARY;
                                                                           136 AAVAAAAAAAA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   || ||||||||||
339 AAVAAAAAAAAA 351
                                               1 AAFAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AAFAAAAAAAA 13
Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 92.3
nes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
STRAIN=PEST;
                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                       STRAIN=PEST:
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                                                                                                                                         ANOGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USTMA
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                                                                                                                      RESULT 27
Q7PPS0 ANO
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ID 04
AC 04
DT 19
DT 19
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SOB_DROME
                                                                                                                                  RAINTE-521;

RA Birren B.W., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,

RA Ait-Zahra M., Allen T., Allen T., An P., Anderson M., Anderson S.,

RA Ait-Zahra M., Allen T., Allen T., An P., Anderson M., Anderson S.,

RA Garchchi H.W., Armbruster J., Bachanteans P., Baldwin J., Barry A.,

RA Bayul T., Blitsheteyn B., Bloom T., Blye J., Boquslavskiy L.,

RA Calvo S.E., Camarata J., Cango, K., Chang J., Chelatsan Y.,

RA Calvos C., Camarata J., Considine T., Cook A., Cooke P., Corum B.,

RA Calvos C., David R., Davoe T., Dagray S., Dodges S., Dodges S.,

ROJOTIP P., Doziek K., Davoe T., Dagray S., Dodges S., Dodges S.,

RA Dozie P., Doziek K., Davoe T., Dagray S., Dodges S., Dodges S.,

RA Figgerald M., Foley K., Gage D., Galagan J.E., Gaalten K., Hafez N.,

RA Figgerald M., Foley K., Gage D., Galagan J.E., Gaalten K., Hafez N.,

RA Honan T., Horn A., Houde N., Hughes L., Hulbe W., Husby E., Illev I.,

RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis D.,

RA Lidblad-for K., Lorikiteang T., Lokytsang Y., Ludien O.,

RA Mening J., Marbella R., Maru K., Matchews C., Maucell E.,

RA Mening J., Marbella R., Maru K., Matchews C., Maucell E.,

RA Mening J., Marbella R., Maru K., Matchews C., Maucell E.,

RA Moryen N., Mulrain L., Munson G., Naylor J., Newes C., Mayor J.,

RA Moryen N., Nguyen T., Nicole T., Mikkeleen T., Mlenga V., Moru K.,

RA Moryen N., Nguyen T., Nicol R., Nicles S., Conctosho B.,

RA Moryen N., Schupbach R., Semman C., Settipalli S., Sharpe T.,

RA Retera R., Stalker J., Stanger T., Dander S., Smith C., Sougez C.,

RA Retera R., Stalker J., Stanger T., Made C., Mang S., Mangchuk T.,

RA Powey S., Theodoca T., Thoulutean D., Thoulutang P., Rameran N., Schupbach R., Stance S., Theodoca T., Thoulute D., Wassiltev H.,

RA Powey S., Theodoca S., Theodoca S., Thoulut S., Mangchuk T.,

RA Verkataraman D. Y., Whithinson J., Wade C., Wang S., Wangchuk T.,

RA Yang S., Yang S., Yangon S., Yeager S., Yeang S., Wade S., Yeager S., Yeager S., Yeager S., Yeang S., Yeang S., Yeages S., Theodoca S., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO:0005634; C:nucleus; IEA.
GO:0003700; F:transcription factor activity; IEA.
GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e genome sequence of Ustilago maydis.";
mitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
              Eukaryoca, Fungi, Basidiomycota, Ustilaginomycetes,
Ustilaginomycetidae, Ustilaginales, Ustilaginaceae, Ustilago.
NCBI_TaxID=237631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 529;
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87.0%; Score 47; DB 2; Lengtn ....
7. 1%: Pred. No. 1.6e+02;
7. 1%: Pred. No. 1.6e+02;
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529 AA; 53820 MW; D5ABC2C8EA96B06D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AACP01000212; EAK86012.1; -; Genomic_DNA.
                                                                                                            NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000679; Znf_GATA.
Pfam; PF00320; GATA; 1.
SMART; SM00401; ZnF_GATA; 1.
PROSTIE; PS50114; GĀTA_ZN_FINGER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preliminary data.
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MARIAINE-ZUJAUSUOUS, FUNDEGE=10/13113/, DUJZ-10.1126/SGOEDRIC-2/81/37911-1212/
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams A.D., Celniker S.E., Holt R.A., Evans C.A., Canal E.R.F.,
RA Gutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Batton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Abril J.P., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Abril J.P., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Beson K.Y. Benco P.V., Barman B.P., Bhandari D., Bolahakov S.,
RA Berlow R.M., Batt M.R., Bouck J., Boystkatoglu L., Besaley E.M.,
RA Berry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P.,
RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chadra I.,
RA Dodson K., Doup L.E., Downes M., Dayan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dayan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Ooup L.E., Downes M., Dayan-Rocha S., Dunkov B.C., Dunn P.,
RA Frosler C., Gabrielian A., Extract C.C., Ferract C., Ferract C., Ferract C.,
RA Hostin D., Harvey D.A., Heiman T.J., Hernandez J.R., Hock M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
Atlanel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
Atlanel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
Atlanel B.E., Kodira C. D., Wobarry C., Morris J., Moshrefi A.,
Nelson D.M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Shue B.C., Siden-Kamos I., Simpson M., Strong A.H., Wen Schen J.,
RA Shieber K., Ramington K.A., Nixon K., Mulb., Shup B.C., Siden-Kamos I., Simpson M., Strong A.H., Wen Schen D.,
RA Hiliams S.M., Woodage T., Worley K., Wu D., Yang S., Yao Q.A.,
RA Hiliams S.M., Woodage T., Worley K., Wu D., Stang S., Zhan X., Zhan M., Shub B.C., Siden-Kamos I., Simpson M., Shupski M., Shub B.C., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENOME REANNOTATION.
MEDLINE=22426069; PubWed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Misra S., Crosby W.A., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whittield B.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hart M.C., Wang L., Coulter D.E.; "Comparison of odd-skipped and two related genes that encode a new family of zinc finger proteins in
                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [MRNA], AND TISSUE SPECIFICITY
                                                              16-AUG-2005, integrated into UniProtKB/Swiss-Prot. 01-MAY-2000, sequence version 1. 07-MAR-2006, entry version 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
578 AA.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Canton-S; TISSUE=Embryo;
MEDLINE=97032935; PubMed=8878683;
                                                                                                                                                                                   Protein sister of odd and bowel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetics 144:171-182(1996).
                                                                                                                                                                                                                          Name=sob; ORFNames=CG3242
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=7227;
                                       Q9VQS7; Q24571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila.
       DROME
                                   RARREN REPRENTED FOR THE PROPERTY OF THE PROPE
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Gaps

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1 AAFAAAAAAAA 13 AAVAAAAAAAA 88

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Best Local Similarity 92.3 Matches 12; Conservative

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HUMAN
                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                       DDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDD
                                                                                                                                                                                                                                                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proximal Malphighian tubules, brain and pharyngeal muscles during late embryogenesis. Expressed weakly in a segmentally repeated pattern in the leg disk at the distal edge of each presumptive leg segment except in tareal segments 1 to 4.
                                                                                 STRAIN-BERKELEY, TISSUE-Embryo;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R.A., Gonzalez M., Guarin H., Krommiller B., Li P.W., Liao G.,
Miranda A., Mungall C.J., Nunoo J., Pacleb J.M., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K.H., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                    POSSIBLE FUNCTION, AND TISSUE SPECIFICITY.
PubMed=1459720; DOI=10.1016/j.ydbio.2003.07.011;
Hao I., Green R.B., Dunaevsky O., Lengyel J.A., Rauskolb C.;
"The odd-skipped family of zinc finger genes promotes Drosophila leg
                                                                                                                                                                                                                                                                       MEDLINE=22930851; PubMed=14568103; DOI=10.1016/j.mod.2003.08.001; Johansen K.A., Green R.B., Iwaki D.D., Hernandez J.B., Lengyel J.A., "The Drm-Bowl-Lin relief-of-repression hierarchy controls fore- and
                                "Annotation of the Drosophila melanogaster euchromatic genome: a
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ensembl; CG3242; Drosophila melanogaster.
FlyBase; FBgn0004892; sob.
GO; GO:0003677; F:DNA binding; ISS.
GO; GO:0016563; F:transcriptional activator activity; ISS.
GO; GO:0016564; F:transcriptional repressor activity; ISS.
GO; GO:000350; P:blastoderm segmentation; ISS.
                                                                                                                                           Patel S., Phouanenavong S., Wan K.H., Yu C., Lewis S.E.,
Celniker S.E.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                    Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Contains 5 C2H2-type zinc fingers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE003579; AAF51087.1; -; Genomic_DNA.
EMBL; BT003205; AA024960.1; -; mRNA.
PLR; 57227; 572227
HSSP; P07248; 2ADR.
                                                                          NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U62004; AAC47282.1; -; mRNA.
                                                                                                                                                                                                                                          Dev. Biol. 263:282-295(2003).
                                                                                                                                                                                                                                                               TISSUE SPECIFICITY.
                                             systematic review
                                                                                                                                                                                                                                segmentation.
                        Lewis S.E.;
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GO; GO:0016348; P:leg joint morphogenesis (sensu Endopterygota); IMP.

RO; GO:000122; P:negative regulation of transcription from R. .; ISS.

RO; GO:0001366; P:periodic partitioning by pair rule gene; ISS.

RO; GO:0045944; P:positive regulation of transcription from R. .; ISS.

InterPro; IPR07087; Znf C2H2.

R Probom; P0000003; Znf C2H2; 2.

R PROSITE; PS00026; Znf C2H2; 2.

R PROSITE; PS00028; Znr C7H2; 2.

R PROSITE; PS00020000000000000000000
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                                                                                                                                                                                                . . ; ISS.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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SS -> G (in Ref. 1).
P -> L (in Ref. 1).
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07-MAR-2006, entry version 27.
Hypothetical protein FLJ10572 (Kelch-like 11)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58455 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      578 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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Q9NVRO;
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01-MAR-2003, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                            MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

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Klausner R.D., Collins F.S., Magner L., Sheamen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

HOpkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Martslina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M.J., Usdin T.B., Toohiyuki S., Carninoi P., Prange C.,

Rohas S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

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Rohas S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rohiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rohiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rohiting W.W., Touchman J.W., Green E.D., Dickson M.C.,

Rohiting W.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rohnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

The Green E.D., Smailus D.E.,

Rohnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Rohnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Makagawa K., Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamagaita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S., "Complete sequencing and characterization of 21,243 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 47; DB 2; Length 708;
Pred, No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH MGC Project; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO, GO:0005515; F:protein binding; IEA.
InterPro; IPR011705; BACK.
InterPro; IPR001210; BTB.
InterPro; IPR013069; BTB.
InterPro; IPR00652; Kelch_rep.
Pfan; PP07707; BACK; 1.
Pfan; PF00651; BTB; 1.
Pfan; PF00651; BTB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; BC034470; AAH34470.1; -; mRNA.
Ensembl; ENSG00000178502; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AK001434; BAA91689.1; -; mRNA.
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92.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sednences.";
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Best Local Similarity 92.5.
Best Local 2; Conservative
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PROSITE; PS50097; BT
SEQUENCE 708 AA;
                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
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RA Carninci P., Kaaukawa T., Katayama S., Gough J., Frith M.C., Maeda N., RA Garninci P., Kaaukawa T., Katayama S., Gough J., Frith M.C., Maeda N., RA Balic V.B., Berner S.E., Batalov S., Forrest A.R., Sahimokawa K., RA Balic V.B., Brenner S.E., Batalov S., Forrest A.R., Sahimokawa K., RA Balic V.B., Wilming L.G., Ajdnins V., Allen J.E.,
RA Bansal M., Baxter L., Beisel K.W., Allen J.E.,
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RA Ghiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
Chiu K.P., Dalla E., Dalrymple B.P., Ge Bono B., Della Gatta G.,
RA Georgil-Hemming P., Engistrom P., Fagiolini M., Faulkner G.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Huminecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katch M., Kasaawa Y., Kelso J., Kitamura H.,
RA Kurcchkin I.V., Larazaveir D., Lipovitch L., Liu J.,
RA Milson R., Mishiguchi S., Miki H., Mignone F., Miyake S., Morris K.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Nordaliliam S., Madan Babu M., Makaroh M., Marchhonni L.,
RA Rosta B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Schobach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Schobach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Rhaman S., Shubara Y., Shimada H., Shimada H., Shimada K., Tans S.L., Tang S., Taylor M. S., Tegen Y., Hide M.K., Van Minwegen E., Valanic K., Salamer A., Hide W., Bult C.,
RA Sperling S., Stupka E., Sugiura K., Silamer A., Hide W., Bult C.,
RA Wannishi H., Zabarcovsky E., Zhu S., Kanamori-Katayama M., Stuch M., Kato T., Hadawa D., Takawa T.,
RA Wannishi H., Zabarcovsky E., Zhuye D., Liu E.T., Pusakawa T.,
RA Wannishi H., Zabarcovsky E., Zhuye D., Liu R., Kawashima T., Kojima M., Storl H., Kawashima T., Kojima M., Storl H., Kawashima T., Kojima M., Plessy C., Shibatra K., Shiraki T., Rawashima T., Kojima M., Plessy C., Shibatra K., Shiraki Y.,
RA Hagami M., Waki K
                                                                                                                                                     Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                       STRAIN-C57BL/6J, TISSUE-Corpora quadrigemina;
MEDLINE-99279253; PubMed-10349636; DOI-10.1016/S0076-6879(99)03004-9;
                                                           Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230201M16 product:Mi-2 autoantigen 240 kDa protein homolog (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=16141073; DOI=10.1126/science.1112009; RIKBN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium; "Antisense Transcription in the Mammalian Transcriptome."; Science 309:1564-1566(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The transcriptional landscape of the mammalian genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-C57BL/6J; TISSUB-Corpora quadrigemina; PubMed=16141072; DOI=10.1126/science.1112014;
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PubMed=16141073, DOI=10.1126/science.1112009;
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STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
                                                                                                                                                                                                                                                                                                                                                                Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
                       01-MAR-2003, sequence version 1. 07-FEB-2006, entry version 21.
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708 AA.

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RESULT 31 QBBR71 MOUSE ID QBBR71 MOUSE AC QBBR71;

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MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
A Nikaldo I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
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RAnai A., Kawaji H., Kawaswa Y., Hirokawa N., Jackson I.J., Jarvis B.D.,
RA Anai A., Kawaji H., Kawaswa Y., Hirokawa N., Jackson I.J., Jarvis B.D.,
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RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
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RA Yananishi A., Yoshinakaki Y., Itohi Y., Itohi Y., Itohi Y., Itohi W., Shinagawa A.,
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Rayasaki Z., Rayaski Z., Ragerston R., Lander E.S., Rogers J.,
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Namania H., Sato K., Schoenbach C., Whittaker C., Willming L.,

Namania H., Sato K., Schoenbach C., Whittaker C., Wilming L.,

Namania H., Sato K., Schoenbach C., Whittaker C., Wilming L.,

Namania H., Sato K., Schoenbach C., Whittaker C., Wilming L.,

Namania H., Sato K., Schoenbach C., Kawaji H., Kohtsuki S.,

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Namania H., Sato K., Sakabanto M.,

Namania H., Sato K., Sayaki K., Kawaji H., Kohtsuki S.,

Namania H., Sato K., Sayaki H., Kawaji H., Kohtsuki S.,

Namania H., Sato K., Sayaki H., Rasegawa Y., Kawaji H., Kohtsuki S.,
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MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60,770 full-length cDNAs.";
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                                                                                                               Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayachida K., Hayatsu N., Hiramoto K., Hiracka T., Hirozane T., Hori P., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Saski D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Lumitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Klhll1;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
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R EASEMD1; ENSWUSG0000018474; Mus musculus.

R GG1; G0:0016585; C:chromatin remodeling complex; IDA.

R GG2; G0:0016581; C:chromatin remodeling complex; IDA.

R GG2; G0:0016581; C:chromatin assembly or disassembly; IDA.

R GG2; G0:000633; P:chromatin assembly or disassembly; IDA.

R InterPro; IPR0012958; CHD_N.

R InterPro; IPR001955; CHP_M.

R InterPro; IPR001955; Chromo.

R Féan; PP00388; Chromo; 1.

R Féan; PP00389; CHromo; 1.
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07-FBB-2006, entry version 20.
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NCBI_TaxID=10090;
                                                            Genome Res. 10:1757-1771 (2000)
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PROSITE; PS50013; CHROMO 2;
PROSITE; PS50016; ZF_PHD 2;
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Matches 12; Conservative
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RYCLEOTIDE SEQUENCE.

RA Carnincip P. Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Carnincip P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., A Oyama R., Ravasi T., Katayama S., Gough J., Frith M.C., Maeda N., RA Oyama R., Ravasi T., Katayama S., Gough J., Frith M.C., Maeda N., A Oyama R., Ravasi T., Katayama S., Gough J., Frith M.C., Maeda N., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Sainley T.L., RA Davis M.J., Milming LG., Aidinis V., Allen J.E., Bailey T.L., RA Ambesi-Impiombato A., Christoffels A., Clutterbuck D.R., Chalk A.M., R. Chiu K.P., Christoffels A., Clutterbuck D.R., Chalk A.M., R. Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gata G., R. Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gata G., R. Crowe M.L., Harbers M., Hayashi Y., Hensch T.K., Hirokawa T., R. Googii-Hemming P., Gingeras T.R., Gojbori T., Green R.E., Gostiincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa T., R. Hill D., Huminlecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T., R. Hill D., Huminlecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T., Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Kurcchkin I.V., Larcau L.F., Lazarevic D., Lipovich L., Liu J., R. Anteudi H., Machan Babu M., Madera M., Marchionni L., R. Anteudi H., Magnon R., Milyake S., Morris K., Mottagui-Tabar S., Mulder N., Nakano N., Nakano H., Matayake S., Morris K., Rottano H., Ralazawa S., Reingel C.A., Senesi L., Sheng Y., Retrough Y., Shimada Y., Shimada K., Sallva D., Sinclair B., Schighara Y., Shimada H., Shimada K., Sallva D., Sinclair B., Rotchmann S.A., Ramond S.M., Takenaka Y., Takenaka Y., Ramond S.M., Taesdaller R.D., Liu B.T., Branci V., Guckenbush J., Ramanda K., Shimata Y., Shimada H., Shimata Y., Shimada H., Shimada M., Raton M., Sabarovsky B., Stuyka B., Zhuya S., Zhuya S., Kari M., Hannola S., Kananishi H., Zabarovsky B., Zhuya S., Kananishi H., Zabarovsky B., Troh M., Yan NCLEMBLING SEAUGHNES.

X NCLEMBLINE=257BL/6J; TISSUE=Skin;

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A Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

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Parker D.S., Jemison J., Cadigan K.M.;
"Pygopus, a nuclear PHD-finger protein required for wingless signaling
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki Y., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takhashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Takhashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Submitted (JUL-2001) to the EMBL/GenBank/DbBJ databases.
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MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
Adama M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
                                                                                                                                                                                                                                                                                                                                                                Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000, sequence version 1.
21-FEB-2006, entry version 39.
Protein pygopus (Gammy legs protein).
Name-pygo; Synonyma-gam, ORFNames-CG11518;
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophila.
                                                                                                                                                                                                                                                                                                                                      87.0%; Score 47; DB 2; Length 709; 92.3%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                              709 AA; 80429 MW; BA3DB8D4CA6FEB7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-SEP-2002, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                 EMBL; AK029101; BAC26297.1; -; mRNA.
Ensembl; ENSWUSG0000048732; Mus musculus.
MG1; MG1:238648; Kll11.
GO; GO:0005515; F:protein binding; IEA.
InterPro; IPR011705; BACK.
InterPro; IPR0103069; BTB.
InterPro; IPR0103069; BTB.
InterPro; IPR006652; Kelch_rep.
Pfam; PF07707; BACK; 1.
Pfam; PF07707; BACK; 1.
Pfam; PF00515; BTB; 1.
Pfam; PF01344; Kelch_1; 3.
SWART; SM00225; BTB; 1.
                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in Drosophila.";
Development 129:2565-2576(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                 AAVAAAAAAAA 15
                                                                                                                                                                                                                                                                                                                                                                                        1 AAFAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                               12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                    Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DROME
                                                                                                                                                                                                                                                                                                              SEQUENCE
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PYGO_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PYG0
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Buncon G.C., Morthan U.R., C'andell N.D., Zhang O. Chon L.N.

Buncon G.C., Morthan U.R., C'Andell N.D., Zhang O. Chon L.N.

Buncon G.C., Adabyoni, A., An H.J., Andrew-Fennkoch C.R., Miklood G.L.C.,

Abril J.G., Adabyoni, A., An H.J., Andrew-Fennkoch C.R., Miklood G.L.C.,

Abril J.G., Adabyoni, A., An H.J., Andrew-Fennkoch C.R., Miklood G.L.C.,

Band N.R., Banu A., Baxendalo J., Bayakateroglu L., Bealadyin D.,

Beason K.R., Banu A., Baxendalo J., Bayakateroglu L., Bealadyin D.,

Band J., Banu A., Baxendalo J., Bandari D., Bolabhakov S.,

Burtis K.C., bausen A., Band B., Mikloof B., Dulkov B.C., Buldaria J.,

Burtis K.C., bauge L.B., Downes M., Dogan Roch S., Dulkov B.C., Dunkov B.C.,

Bandis B., Bartis M., Band A., Band Z., May A.D., Dulkov B.C., Dunkov B.C.,

B. Bartis M., Dough L.E., Downes M., Dogan Roch S., Dulkov B.C., Dunkov B.C.,

B. Bartis M., Jangelise C.C., Ferract C., Ferract S., Felsiahann M.,

B. Bartis M., Jangelise C.C., Perract C., Perract S., Kollp D., Laiz S.,

B. Hartis M., Milaina M.V., Modary C.C., Margon D.,

B. Martis M., Mod W., Modary C.C., Mories G., Mosine G.,

B. M., Martis M., Modary C.C., Mories G., Monie S., Man H.,

B. Mang Z.-Y., Mestelk M., Modary C.C., Mories G., Mosine G.,

B. M., Mang Z.-Y., Massamman D.A., Wellinkor D.A., Mang A.H., Wang X.,

B. M., Mang Z.-Y., Massamman D.A., Wellinkor D.A., Shughad J., Mang A.H.,

B. Mang Z.-Y., Massamman D.A., Wellinkor J.S., Mill M., P., Smith T.,

Spier B., Spradling R., Modary W., Malland M., Strong R., San E.,

B. Mang Z.-Y., Massamman D.A., Wellinkor J.S., Mull M., Park S., Man K.H.,

B. Mang Z.-Y., Massamman D.A., Wellinkor J.S., Mull M., Park S., Man K.H.,

B. Mang Z.-Y., Massamman D.A., Wellinkor J.S., Mull M., Park S., Man K.H.,

B. Mang Z.-Y., Massamman D.A., Wellinkor J.S., Mull M., Park S., Man K.H.,

B. Mang Z.-Y., Massamman D.A., Wellinkor J.S., Shuka G.D., Shuka M., Park S., Man K.H.,

B. Mang Z.-Y., Massamman D.A., Wellinkor J.S., Shuka G.D., Shuka M., Shuka M., Mang Z.-Y., Mang Y., Manhad C., Stapheron M., Strong M., Shuk

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Ensembl; CGI1518; Drosophila melanogaster.

R PlyBase; Regn0043900; pygo.

R BioCyc; DMEL-XXX-02:DMEL-XXX-02-014325-MONOMER; -.

R GO; GO:0005634; C:nucleus; NAS.

GO; GO:0015528; F:transcription regulator activity; IPI.

GO; GO:00317; P:positive regulation of Wnt receptor signali. ..; IPI.

GO; GO:0007167; P:positive regulation of Wnt receptor signali. ..; IPI.

GO; GO:0007367; P:positive regulation of Wnt receptor signaling pathway; IMP.

R GO; GO:0010155; P:Wnt receptor signaling pathway; IMP.

R GO; GO:001655; P:Wnt receptor signaling pathway; IMP.

R PROSITE; PS010155; ZF PHD. 1.

R PROSITE; PS011359; ZF PHD. 1; 1.

R ROSITE; PS011359; ZF PHD. 2; 1.

R Complete protecome; Developmental protein; Metal-binding;
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                                                                                                                                                                                                                                                                                                                                       Nuclear protein; Segmentation polarity protein; Wnt signaling pathway;
Zinc; Zinc-finger.

Protein pydopus.

CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-0cT-2005, integrated into UniProtKB/TrEMBL.
11-0CT-2005, sequence version 1.
07-FEB-2006, entry version 5.
B16 F10Y cells cDNA, RIKEN full-length enriched library,
clone:G370031D15 product:SH3 multiple domains 2, full insert sequence.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi;
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                          Protein pygopus.
/FTId=PRO_0000097124.
PHD-type._
Nuclear localization signal (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.0%; Score 47; DB 1; Length 815; 92.3%; Pred. No. 2.3e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ala-rich.
Asn/Gly/His/Met/Pro-rich.
S -> P (in Ref. 1).
369FD5A5D34BC136 CRC64;
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"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     828 AA.
  EMBL; AY058500; AAL13729.1; -; mRNA.
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39 45 Nuu
48 65 All
123 749 Asi
393 393 S
815 AA; 80493 MW;
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Q3UG42;
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Les 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=Sh3md2;
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MOTIF
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O310542 MOU
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RA Gustincich S., Rarbers M., Hayashi Y., Hensch Tr.K., Hitokkwa N., Railli M., Ramainer, Ekicha W. Kasanasa Y., Relion J., Kitimara H., Richano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Kitano H., Wollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Liunis S., Wollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Liunis S., Wollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Raillason R., Washillason S., Wadara M., Warchionni L., Ray Retuda H., Mateawa S., Walth H., Majoro R., Washchin I.V., Larsey S., Rail B., S., Warther S., Walther S., Stupe B., Bend J., Farby S., Walther S., Walther S., Walther S., Stupe B., Bend J., Farby S., Stupe B., Bend J., Walther S., Taka K., Sample C. A., Sense L., Sheng Y., Randola H., Mitharda K., Shilthan S., Taka K., Speciling S., Stupe B., Stupe S., Payor S., Payor S., Payor S., Payor S., Payor S., Payor S., Sense L., Sheng Y., Randola H., Mitharda K., Shilthan S., Takanada H., Shilthan S., Takanada H., Shilthan S., Takanada K., Taka K., Shilthan S., Mandola H., Mateadala R., Takanada K., Taka K., Shilthan S., Mandola H., Waltharda K., Shilthan K., Mandola H., Waltharda K., Shilthan S., Mandola H., Waltharda K., Waltharda K.,
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Q9VE88 DROME
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A Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
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Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
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Rielschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
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Baka J., Boffelli D., Bojunga N., Canninoi P., Ga Bonahdo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
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Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Austincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
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Sasaki H., Saco K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Whynhaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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Arakwa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
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Muramatsu M., Hayashizaki Y.,
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
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"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
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GO; GO:0030027; C:lamellipodium; IDA.
GO; GO:0030027; C:lamellipodium; IDA.
GO; GO:0005078; F:MAP-Kinase scaffold activity; IDA.
GO; GO:0006328; F:MAP-Kinase scaffold activity; IDA.
GO; GO:0046328; P:rectein binding; IPI.
GO; GO:0046328; P:rectein binding; IPI.
InterPro; IPR00108; Neu Cyt_fact_2.
InterPro; IPR001841; Znf RING.
Pfam; PF00018; SH3 1; 3.
Fram; PF00018; SH3 1; 3.
Fram; PF00097; zf-G3HC4; 1.
FRINTS; PR00499; P67PHOX.
FRINTS; PR00452; SH3DOMAIN.
FRINTS; PR00065; SH3; 3.
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SMART; SM00326; SH3; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name-Sh3md2; Synonyms-POSH;
Mus musculus (Mouse).
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98151363; PubMed=9482736; DOI=10.1093/emboj/17.5.1395; Tapon N., Nagata K., Lamarche N., Hall A.; "A new rac target POSH is an SH3-containing scaffold protein involved in the JNK and NF-kappaB signalling pathways.";
                                                                                                                                                                                        Gaps
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0
                                                                                                                               87.0%; Score 47; DB 2; Length 828; 92.3%; Pred. No. 2.3e+02; ive 0; Mismatches 1; Indels
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HISP, 199071; T09071.

MGI; MGI:1933066; Shand2.

MGI; MGI:1933066; Shand2.

GO; GO:0030027; C:lamellipodium; IDA.

GO; GO:0005718; F:MAP-Kinase scaffold activity; IDA.

GO; GO:0005518; F:MAP-Kinase scaffold activity; IDA.

GO; GO:0005218; F:mAP-Kinase scaffold activity; IDA.

GO; GO:0005218; F:mAP-Kinase scaffold activity; IDA.

GO; GO:000518; F:mAP-Kinase scaffold activity; IDA.

HITEPTO: IPR00108; Neu_Cyt_fact_2.

InterPro; IPR001841; Znf_RING.

FFam; PF00018; SH3 1; 4.

PFam; PF00007; zf-C3HG4; 1.
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                                                                                 72FE525B907FE0FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            070254;
01-AUG-1998, integrated into UniProtKB/TrEMBL.
01-AUG-1998, sequence version 1.
07-FBB-2006, entry version 26.
Plenty of SH38.
                                                                                                                                                                                                                                                                                                                                                                                                                    O70254 MOUSE PRELIMINARY; PRT;
PS50002; SH3; 3.
PS00518; ZF RING 1; 1.
PS50089; ZF RING 2; 1.
828 AA; 86192 MW; '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50002; SH3; 4.
PROSITE; PS00518; ZF RING 1; 1.
PROSITE; PS50089; ZF RING 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBO J. 17:1395-1404 (1998).
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PRINTS; PR00422; SH3DOMAIN.
PRODOM; PD0000666; SH3; 4.
SMART; SW00184; RING; 1.
SMART; SM00326; SH3; 4.
                                                                                                                                                                                                                                                                                          419 AAVAAAAAAAA 431
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                                                                                                                                                          Best Local Similarity 92.3
Matches 12; Conservative
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                                                                                                                                  Query Match
  PROSITE;
PROSITE;
                                                      PROSITE,
SEQUENCE
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RA Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Galle R.F.,
Randon R.C., Lewis S.E., Richards S., Ashburner M. Henderson S.N.,
Randon R.C., Negers Y.-H.C., Blazej R.G., Chango O., Chen L.X.,
RA Ballew R.M., Doyle C. Baxter E.G., Helf G., Change M., Piefiffer B.D.,
RA Ballew R.M., Basu A., Raman B.P., Bhandari D., Belahakov S.,
Ra Besoon K.Y. Benos P.V., Berman B.P., Bhandari D., Bolahakov S.,
RA Burtis R.C., Busem D.A., Burler H., Cadieu E., Center A., Chadra I.,
RA Burtis R.C., Busem D.A., Dallke C., Pevenport L.B., Davies P.,
RA Burtis R.C., Busem D.A., Dallke C., Pevenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dagan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dagan-Rocha S., Dunkov B.C., Dunn P.,
Rosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
A Glodek A., Gong F. Gorrell J.H., Gu Z., Genbart W.M., Glasser K.,
A Hostin D., Harvey D.A., Heiman T.J., Wernison J.A., Ketchum K.A.,
A skimmel B.E., Kaire C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
A Lasko P., Lei Y., Leviteky A.A., Li J.H., Li Z., Liang Y., Lin X.,
Atteris N.L., Harvey D.A., Howland T.J., Wolherson D.L.,
Merkulov G., Milshima N.V., Mobarry C., Morris J., Moshrefi A.,
Romet S.M., Moy M., Murphy B., Murphy L., Murshy D.M., Nelson D.L.,
R. Remington K.A., Nixon K., Nusskern D.R., Parley C., Shen H.,
R. Spier E., Spradling A.C., Stapleton M., Stuong R., Sunh B.,
R. Spier E., Spradling A.C., Stapleton M., Stuong R., Sunh B.,
R. Spier E., Spradling A.C., Stapleton M., Stuong R., Sunh B.,
R. Shirkas R., Wedonger T., Worley K., Murby W., Shirth H.O.,
R. When B.C., Siden-Kiamos I., Simpson M., Stuong R., Shir H.,
R. Spier E., Spradling A.C., Stapleton M., Stuong R., Shir H.,
R. Spier E., Spradling A.C., Stapleton M., Stuong R., Shir H.,
R. Shirkas R., Wedonger T., Worley S., Romer B.,
R. When B.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22426065; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
Celniker S.E., Maeeler D.A., Kronmiller B., Frise B., Hodgson A.,
Batel S., Adams M., Champe M., Dugan S.P., Frise B., Hodgson A.,
George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
Svirskas R., Tabor P.E., Wan K., Staplecon M., Sutton G.G., Venter C.,
Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
"Finishing a whole-genome shotgun: release 3 of the Drosophila
                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
                                                                                                                            Drosophila melanogaster (Frūit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda; Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                  integrated into UniProtKB/TrEMBL
897 AA
                                                                                                         Name=CG15803; ORFNames=Dmel CG15803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22426070; PubMed=12537573;
               O9VE88;
01-MAY-2000, integrated into Uni
01-OCT-2002, sequence version 2.
21-FEB-2006, entry version 28.
PRELIMINARY;
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 Q9VE88_DROME
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genomics perspective.";

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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                            MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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NUCLEOTIDE SEQUENCE.
TISSUE=Embryonic tail;
PubMed=15368895; DOI=10.1093/dnares/11.3.205;
Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
                                                                                                                                                                                                                                                                                                                                                                                                                     Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith J.
Yu C., Rubin G.;
"Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                "Annotation of the Drosophila melanogaster euchromatic genome: a systematic review.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            897 AA; 94372 MW; 3A74789E08FD1A2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9VBP2:CG5053; NbExp=1; IntAct=EBI-172540, EBI-20: Q9VQW7:ed; NbExp=1; IntAct=EBI-172540, EBI-85823; SIMILARITY: Contains 4 PDZ (DHR) domains.
                                                                                                                                                                                                                                                                                                                                               Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87.0%; Score 47; DB 2; I
92.3%; Pred. No. 2.5e+02;
iive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE003721; AAF55539.2; -; Genomic_DNA.
HSSP; Q64512; 1021.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FlyBase, FBG0038606, CG15803.

GO; GO:0005515; F:procein binding; IPI.
InterPro; IPR001478; PDZ.
Ffam; PF00595; PDZ; 4.
SMART; SM00228; PDZ; 4.
FROSITE; PSS0106; PDZ; 4.
SEQUENCE 897 AA; 94372 MW; 3A74789E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q69ZII MOUSE PRELIMINARY; PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IntAct; Q9VE88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FlyBase;
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                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-OCT-2005, integrated into UniProtKB/TrEMBL.
11-OCT-2005, sequence version 1.
07-FEB2-2006, entry version 2.
Adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:6330596E03 product:hypothetical Transforming protein Ski/SAND-like/Putative DNA binding containing protein, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
PubMed=16141072; DOI=10.1126/science.1112014;
Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
Saga Y., Seino S., Nishimura M., Kaisho T., Hoshino K., Kitamura H., Nagase T., Ohara O., Koga H.;
Nagase T., Ohara O., Koga H.;
Prediction of the coding sequences of mouse homologues of KIAA gene:
IV. The complete nucleotide sequences of 500 mouse KIAA-homologous cDNAs identified by screening of terminal sequences of cDNA clones randomly sampled from size-fractionated libraries.";
DNA Res. 11.205-218(2004).
-! SIMILARITY: Contains 1 RING-type zinc finger.
-! SIMILARITY: Contains 4 SH3 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6J; TISSUB=Medulla oblongata;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
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0
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                                                                                                                                                                                                                                                                                  EMBL, AK173185; BAD32463.1; -; mRNA.

R GO; GO:0030027; C.1amellipodium; IDA.

GO; GO:0030027; C.1amellipodium; IDA.

GO; GO:0005515; F:Protein binding; IPI.

GO; GO:0046328; P:requilation of JNK cascade; IDA.

R GO; GO:0046328; P:requilation of JNK cascade; IDA.

R InterPro; IPR00108; New cyt_fact_2.

R InterPro; IPR001081; New cyt_fact_2.

R InterPro; IPR001452; SH3.

R Pfam; PF00018; SH3.1 4.

P Ffam; PF00018; SH3.4 1.

R RNNTS; RN0184; RING; 1.

R RNAT; SN0184; RING; 1.

R RNAT; SN0184; RING; 1.

R RNAT; SN0186; SH3, 4.

R RNAT; SN0186; SH3, 4.

R RNOSITE; PS50018; ZF RING 1; 1.

R PROSITE; PS50018; ZF RING 1; 1.

R PROSITE; PS50089; ZF RING 2; 1.

R Metal-binding; SH3 domain; Zinc; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 914 AA; 95963 MW; 0D3F7A4B4AD9E067 CRC64;
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QJUYA4;
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nes 12; Conservative
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KEATIMECSTED. SEQUENCE.

KENDINE-2708560; PubMed=11217851; DOI=10.1038/3505500;

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Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoco N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shipata Y., Storch K.-F.,

Nornokan H., Sato K., Schoenbach C., Seya T., Shipata Y., Storch K.-F.,

M. Wanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

M. Havashi P., V.
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Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
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GO:0005634; C:nucleus; RCA.
GO:0005634; C:nucleus; IDA.
GO:0005667; C:transcription factor complex; IDA.
GO:0005615; F:protein binding; IPI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 409:685-690(2001).
                                                                                                                                             Nature 420:563-573(2002).
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Drosophila melanogaster (Fruit fly).
Bukaryyota; Matazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Nooptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
GO; GO:0003714; F:transcription corepressor activity; IDA. GO; GO:0050875; P:cellular physiological process; RCA. GO; GO:0016481; P:negative regulation of transcription; IDA. Interpro; IPR003380; Transform_Ski. Pfam; PR02437; Ski. Sno; 1.
                                                                                                                                                                                                                                                                                                       Length 935;
                                                                                                                                                                                                                                 935 AA; 96933 MW; A9C2953F4A77E367 CRC64;
                                                                                                                                                                                                                                                                                                           87.0%; Score 47; DB 2; I
92.3%; Pred. No. 2.5e+02;
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Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
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NUCLECTIDE SEQUENCE.
MEDLINE=22456065; PubMed=12537568;
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                                                                                                                                                                                                                                                                                            MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.B.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.
                                                                                                                                                                                                                                                                                                                                                                                                    "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE003672; AAF54032.3; -; Genomic_DNA.
Flybase, FBgn000263; rn.
Flybase, FBgn000263; rn.
GO; GO:0007480; Fleg morphogenesis (sensu Endopterygota); IMP.
GO; GO:0007480; P:leg morphogenesis (sensu Endopterygota); IMP.
InterPro; IRRO07081; Znf_CZH2.
Pfam; PF00096; zf-CZH2; 6.
ProDom; PD000003; Znf_CZH2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 47; DB 2; Length 946; Pred. No. 2.6e+02; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases.
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PROSITE; PSO157; ZINC_FINGER_C2H2_2; 6.
Metal-binding; Nuclear_protein; Zinc; Zinc-finger.
PROFIENCE 946 AA: 100948 MW; 05EA01C8F64F61A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Biol. 3: RESEARCH0083.1-RESEARCH0083.22 (2002).
                                                                                                                                                                                                                                         a genomics perspective.";
Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002)
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nes 12, Conservative
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RC STRAIN-GSTBLE-GEROBELIUM, and Testis;
RD GALLOCTIDE SEQUENCE ILARGE SCALE MRNA] (ISOPCOME) I AND 3).
RD MUNICACTIDE SEQUENCE ILARGE SCALE MRNA]
RA GAITOT2; DOI-10.1126/GEGENCE 1112014;
RA GAITOT2; DOI-10.1126/GEGENCE 1112014;
RA GAITOT3; DOI-10.1126/GEGENCE 1112014;
RA GAITOT3; DOI-10.1126/GEGENCE 1112014;
RA GAITOT3; DOI-10.1126/GEGENCE 1112014;
RA GAITOT3 DOI-10.126/GEGENCE 1112014;
RA GAITOT3 DOI-10.126/GEGENCE 1112014;
RA GAITOT3 DOI-10.126/GEGENCE 1112014;
RA GAITOT3 DOI-10.126/GEGENCE 112014;
RA GAITOT3 DOI-10.126/GEGENCE 112014;
RA GAITOT3 DOWN T., BEIGEN R., ALUTALIDAR D., DEIDA GATLA G.,
RA GUSTINICICH S., Harbers M., Targetrom P., Fegiolini M., Faulkner G.,
RA GUSTINICICH S., Harbers M., Ingernom P., Fegiolini M., Faulkner G.,
RA GUSTINICICH S., Harbers M., Ingernom P., Hensch T.K., Hirokawa N.,
RA Hill D., Hunninecki L., Iaconom M., Ikeo J., Kitamura H.,
Aukt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
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                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                Ladybird homeobox corepressor 1 (Transcriptional corepressor Corll).
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-!- FUNCTION: Acts as a transcriptional corepressor of LBX1-!- SUBUNIT: Interacts with LBX1.
-!- INTERACTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 3)
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LOCATION, TISSUE SPECIFICITY, AND INTERACTION WITH LBX1
QBBX45; QSW012; Q8C0T2; 21-JUN-2005, integrated into UniProtKB/Swiss-Prot. 01-MAR-2003, sequence version 1. 07-FEB-2006, entry version 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Embryonic brain;
PubMed=15528197; DOI=10.1074/jbc.M411652200;
                                                                                                                                                                                                                                  Name=Lbxcorl; Synonyms=Corll;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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Gaps

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RESULT 40

Matches

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                                                                                                                                        Isold-QBRX46-3; Sequence=VSP_014178, VSP_014180, VSP_014181; Note=No experimental confirmation available; Note=No experimental confirmation available; TISSUE SPECIFICITY: Expressed in brain with higher levels in embryo than adult. Also expressed in adult testis. In embryonic brain, expressed in a subset of postmitotic neurons generated posterior to the midbrain-hindbrain border. In the developing spinal cord, selectively expressed in dorsal horn interneurons. SIMILARITY: Belongs to the SKI family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Missing (in isoform 3).
/FTId=VSP 014178.
Missing (in isoform 2).
/FTId=VSP 014179.
LQGGGCGGA -> PARGERERER (in isoform 3).
/FTId=VSP 014180.
Missing (in isoform 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF02437; Ski Sno; 1. Alternative splicing; Coiled coil; Nuclear protein; Repressor; Transcription; Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ladybird homeobox corepressor 1. /FTId=PRO_0000129391.
                                                                                                                                                                                                                                                                                                                                                                                                                       Ensembl; Poenavo; — Ensembl; ENSUNGS0000022245; Mus musculus.

BNG1: 2443473; Lbxcor1.

GO; GO:0005634; C:nucleus; IDA.

GO; GO:0005667; C:transcription factor complex; IDA.

GO; GO:0005515; F:proctein binding; IPI.

GO; GO:000714; F:transcription corepressor activity; IDA.

GO; GO:0016481; P:negative regulation of transcription; IDA.

InterPro; IPR003380; Transform_Ski.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 47; DB 1; Length 964; Pred. No. 2.6e+02; 0; Mismatches 1; Indels
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                                                                            Note=No experimental confirmation available;
-!- SUBCELLULAR LOCATION: Nucleus.
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /FTId=VSP 014181.
Q -> P (in Ref. 1)
                                                                                                                IsoId=08BX46-2; Sequence=VSP_014179;
                                                                IsoId=Q8BX46-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                                               EMBL, AB185113; BAD69568.1; -; mRNA.
EMBL, AK029916; BAC26674.1; -; mRNA.
EMBL, AK049035; BAC33520.1; -; mRNA.
HSSP; P12755; 1MR1.
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92.3%;
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Search completed: September 9, 2006, 23:00:21 Job time : 120.139 secs 512 AAVAAAAAAAA 524 a

1 AAFAAAAAAAA 13 12; Conservative

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Matches

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Gaps

Breast an IPT-like 0 Isopenten Pseudomon Protein e Human MHC

Human lun Human lun Human lun Drosophil Plant pol Pseudomon

Human pro Human sto Listeria

Lung spec Drosophil

Protein e Spider (E Human hom Human NKX

Human NK-

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Lung canc Prostate Human lun Human gen Human lun

Human lun Tumour-as Plant ful Human sex Cyclin-de

Title: Perfect score:

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protein

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Scoring table:

Searched:

Minimum DB Maximum DB 8

Database

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Aay44712
Adx71924
Aau57985
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Adv80259 Streptoco
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Adv803010 Thalecres
Ado62431 Transcrip
Abb58866 Drosophil
Abm89198 Rice abio
Adi29006 Human MHC
Abb49912 Listeria
Abb71345 Drosophil
Abr40698 Glycine m
Abm87998 Rice abio
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         GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
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                                                protein search, using sw model
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1: geneseqp1980s:*

2: geneseqp2000s:*

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Gaps

ADO03023 AAY37630 AEF77642 AEF77640

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ADI29009 standard; peptide; 13 AA

(first entry)

15-APR-2004

ADI29009;

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL3011), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
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Score 54; DB 8; Length 13;
Pred. No. 0.024;
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Pred. No. 8
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  100.08;
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11-JUL-2000; 2000US-00614150.
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genes from Drosophila and
interactions.
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N-PSDB; ABL14986.
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                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes an isolated MHC class II compound (I) comprising: (a) an MHC class II component comprising at least a portion of an MHC class II alpha chain and at least a portion of an MHC class II beta beta chain, such that the MHC class II alpha chain and MHC class II beta chain form a peptide binding groove; (b) a spaceholder molecule; and (c) an effector component, Also described; (l) a pharmaceutical composition class II component. Also described: (l) a pharmaceutical composition comprising the MHC class II molecule and a carrier; (2) a method of producing an MHC class II compound; (3) a method of directly identifying an antigan-specific T cell; (4) a method of directly identifying an autigan-specific T cell; (4) a method of regulating an immune response ex vivo in a subject; and (c) a method of treating an immune response ex vivo in a subject; and continued, antibacterial, antiparasitic, cytostatic and immunosuppressive activities, and can be used in gene therapy. The MHC class II compound (I) can be used for preparing a composition for treating immune classifications, neoplastic disease, autoimmunity or toxicity. The present configurations, neoplastic disease, autoimmunity or toxicity. The present sequence represents a spaceholder molecule peptide, which can be used in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                               MHC class II compound; MHC class II component; MHC class II alpha chain; MHC class II beta chain; peptide binding groove; spaceholder molecule; effector component; immune response; immune disorder; virucide; antibacterial; antiparasitic; cytostatic; immunosuppressive; gene therapy; viral infections; bacterial infection; parasitic infection; neoplastic disease; autoimmunity; toxicity; human.
                       Aay37630 Chlamydia
Aef77642 Rat 3-hyd
Aef77640 Mouse 3-h
           Ado03023 Thalecres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New MHC class II compound, useful for preparing a composition for treating immune disorders e.g. viral infections, bacterial infections, parasitic infections, neoplastic disease, autoimmunity or toxicity.
                                                                                                                                                                                                                                                                                                                                                                                                         Human MHC class II compound spaceholder molecule SEQ ID NO:5.
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Gaps

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Claim 11; SEQ ID NO 5; 92pp; English

Sequence 13 AA;

(DAND ) DANA FARBER CANCER INST INC.

Seth N;

RESULT 1

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AD129009

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AD129009

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AD129009

Exp. Title 15-A

AD129009

AD129

WPI; 2004-122876/12. Wucherpfenning KW,

12-JUL-2002; 2002US-0395494P. 22-JUL-2002; 2002US-0397893P. 11-JUL-2003; 2003WO-US021767

22-JUL-2002;

WO2004007528-A2

22-JAN-2004.

sapiens

Homo

Synthetic.

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New nucleic acid molecule encoding a hyperimmune serum reactive antigen, useful for the manufacture of a vaccine against Streptococcus agalactiae
                         immune stimulation; antigen; bacterial surface display; hyperimmune serum reactive antigen; vaccine; bacterial infection; antibacterial; infection.
  S agalactiae hyperimmune serum reactive antigen seqid 326.
                                                                                                                                                                                                                                                                                                                                                                                                         Claim 12; SEQ ID NO 326; 221pp; English.
                                                                                                                                                                                                                                                                           Meinke A, Nagy E, Hanner M,
                                                                                                                                                                       06-MAY-2004; 2004WO-EP004856.
                                                                                                                                                                                                 07-MAY-2003; 2003EP-00450112.
28-NOV-2003; 2003EP-00450266.
                                                                                    Streptococcus agalactiae
                                                                                                                                                                                                                                             (INTE-) INTERCELL AG
                                                                                                                                                                                                                                                                                                       WPI; 2004-821662/81.
                                                                                                                                                                                                                                                                                                                    N-PSDB; ADU69414
                                                                                                                WO2004099242-A2.
                                                                                                                                             18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                             infection.
 The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN6604-ABN7126 and antibacterial bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a bilogical sample. (I) is used to detecmine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity charted may be used in gene therapy, humunoassays, and distinguishing/identifying
                                                                  Streptococcus, GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                  New Streptococcus protein for the treatment or prevention of infection disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 42; DB 5; Length 970;
Pred. No. 2.1e+02;
1; Mismatches 0; Indels
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                                           Streptococcus polypeptide SEQ ID NO 4012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 3556; 4525pp; English
                                                                                                                                                                                                                                            2000GB-00026333
                                                                                                                                                                                                               29-OCT-2001; 2001WO-GB004789
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Best Local Similarity 69.47
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                                                                                                                            Streptococcus agalactiae.
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(GENO-) INST GENOMIC RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 970 AA;
                                                                                                                                                        WO200234771-A2
             02-JUL-2002
                                                                                                                                                                                                                                            27-OCT-2000;
                                                                                                                                                                                                                                                          24-NOV-2000;
                                                                                                                                                                                     02-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                              Tettelin H;
                                                                                                                                                                                                                                                                                                                                              Telford J,
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Prustomersky S;

Kallenda S,

Horky M,

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The invention describes an isolated nucleic acid molecule encoding a hyperimmune serum reactive antigen or its fragment. Also described are: a vector comprising the nucleic acid molecule; a host cell comprising the vector, a hyperimmune serum-reactive antigen comprising a sequence encoded by the nucleic acid molecule and consisting of e.g., 85, 299, 467 or 812 amino acids; fragments of hyperimmune serum reactive antigens consisting of peptides comprising e.g., 76, 114, 221 or 576 amino acids; a process for producing a Streptococcus agalactiae hyperimmune serum reactive antigen; a process for producing a cell that expresses a S. C. agalactiae hyperimmune serum reactive antigen; a pharmaceutical composition, especially a vaccine, comprising the hyperimmune serum cactive antigen; a part of the hyperimmune serum-reactive antigen; a method for nucleic acid molecule; an antibody that binds at least to a selective part of the hyperimmune serum-reactive antigen; a method for identifying an antagonist capable of binding to the hyperimmune serum-reactive antigen; a method for identifying an antagonist capable of binding to the hyperimmune serum-reactive antigen to its interaction partner; a process for in vitro diagnosis of a bacterial infection, especially a S. agalactiae infection. The hyperimmune serum reactive antigen is useful for searching and/or identifying an interaction partner; and/or identifying an interaction partner of the hyperimmune serum reactive antigen, and a process for in vitro diagnosis and/or identifying an interaction partner of the hyperimmune serum reactive antigen, eactive antigen, eactive antigen, eactive antigen, eactive antigen, especially a S. agalactiae in sectul for reactive antigen, eactive encomprises anticalines or for the manufacture of a functional nu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acid comprising ribozymes, antisense nucleic acids or siRNA. The nucleic acid molecule, hyperimmune serum-reactive antigen or antibody is useful for the manufacture of a vaccine against S. agalactiae infection. This is the amino acid sequence of a Streptococcus agalactiae hyperimmune serum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 2.9e+02;
4; Mismatches 0; Indels
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Best Local Similarity 69.23,
Best Local Similarity 69.43,
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Gaps

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4; Mismatches

||||||:::||||: 881 ASMSASTSASMSA 893

1 ASMSAASAASMAA 13

ઠે 셤 ADU69631 standard; protein; 1310 AA.

RESULT 4 ADU69631 (first entry)

10-FEB-2005

ADU69631;

1 ASMSAASAASMAA 13 

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ADV89548;

ADV89548 RESULT

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The present invention relates to novel Streptococcus agalactiae

uncleotide sequences (1; ADV78860-ADV78998 and ADV83341-ADV85496) and

uncleotide sequences (1; ADV78899-ADV81203 and ADV81205-ADV83340). The

nucleotide sequences encode polypeptides of S. agalactiae involved in the

synthesis of amino acids, cell membranes, intermediate (central)

metabolism, energetic metabolism, fatty acid and phospholipid metabolism,

cucleotide metabolism including purines, pyrimidines and/or nucleosides,

regulatory functions, replication, transcription, translation, protein

transport, adaptation to atypical conditions, sensitivity to medicines

cofactors, prosthetic groups and transporters, cell membrane proteins and

cofactors, prosthetic groups and transporters, cell membrane proteins and

cofactors, prosthetic groups and transporters, cell membrane proteins and

colactors, prosthetic groups and transporters, cell membrane proteins and

colactors, prosthetic groups and transporters, cell membrane proteins

colactors prosthetic groups and transporters, cell membrane process

colactors process agalactical composition comprisingly (1) or (11) are

general for treatment of a bacterial is given in ADV81204, Note: The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomic nucleotide sequences encoding polypeptides of Streptococcus agalactiae for the development of vaccines, diagnostic tools, DNA chips and identification of therapeutic targets.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rusniok C, Chevalier F, Frangeul L, Lalioui L, Couve E, Buchrieser C, Poyart C, Trieu-Cuot P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 42; DB 8; Length 1310;
Pred. No. 2.9e+02;
4; Mismatches 0; Indels
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                                                                        Streptococcus agalactiae protein, SEQ ID 1942.
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                                                                                                                          Antibacterial; vaccine; bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; SEQ ID NO 1942; 439pp; French
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(CNRS ) CNRS CENT NAT RECH SCI
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contains only 2344 sequences.
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781 ASMSASTSASMSA 793
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                         24-FEB-2005 (first entry)
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Best Local Similarity 69.2
Matches 9; Conservative
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                                                                                                                                                                                    Streptococcus agalactiae.
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Zouine M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to novel Streptococcus agalactiae
nucleotide sequences (1; ADV87607-ADV87745) and novel polypeptides (II;
ADV87746-ADV89550). The nucleotide sequences encode polypeptides of S.
agalactiae involved in the synthesis of amino acids, cell membranes, intermediate (central) metabolism, energetic metabolism, fatty acid and phospholipid metabolism, nucleotide metabolism including purines, cpyrimidines and/or nucleosides, regulatory functions replication, transportion, transport, adaptation to atypical conditions, sensitivity to medicines and/or analogues, functions related transporters, cell membrane proteins and cellular machinery. (I) are useful for the detection and/or amplification of nucleic acids. Pharmaceutical composition comprising (I) or (II) are useful for the present basic patent FR2824074A1. WO200292818A2 is equivalent for the present basic patent FR2824074A1. WO200292818A2 contains 6617 sequence whereas the present patent only contains 2344
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Poyart C, Trieu CP, Kunst F;
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Pred. No. 2.9e+02;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                 Streptococcus agalactiae protein sequence, SEQ ID 1942.
                                                                                                                                                                                                                                                                                                                                                         Antibacterial, Vaccine, bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; SEQ ID NO 1942; 2687pp; French
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                                                                                                                                           ADV89548 standard; protein; 1310 AA.
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(CNRS ) CNRS CENT NAT RECH SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-APR-2001; 2001FR-00005642.
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781 ASMSASTSASMSA 793
     781 ASMSASTSASMSA 793
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                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus agalactiae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                  24-FEB-2005
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Glaser Zouine

Kunst F;

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Gaps

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RESULT 6 ADV80801

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WO200292818-A2

21-NOV-2002

Glaser P, Zouine M,

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABBS7777-ABBS2072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     osteopathic; vulnerary; cytostatic; gene therapy; diagnosis; forensics; gene mapping; mutation identification; biodiversity; chromosome marker; immune response; myeloid cell disorder; lymphoid cell disorder; bone cartilage; tendon; ligament; nerve tissue growth; wound healing; burns; incision; ulcer; cancer.
                                                                                                                                                                                                                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                           Disclosure, SEQ ID NO 21255, 21pp + Sequence Listing, English.
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ou P, Drmanac RT;
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Xue AJ, Wehrman T, Weng G, Zhou P,
                                                                                                                                  Myers EW;
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                                                                                                                                  Li PWD,
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23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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16-SEP-2002; 2002US-00323349.
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                                                                                                                                  Venter JC, Adams M,
                                                                                                                                                                                    WPI; 2001-656860/75.
N-PSDB; ABL08924.
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N-PSDB; ADI60483.
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                                                                                (PEKE ) PE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 510 AA;
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interactions.
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Ghosh M,
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ADI60138
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                                                                                                                                                                                                                                                                                                                                                     Kunst F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention relates to novel Streptococcus agalactiae
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                                                                                                                                                                                                                                                                                                                       Frangeul L, Lalioui L;
Poyart C, Trieu-Cuot P,
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Pred. No. 2.9e+02;
4; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                Poyart C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; SEQ ID NO 4100; 439pp; French.
                                                                                                                                                                                                                                                                                                                    Chevalier F,
                                                                                                                                                                                                                                                                                                                                             Buchrieser C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB64821 standard; protein; 510 AA.
                                                                                                                                                                                                                                   (INSP ) INST PASTEUR.
(CNRS ) CNRS CENT NAT RECH SCI
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                                                                                                                                                                                 26-APR-2001; 2001FR-00005642.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contains only 2344 sequences.
                                                                                                                             26-APR-2002; 2002WO-IB003059
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781 ASMSASTSASMSA 793
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les 9; Conservative
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                                                                                                                                                                                                                                                                                                                       Rusniok C,
                                                                                                                                                                                                                                                                                                                                             Couve E,
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Gaps

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Wang J;

pharmaceutical

26-MAR-2002

ABB64821;

Query Match Best Loc Matches

g 8

WO200171042-A2

27-SEP-2001

Sequence 276 AA; 06-JAN-2005. replacement ADW17198; Query Match RESULT 10 ADW17198 8 셤

The invention relates to novel isolated polymucleotides or a sequence encoding a polypeptide with biological activity, where the polymucleotide with biological activity, where the polymucleotide or the polymucleotide under stringent hybridization conditions or has greater than 99% sequence identity with the polymucleotide. The conjunction of mutations responsible for genetic gene mapping, identification of mutations responsible for genetic disorders and other traits, to assess biodiversity, as nutritional sources or supplements. The polymucleotides may also be used as molecular course, chromosome markers or map related gene positions, or as an antigen to raise anti-DNA antibodies or elicit immune response. The polymothides are useful for raising antibodies, as markers for tissues in which the corresponding polypeptide is expressed, for re-engineering damaged or diseased tissues, for treating myeloid or lymphoid cell cliscues; in home cartilage, tendon, ligament and/or nerve tissue growth or regeneration, in wound healing, in tissue repair and replacement, in the reginer or this course. This New polynucleotides and secreted proteins, useful for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve tissue growth or regeneration, in wound healing, and in tissue repair and sequence corresponds to a protein sequence of the invention. Claim 20; SEQ ID NO 173; 243pp; English.

72.2%; Score 39; DB 7; Length 276; 61.5%; Pred. No. 1.7e+02; ive 5; Mismatches 0; Indels 1 ASMSAASAASMAA 13 Best Local Similarity 61.5 Matches 8; Conservative

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Gaps

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|::|||:||:|| | AALSAAAAAALAA 17

plant; transcription; gene regulation; gene expression; transgenic plant; drought resistance; disease resistance; salt tolerance; cold tolerance; freezing tolerance; flowering; flavor enhancer; flower color. E\_grandis transcription factor protein C2C2 (co-like) family Seq 948. ADW17198 standard; protein; 311 AA. 24-MAR-2005 (first entry) Eucalyptus grandis

07-JUN-2004; 2004WO-US017965. 06-JUN-2003; 2003US-0476189P. (ARBO-) ARBORGEN LLC. WO2005001050-A2.

New polynucleotides isolated from plants encoding transcription factors, and polypeptides encoded by such polynucleotides, useful for regulating gene transcription and gene expression. Magusin A; K, Wood M; Emerson SJ, Fror Lund ST, Mague. Gause K, Connett MB, Emerson SJ, Higgins C, Lasham A, Lund Veerakone S, Westwood C, Bryant C, Grigor M, F Puthigae S, WPI; 2005-075542/08. N-PSDB; ADW16412. Bloksberg LN, Forster RLS, G Phillips J, Pu

This invention relates to novel isolated plant nucleic acid molecules, or variants thereof, that encode transcription factors. Specifically, it refers to transcription factor proteins that are capable of binding to DNA in order to require gene transcription and gene expression in a plants, in particular Eucalyptus grandis and Pinus radiata. The present invention describes DNA constructs containing DNA encoding a transcription factor that regulates the promoter, which is operably linked to the desired nucleic acid to be expressed. It further provides transgenic plants expressing a transcription factor that confers a trait to the plant such as increased drought, salt or disease tolerance, height nucleic, enhanced cold, frost tolerance, enhanced color, health and nutritional characteristics, as well as improved taste, starch 占 composition, flower longevity and germination, amongst others.
Accordingly, such plants that are successfully transfected with a DNA construct can be characterized by a difference in flower color, petal or leaf shape and size, aroma or plant height. This polypeptide is a plant transcription factor protein sequence of the invention. Claim 31; SEQ ID NO 948; 1265pp; English. 

Gaps ö Score 39; DB 9; Length 311; Pred. No. 1.9e+02; Mismatches 2; Indels 1; Mismatches 72.2%; 76.9%; 1 ASMSAASAASMAA 13 Best Local Similarity 76.9 Matches 10; Conservative Sequence 311 AA; Query Match ð

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ADI42807 standard; protein; 395 AA. 155 AAASAASAAA 167 22-APR-2004 (first entry) AD142807; RESULT 11 ADI42807 엄

Plant transcription factor #459.

transgenic; plant; enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone sensitivity; disease resistance; sugar sensing; flower structure; stem bifurcation; branching pattern; apical dominance; trichome; stem morphology; root growth; root hair; seed development; call proliferation; cell differentiation; premature senescence; necrosis; plant size; leaf morphology; seed morphology; seed biochemistry; root anthocyanin; plant enthocyanin; lapt response; shade avoidance; bioinformatic; transcription factor; gene; ds

25-FEB-2003; 2003US-00374780. US2004019927-A1 Oryza sativa. 29-JAN-2004. 

SHERMAN B K. RIECHMANN J L. HEARD J E. HAAKE V. CREELMAN R A. RATCLIFFE O. ADAM L J. REUBER T L. KEDDIE J. JIANG (HAAK/) (CREE/) (RATC/) (ADAM/) (REUB/) SHER/) (JIAN/) (HEAR/) RIEC/)

18-APR-2001; 2001US-00837944

BROUN P E. (KEDD/) (BROU/) (PILG/) 10-APR-2003; 2003US-00412699

04-MAR-2004

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The invention describes a transgenic plant comprising a recombinant belonged of any one of more than 500 nucleotide sequences fully defined in the specification or its complement. The method of the invention can be used to produced a plant having altered traits such as: chhanced tolerance to abiotic stress; glyphosphate tolerance; hormone sensitivity; disease resistance; sugar sensing; early or late flowering; altered flower structure, change in steem bifurcations, altered branching pattern, reduced apical dominance, reduced trichome density; lack of trichomes; reduced crichome development; altered trichome trichome trichome number; altered stem morphology; cincreased root growth; increased root hairs; altered seed development; caltered cell proliferation or cell differentiation; rapid development; premature senescence; increased nor cell differentiation; rapid development; premature senescence; increased necrosis; increase in seedling or plant of size; decreased plant size; leaf morphology; seed morphology; seed conthocyanins, or alteration in light response or shade avoidance. The anthocyanins; increase in plant can be useful in bioinformatic search methods. This is the amino acid sequence of a plant transgenic plant with altered traits can be used in the transcription factor, and an orthologue of Arabiodopsis thaliana creation of a transgenic plant with altered traits.
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                                                                                                                                                                                                     New transgenic plant comprising a recombinant polynucleotide of any one of more than 500 nucleotide sequences, useful in bioinformatic search methods.
                                                                                 Haake V;
Keddie J, Broun PE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 39; DB 8; Length 395;
Pred. No. 2.5e+02;
3; Mismatches 1; Indels
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                                                                                 Jiang C, Heard JE, Adam LJ, Reuber TL,
                                                                                                                       Pineda O, Yu G
                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 1270; 435pp; English.
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                                                                               Riechmann JL,
                                                                                                    Creelman RA, Ratcliffe O,
Pilgrim ML, Dubell AN, P
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Best Local Similarity 69.2
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DUBELL A N.
PINEDA O.
                                                                                                                                                               WPI; 2004-132245/13
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(DUBE/) DUBELL (PINE/) PINEDA (YUGG/) YU G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa.
                                                                                 Sherman BK,
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polymucleotide having a polymucleotide sequence or its complementary sequence comprising a sequence encoding a polypeptide, that initiates transcription (i.e. a transcription factor) from Arabidopsis, Soybean, Nic., Rape or Corn, comprising any of the sequences appearing as AD001588 -AD003527 or AD003530-AD003559. Also included are using a transgenic plant to grow a progeny plant, an expression cassette (comprising a constitutive, inducible or tissue-specific promoter and a recombinant polymucleotide described above), a host cell comprising the expression cassette, producing a modified plant having a modified trait, identifying a factor that is modulated by or interacts with a polypeptide encoded by the polymucleotide sequence and identifying at least one downstream polymucleotide sequence that is subject to a regulatory effect of any of the polypeptides encoded by the polymucleotide described above. The transgenic plant is useful for producing a plant that has an altered transgenic plant, susful for producing a plant that has an altered transgenic plant, and encoded polymucleotide sequence to abjoric stress (increased tolerance to chilling, germination in cold conditions, freezing tolerance to theat, tolerance to the heat, tolerance to semotic stress, tolerance to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New transgenic plant, useful in developing phenotypes with altered or improved characteristics or traits.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fromm ME, Heard JE, Riechmann JL, Adam LJ, Broun PE; Reuber TL, Keddie JS, Yu G, Jiang C, Samaha RS; L, Creelman RA, Dubell AN, Ratcliffe O, Kumimoto R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 1424; 213pp; English.
                                                                                                                                         22 - MAR. - 2000; 2000US-00533030.
22 - MAR. - 2000; 2000US-00533030.
22 - MAR. - 2000; 2000US-00533032.
22 - MAR. - 2000; 2000US-00533032.
16 - NOV. - 2000; 2000US-00713994.
27 - MAR. - 2001; 2001US-00819142.
17 - AFR. - 2001; 2001US-00819142.
17 - AFR. - 2001; 2001US-00958131.
14 - JUN - 2002; 2002US-00958131.
14 - JUN - 2002; 2002US-0025506.
09 - AUG-2002; 2002US-00225068.
17 - DEC - 2002; 2002US-041466P.
25 - FEB-2003; 2003US-0434166P.
                                                                             21-JAN-2000; 2000US-00489376.
17-FEB-2000; 2000US-00506720.
22-MAR-2000; 2000US-00532591.
22-WAR-2000; 2000US-00533029.
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DUBELL A N.
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SAMAHA R S.
PILGRIM M L.
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FROMM M E.
HEARD J E.
RIECHMANN J I
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BROUN P E.
PINEDA O.
REUBER T L.
KEDDIE J S.
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Pilgrim ML,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BROU/)
(PINE/)
(REUB/)
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(YUGG/)
(JIAN/)
(SAMA/)
(PILG/)
(CREE/)
(DUBE/)
(RATC/)
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(HEAR/)
(RIEC/)
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biochemistry, an increase in seed oil content, decrease in seed oil content, increase in seed fatty acid content, decrease in seed fatty acid content, increase in seed protein content, decrease in seed protein content, alteration in seed promyl lipid content, increase in seed sterols, upregulation of genes involved in secondary metabolism, increase in root anthocyanins, increase in plant anthocyanins, and alteration in light response or shade avoidance. The present sequence represents an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant; transcription factor; transgenic plant; abiotic stress tolerance; osmotic stress tolerance; cold tolerance; heat tolerance; low nitrogen tolerance; low phosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development.
                                                                                                                                                                                                                                                                                                                                             or shade avoidance. The present sequence represents an thalecress transcription factor isolated from Rice.
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to phosphate limitation, tolerance to potassium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADO62431 standard; protein; 395 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-DEC-2002; 2002US-0434166P.
24-APR-2003; 2003US-0465809P.
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264 AAMSASSAAAAAA 276
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nes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 395 AA;
                                                                                                                                                                                                                                                                                                                                                              orthologue of a
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                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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ADO62431
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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The present invention relates to novel plant transcription factor proteins (I) and nucleotide sequences (II) (ADO61384-ADO6379). The equences can be used to produce transgenic plants, which overexpress (II), where the transgenic plant has an altered trait as compared to a nathered trait selected from increased tolerance to abiotic stress, increased tolerance to cold, increased tolerance to disease, including increased tolerance to disease, including disease and particularly Erysiphe, Pusarium and Botrytis, cold particularly Erysiphe, Pusarium and Botrytis, increased sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABC, altered sugar sensing, increased tolerance to cold sease and particularly Erysiphe, Pusarium and Botrytis, cold sensitivity to ABC, altered sugar sensing, increased tolerance to calcard sensitivity to ABC, altered sugar sensing, increased tolerance to calcard sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ABC, altered sugar sensing, altered shoot meristem development, altered branching pattern, altered shown morphology, altered vascular tissue structure, reduced tertility altered shoot meristem development, altered branching pattern, altered seed trichome structure, altered cold proliferation, altered cold expendition, altered cold expendition, altered cell expension, altered bhase calcarded blomass, large seedlings dwarfed plants, dark growth, altered cell proliferation, altered cell expension altered sensecence, abnormal embryo development, altered bhase, large seed sensecence, abnormal embryo development, altered phase of altered sensecence, abnormal embryo development, altered phase, large seed large and mass, large seed increased leaf prant, large seed large and mass, large seed increased ant
                                                                                                       New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.
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Reuber TL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
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                        Sherman BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39; DB 8; Length 395;
Pred. No. 2.5e+02;
3; Mismatches 1; Indels
  Adam LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster polypeptide SEQ ID NO 3390.
Jiang C, Heard JE, Ratcliffe O, Creelman RA, Riechmann JL, Haake V, Dubell AN, Keddie JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                Claim 1; SEQ ID NO 898; 510pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB58866 standard; protein; 793 AA.
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Best Local Similarity 69.4.
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ASMSAASAASMAA 13
                                                                    WPI; 2004-330163/30
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ABB58866
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The invention relates to novel abiotic stress responsive polynucleotides and polypeptides. Also disclosed are vectors, expression cassettes, host cells, and plants containing such polynucleotides. Also disclosed are methods for using the polynucleotides and polypeptides to alter the responsiveness of a plant to abiotic stress. The invention is useful in agriculture. The nucleic acid is useful for determining whether a test plant has been exposed to an abiotic stress condition. It is also useful for selecting an agent that alters abiotic stress regulated polynucleotide expression in a plant cell, and to identify a homolog or ortholog to an abiotic stress responsive polynucleotide. The nucleic acid molecule and the polypeptide encoded by it are useful in altering the responsiveness of a plant to an abiotic stress, such as cold stress, salt stress, osmocic stress cany of their combinations. The present sequence is used in the exemplification of the invention
                                                                                                                              responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold stress, salt stress or osmotic stress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MHC class II compound; MHC class II component; MHC class II alpha chain; MHC class II beta chain; peptide binding groove; spaceholder molecule; effector component; immune response; immune disorder; virucide; antibacterial; antiparasitic; cytostatic; immunosuppressive; gene therapy; viral infections; bacterial infection; parasitic infection; neoplastic disease; autoimmunity; toxicity; human.
  Katagiri F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New MHC class II compound, useful for preparing a composition for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human MHC class II compound spaceholder molecule SEQ ID NO:2.
                                                                                                          New stress-responsive nucleic acid, useful for altering the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.2%; Score 39; DB 7; Length 930; 76.9%; Pred. No. 6.1e+02; tive 1; Mismatches 2; Indels
  Goff SA,
Glazebrook J,
J, Zhu T;
                                                                                                                                                                                              Claim 1; SEQ ID NO 7444; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DAND ) DANA FARBER CANCER INST INC.
  Kreps J, Briggs SP, Cooper B, Gl
Moughamer T, Provart N, Ricke D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-JUL-2003; 2003WO-US021767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-JUL-2002; 2002US-0395494P.
22-JUL-2002; 2002US-0397893P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-248011/24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 930 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2004007528-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JAN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADI29006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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ADI29006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                      new isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  abiotic stress tolerance; transgenic plant; plant; cereal; agriculture.
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Pred. No. 5.2e+02;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rice abiotic stress responsive polypeptide SEQ ID NO:7444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 3390; 21pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABM89198 standard; protein; 930 AA.
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26-SEP-2001; 2001US-0325277P.
                                                                                                                                                                   23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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                                                                                                                           23-MAR-2001; 2001WO-US009231
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Drosophila melanogaster
                                                                                                                                                                                                                                                                             Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                     WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                   (PEKE ) PE CORP NY
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                                       WO200171042-A2
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The present invention describes an isolated WHC class II compound (I) comprising: (a) an MHC class II component comprising at least a portion of an MHC class II alpha chain and at least a portion of an MHC class II beta beta chain, such that the MHC class II alpha chain and MHC class II beta chain form a peptide binding groove; (b) a spaceholder molecule; and (c) an effector component, where the effector component is linked to the MHC class II component. Also described: (l) a pharmaceutical composition comprising the MHC class II molecule and a carrier; (2) a method of producing an MHC class II compound; (3) a method of directly identifying in a subject; (5) a method of treating an immune disorder in a subject; and can be used for treating an immune esponse ex vivo in a subject; and (7) a method of treating an immune response ex vivo in a subject; and (7) a method of treating an immune disorder ex vivo in a subject; and (7) a method of treating an immune disorder and immunosuppressive activities, and can be used in gene therapy. The MHC class II compound (I) can be used for preparing a composition for treating immune catcivities, and can be used in gene therapy. The MHC class II compound infections, parasitic infections, neoplastic disease, autoimmunity or toxicity. The present sequence represents a spaceholder invention.

The MHC class II compound from the present invention.
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treating immune disorders e.g. viral infections, bacterial infections, parasitic infections, neoplastic disease, autoimmunity or toxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
vitamin B12; bacterial infection; disease.
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Pred. No. 8.5;
1; Mismatches 0; Indels
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                                                            Claim 11; SEQ ID NO 2; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB49912 standard; protein; 328 AA
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1 AAMAAAAAAAAA 12
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12 AA;
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The present invention relates to the genome sequence of Listeria

CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of

CC it are useful for selecting probes and primers for detecting genes in L.

CC monocytogenes and related organisms, and for studying genetic

monocytogenes and related organisms, and for studying genetic

CC polymorphisms and other genomes. The present sequence is a protein

CC polymorphisms and other genome sequence of the present invention. Proteins

CC antibodies, identification of L. monocytogenes and related organisms, and

CC antibodies, identification of L. monocytogenes and related organisms, and

CC in biosynthesis and biodegradation, especially biosynthesis of vitamin

CC antibodies is and biodegradation, especially biosynthesis of vitamin

CC in biosynthesis and biodegradation, especially biosynthesis of vitamin

CC selecting compounds that regulate gene expression and cell replication

CC selecting compounds that regulate gene expression and cell replication

CC selecting compounds that regulate gene expression and cell replication

CC selecting compounds that regulate gene expression and cell replication

CC selecting compounds that regulate gene expression and cell replication

CC selecting compounds that regulate gene expression and cell replication

CC sequence and proteins encoded by it are useful in pharmaceutical and

CC vaccines compositions for the treatment or prevention of infections by L.

CM monocytogenes and related organisms. Note: The sequence data for this

CM patent did not form part of the printed specification, but was obtained

CM patent form part of the printed specification, but was obtained

CM patent form part of the printed specification, but was obtained

CM patent form part of sequences
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Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related polypeptides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 328;
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Pred. No. 2.9e+02;
3; Mismatches 1;
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                                                                                                                Claim 6; SEQ ID NO 2617; 192pp; French.
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sest Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes an isolated nucleotide fragment (I) comprising a nucleic acid sequence (NS) chosen from a NS encoding a polypeptide (PP) having receptor-like protein kinase activity, mitogen activated protein (MAP)-kinase activity, LIPI5-like transcription factor activity, caleosin-like activity, ATP citrate lyase activity, SNF1-like activity and CKC-like transcription factor activity and CKC-like transcription factor activity. Also described: (1) complement (II) of (I); (2) a chimeric construct (III) comprising (I) or (III), operably linked to a regulatory sequence; (3) a plant (IV); and (5) comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleotide fragment encoding polypeptides having receptor-like protein kinase activity, caleosin-like activity, useful for altering oil phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B;
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapoutics and pharmaceutical drugs. The invention siscloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB27737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S, Famodu OO, Harvell LT; iveira IC, Sakai H, Shen I
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plant, oil trait; oil phenotype; altered lipid profile; MAP kinase; receptor-like protein kinase; mitogen activated protein kinase; oil; LIP15-like transcription factor caleosin; ATP citrate lyase; SNP1; CKC-like transcription factor; antisense inhibition; co-suppression;
                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycine max oil trait related protein sequence SEQ ID NO:216.
                                                                                                                                                                                                                                                      Length 508;
                                                                                                                                                                                                                                                      Score 38; DB 4; Length 508
Pred. No. 4.7e+02;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Epelbaum S, Famodu Li C, Oliveira IC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12; Page 248-250; 542pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΞΊ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABR40698 standard; protein; 589 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cahoon RE,
Klein TM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DUPO ) DU PONT DE NEMOURS & CO (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-JUN-2002; 2002WO-US020152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JUN-2001; 2001US-0301913P.
                                                                                                                                                                                                                                                      70.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                     449 ASVAAASAAAAA 461
                                                                                                                                                                                                                                                                                                                                  1 ASMSAASAASMAA 13
                                                                                                                                                                                                                                                                    Local Similarity 69.2
les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kinney AJ,
MC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2003-201509/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Allen SM, Allen WB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-201509/
N-PSDB; ACC00733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transgenic plant
                                                                                                                                                                                                                   Sequence 508 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003002751-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycine max
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                                                                                                                                                                                                                                                      Query Match
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ABR40698
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oil obtained from (V). (I) or its part can be used in antisense inhibition or co-suppression in a transformed plant. (III) is useful for altering the oil phenotype in a plant such as corn, soybean, wheat, rice, canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for creating transgenic plants having altered lipid profiles. (I) can also be used as a hybridisation probe. ACCOOGSE to ACCOOGSE and ABR40591 capesent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to novel abiotic stress responsive polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     stress tolerance; transgenic plant; plant; cereal; agriculture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goff SA, Katagiri F;
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for altering the
an abiotic stress such as
                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rice abiotic stress responsive polypeptide SEQ ID NO:6244.
                                                                                                                                                                                                   Length 589
                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                 Score 38; DB 6; 1
Pred. No. 5.5e+02;
2; Mismatches 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glazebrook J,
J, Zhu T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New stress-responsive nucleic acid, useful responsiveness of a plant, e.g. cereal, to stress, salt stress or osmotic stress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 6244; 89pp; English:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SYGN ) SYNGENTA PARTICIPATIONS AG.
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                                                                                                                                                                                                                                                                                                                                                                                                        Ą.
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                                                                                                                                                                                                                                                                                                                                                                                                        ABM87998 standard; protein; 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-JUN-2001; 2001US-0300112P.
24-AUG-2001; 2001US-0314662P.
26-SEP-2001; 2001US-0325277P.
21-NOV-2001; 2001US-0332132P.
                                                                                                                                                                                                   70.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUN-2002; 2002WO-US019668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                            67 ASFRSASASSMAA 79
                                                                                                                                                                                                                                                                          1 ASMSAASAASMAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kreps J, Briggs SP, Coo
Moughamer T, Provart N,
                                                                                                                                                                                                                                     9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-248011/24.
                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                 Sequence 589 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003008540-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2003
                                                                                                                             invention
                                                                                                                                                                                                                                                                                                                                                                                                                                          ABM87998:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     abiotic
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Matches

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RESULT 21

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL35511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense, prokaryotic essential gene, cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                                     developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 22404; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37; DB 4; Length 285;
Pred. No. 3.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein encoded by Prokaryotic essential gene #35899.
                                                   Drosophila melanogaster polypeptide SEQ ID NO 22404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABU50372 standard; protein; 375 AA.
                                                                                                                                                                                                                                                                                                                                                                                   Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2002; 2002WO-US009107.
                                                                                                                                                                                                                                                        23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                        23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68.5%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158 AAVAAASAAVAA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid
genes from Drosophila and
               26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ASMSAASAASMAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Conservative
                                                                                                                                            Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                     Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                     2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                 (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABL09307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 285 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yersinia pestis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200277183-A2
                                                                                                                                                                                WO200171042-A2
                                                                                                            pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genes from Dr
interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-OCT-2002
                                                                                       Drosophila;
                                                                                                                                                                                                                    27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                     Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU50372;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a substantially purified nucleic acid molecule encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a recombinant DNA construct for expression of a nitrite reductase gene in a plant cell, and a plant cell comprising the recombinant DNA construct. The nucleic acid is useful for determining gene expression, identifying mutations in a gene of interest, and for constructing mutations in a gene of interest and for sEQ IDS 9692-16825 represent a group of 7134 Mxyococcus xanthus proteins and peptides. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New substantially purified Myxococcus xanthus nucleic acid molecule encoding a nitrite reductase, useful for determining gene expression, identifying mutations in a gene of interest, and for constructing mutations in a gene of interest.
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                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                       Transgenic plant; DNA replication; gene regulation; gene expression.
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                                     Length 45;
                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wiegand RC;
                                    DB 7;
51;
                                    Score 37; DB 7
Pred. No. 51;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; SEQ ID NO 11882; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                     M. xanthus protein sequence, seq id 11882.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Slater SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB65204 standard; protein; 285 AA.
                                                                                                                                                                                                                                           ABM92683 standard; protein; 170 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MONS ) MONSANTO TECHNOLOGY LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-JUL-2001; 2001US-00902540.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-JUL-2000; 2000US-0217883P.
                                    68.5%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 75...
9, Conservative
                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                            1 ASMSAASAASMAA 13
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| ASLTAASASAMIA 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hinkle GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2005-028716/03.
                                                                                                                                                                                                                                                                                                                                                                                                                               Myxococcus xanthus,
                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 170 AA;
   Sequence 45 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US6833447-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-DEC-2004
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ABB65204;

ABB65204

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99US-0124270P

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New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and
                                    nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant;
                                                                      antibacterial; antifungal; antiparasitic; cardiant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; amultiple sclerosis; rheumatoid arthritis; ulcerative colltis; cardiovascular disorder; wound healing; neurological disease.
                                                                                                                                                                                                                                                                                        08-MAR-2000, 2000WO-US005881.
                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurological diseases.
                                                                                                                                                                                                                                                                                                                                                                                                 Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-611515/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAF21701.
                                                                                                                                                                                                                  WO200055173-A1
                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                           12-MAR-1999;
                                                                                                                                                                                                                                                     21-SEP-2000.
                      Human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                    The invention features to an isolated muclead acta compirising any one of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid conformation and inhibited by the antisense accidenceding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated conformation and inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular contineration; (7) identifying a compound that influences the activity of the polypeptide for proliferation or that has an activity against a biological pathway required for that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) contained for proliferation or the biological pathway in which a proliferation required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibictic; (10) profiling a compound; activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or organism acts; (9) manufacturing an antibictic; (10) profiling a compound; activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or organism. The strains; or compound that inhibits the conformation of an organism. The antitiense nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, conformative for proliferation in cells other than S. aureus, S. typhimurium, conformation in electronic format directly from MIPO at equired format dined formation or the parent sequence is encoded by one of the print in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Breast and ovarian cancer associated antigen protein sequence SEQ ID 506.
                                                                                                                                                                                                                                                                                                                                                                            invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                          Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                              New antisense nucleic acids, useful for identifying proteins or so for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB 6; Length 375; Pred. No. 4.9e+02;
                                                                                                                                                            Haselbeck R, Ohlsen KL,
Yamamoto R, Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                      Claim 25; SEQ ID NO 78296; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB58798 standard; protein; 434 AA.
                                                                                                                                                          Malone C,
Carr GJ,
                               06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
                                                                    08-FEB-2002; 2002US-00072851.
                  21-MAR-2001; 2001US-00815242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180.06
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                                                                                                                       (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 SAASVASMAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 SAASAASMAA 13
                                                                                                                                                          Zamudio C,
Trawick JD,
                                                                                                                                                                                                                2003-029926/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                N-PSDB; ACA54242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 375 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB58798;
                                                                                                                                                          ů,
                                                                                                                                                          Wang I
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isolation and characterisation of the DNA and protein sequences of the invention. The breast and ovarian cancer associated DNA, protein, agonist or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antialergic; hepatotropic; antidiabetic; antiinflammatory; antiviral; antialergic; hepatotropic; antidiabetic; antifinflammatory; antiviral; antionavulsant; antibacterial; antibacterial; antitungal; antiparasitic and cardiant activity. The polymucleotide and protein sequences are used in the diagnosis of cancer, particularly breast and ovarian cancer. The mucleic acid sequences, proteins, agonists and agonists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's datisease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; neurological diseases such as cerebral anoxia and epilepsy; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                               Sequences AAF21614 - AAF22031 represent DNA sequences encoding human proteins ABES9711 - AAB59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are sequences AAF22032 - AAF22040 and AAB59129 which are used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 5.7e+02;
4; Mismatches 1; Indels
Claim 11; Page 940-942; 1299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADR43053 standard; protein; 455 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68.5%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 61...
8; Conservative
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8 ASVSTAAAAALAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         infectious diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 434 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 25
ADR43053
ID ADR43
XX
AC ADR43
XX
DT 18-NO
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The present invention relates to a novel recombinant DNA polynucleotide comprising a cell cycle regulated promoter, such as a cyclin promoter, that functions in plants operably linked to a DNA polynucleotide encoding an isopentenyl transferase. The present sequence is one such isopentenyl transferase. The present sequence is one such isopentenyl transferase. Also claimed are transgenic plants comprising the recombinant DNA polynucleotide. The recombinant polynucleotide is useful for producing transgenic plants expressing cytckinin biosynthetic genes, and also provides an improved method of producing transgenic plants with increased yield and vigor. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to Pseudomonas aeruginosa polypeptides and the polymucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics.
                                                                                              New recombinant DNA polynuclectide comprising a cell cycle regulated promoter and encoding an isopentenyl transferase, useful for producing transgenic plants expressing cytokinin biosynthetic genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37; DB 10; Length 455; Pred. No. 6e+02; i, Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas aeruginosa polypeptide #4050.
                                                                                                                                                                                        Disclosure, SEQ ID NO 128; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Deloughery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABO71875 standard; protein; 493 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 SMSAASAASMAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa
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                                                             WPI; 2006-088763/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABD05446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 455 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rubenfield MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABO71875;
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                     He SS;
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Matches
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ABO71875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to an isolated polynucleotide comprising a plant promoter directing transcription of an operably linked polynucleotide in at least one of the tissues selected from abscrission zone, root, pod, wall, apical meristem, and flower of plants. The polynucleotides and methods are useful for producing a plant having increased yield or a trait of agronomic interest when compared to a nontransformed plant of the same genotype. The present sequence represents a IPP-like structural protein. The sequence data for this patent is not represented in the printed specification but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transgenic plant; plant breeding; isopentenyl transferase; enzyme; plant
                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotides comprising a plant promoter that directs its transcription into abscission zone(s), root, pod, wall, apical meristem, or flower of plants, useful for producing a plant having increased yield or agronomic trait.
                                       abscission zone; apical meristem; Plant Growth Regulant; Gene Therapy; A6; abscission zone promoter; IPT; isopentyl transfease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                     Tennessen DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  Nelson DE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 21; SEQ ID NO 135; 63pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isopentenyl transferase, SEQ ID 128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEF15580 standard; protein; 455 AA.
    IPT-like structural protein #112
                                                                                                                                                                                                                                                                                                                           (MONS ) MONSANTO TECHNOLOGY LLC.
                                                                                                                                                                                                                                                                                                                                                                     Eilers RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JUN-2005; 2005US-00156084.
                                                                                                                                                                                                                                                                               14-FEB-2003; 2003US-0447833P.
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                                                                                                                                                                                                                                        13-FEB-2004; 2004WO-US004499.
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Best Local Similarity 66...
8; Conservative
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| SLAAATAASIAA 121
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                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-635562/61.
                                                                                                                                                                                                                                                                                                                                                                     Deng M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 455 AA;
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                                                                                                                                                    WO2004074442-A2
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                                                                                                           Unidentified
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                                                                                                                                                                                              02-SEP-2004.
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prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABO67826-ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antisense, prokaryotic essential gene; cell proliferation, drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                Score 37; DB 7; Length 493; Pred. No. 6.5e+02; 0; Mismatches 3; Indels
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein encoded by Prokaryotic essential gene #7794.
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 25; SEQ ID NO 50191; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU22267 standard; protein; 533 AA.
                                                                                                                                                                                                                        seqdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                68.5%;
76.9%;
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                                                                                                                                                                                                                                                                                            Query Match 68.5
Best Local Similarity 76.9
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burkholderia mallei
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N-PSDB; ACA26137.
                                                                                                                                                                                                                                                              Sequence 493 AA;
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Wall
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the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway is dentifying a gene required for cellular proliferation; (8) constitution or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound; sactivity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimmrium, K. pneumoniae or P. aeruginesa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MHC class II compound; MHC class II component; MHC class II alpha chain; MHC class II beta chain; peptide binding groove; spaceholder molecule; effector component; immune response; immune disorder; virucide; antibacterial; antiparastic; cytostatic; immunosuppressive; gene therapy; viral infections; bacterial infection; parasitic infection, neoplastic disease; autoimmunity; toxicity; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New MHC class II compound, useful for preparing a composition for treating immune disorders e.g. viral infections, bacterial infections, parasitic infections, neoplastic disease, autoimmunity or toxicity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37; DB 6; Length 533
Pred. No. 7.1e+02;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADI29007 standard; peptide; 13 AA.
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61.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 533 AA;
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The present invention describes an isolated MHC class II compound (I) comprising: (a) an MHC class II component comprising at least a portion of an MHC class II clapha chain and at least a portion of an MHC class II alpha chain and MHC class II beta chain, such that the MHC class II alpha chain and MHC class II beta chain form a peptide binding groove; (b) a spaceholder molecule; and (c) an effector component. Also described: (1) a pharmaceutical composition class II component. Also described: (1) a pharmaceutical composition comprising the MHC class II molecule and a carrier; (2) a method of producing an MHC class II compound; (3) a method of directly identifying an antigen-specific T cell; (4) a method of regulating an immune disorder in a subject; (6) a method of regulating an immune response ex vivo in a subject; and concept composition for treating an immune disorder ex vivo in a subject; (1) has vivoide, antibacterial, antiparasitic, cytostatic and immunosuppressive civicuites, and can be used in gene therapy. The MHC class II compound (1) can be used for preparing a composition for treating immune cativities, and can be used in gene therapy. The MHC class II compound for infections, parasitic infections, neoplastic disease, autoimmunity or toxicity. The present sequence represents a spaceholder molecule peptide, which can be used in the present invention. Claim 11; SEQ ID NO 3; 92pp; English 

Sequence 13 AA;

66.7%; Score 36; DB 8; Length 13; 61.5%; Pred. No. 19; 1; Indels 4; Mismatches Query Match
Best Local Similarity 61...
Best Conservative
8; Conservative 1 ASMSAASAASMAA 13 1 AAMAAAAAAAA 13 8 셤

RESULT 30 ADH47583

ADH47583 standard; peptide; 20 AA. (first entry) 25-MAR-2004 ADH47583; 

Human lung tumour clone peptide, SEQ ID No 2064.

cancer; tumour; cytostatic; immunostimulant; vaccine; gene therapy; human; clone nng

Homo sapiens.

WO2003037267-A2.

08-MAY-2003

28-OCT-2002; 2002WO-US034777.

29-OCT-2001; 2001US-00017754 28-MAR-2002; 2002US-00113872

(CORI-) CORIXA CORP.

Fanger GR, Vedvick TS; Sleath PR; Kalos MD, Carter D, Watanabe Y, Durham M, Henderson RA, Wang T, I Johnson JC, Retter MW, Johnson JC, Retter M Bangur CS, Mcnabb A;

WPI; 2003-468346/44.

New polypeptides and encoding polynucleotides, useful for diagnosing, preventing and/or treating lung cancer.

Example 38; SEQ ID NO 2064; 258pp; English.

The invention relates to novel compositions and methods for the therapy

and diagnosis of cancer, particularly lung cancer. The compositions comprise one or more lung tumour polypeptides, immunogenic portions therof, polynucleotides that encode such polypeptides, antigen presenting cells that expressing such polypeptides, and T cells that are specific for cells expressing such polypeptides. The novel compositions have cytostatic and immunostimulant activity. The lung tumour antigens can be used in the creation of a vaccine. The polynucleotides that encode the lung tumour polypeptides can be used in gene therapy to help in the treatment of lung tumours. This sequence represents a human lung tumour clone polypeptide of the invention. This sequence was not shown in the specification. It has been taken from a World Intellectual Property Organization CD ROM supplied with the specification.

0222222222222228

Sequence 20 AA;

Gaps ; 0 Length 20; 2; Indels Score 36; DB 7; Pred. No. 31; 2; Mismatches DB 31; 66.7%; Ouery Match
Best Local Similarity 6>...
Best Joy 9; Conservative

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RESULT 31 ADH47584

Ä ADH47584 standard; peptide; 20 25-MAR-2004 (first entry) ADH47584;

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Gaps

., 0

Human lung tumour clone peptide, SEQ ID No 2065.

lung cancer; tumour; cytostatic; immunostimulant; vaccine; gene therapy; human; clone

Homo sapiens.

WO2003037267-A2 08-MAY-2003. 28-OCT-2002; 2002WO-US034777.

29-OCT-2001; 2001US-00017754. 28-MAR-2002; 2002US-00113872.

(CORI-) CORIXA CORP.

Sleath PR; Fanger GR, Vedvick TS; Watanabe Y, Kalos MD, Durham M, Carter D, Henderson RA, Wang T, Johnson JC, Retter MW, Johnson JC, Retter M Bangur CS, Mcnabb A; X \$\forall \text{B} \times \te

WPI; 2003-468346/44.

encoding polynucleotides, useful for diagnosing, preventing and/or treating lung cancer. polypeptides and New

Example 38; SEQ ID NO 2065; 258pp; English.

The invention relates to novel compositions and methods for the therapy and diagnosis of cancer, particularly lung cancer. The compositions comprise one or more lung tumour polypeptides, immunogenic portions therof, polynucleotides that encode such polypeptides, antigen presenting cells that express such polypeptides, and T cells that are specific for cells expressing such polypeptides. The novel compositions have cytostatic and immunostimulant activity. The lung tumour antigens can be used in the creation of a vaccine. The polynucleotides that encode the lung tumour polypeptides can be used in gene therapy to help in the treatment of lung tumoure. This sequence represents a human lung tumour clone polypeptide of the invention. This sequence was not shown in the specification. It has been taken from a World Intellectual Property

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US2003211510-A1.
                                                                       Sequence 20 AA;
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                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence chosen from any one of 40 lung tumour polypeptides or its complements, fragments or degenerate variants. The method of the invention has cytostatic applications and may be useful for detecting and treating lung cancer in a patient, as well as for inhibiting the development of lung cancer in a patient via incubating CD4+ and/or CD8+ T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel isolated polynucleotide comprising a
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vedvick
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                                                                                                                                                                                        Human lung cancer-related L978P peptide fragment - SEQ ID 2064.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polynucleotide encoding lung tumor polypeptides, useful diagnosing, preventing and treating cancer e.g. lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PR;
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                                    Length 20
                                                     2; Indels
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Organization CD ROM supplied with the specification.
                                                                                                                                                                                                        lung tumour; cytostatic; lung cancer; human; L978P.
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Carter D,
                                    7;
                                  ore 36; DB 7
ed. No. 31;
Mismatches
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                                    Score
Pred.
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                                                                                                                                    ADJ21502 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                         26-SEP-2000; 2000US-00671325.
06-OCT-2000; 2000US-00677419.
30-OCT-2000; 2000US-00702705.
13-DEC-2000; 2000US-007136457.
03-MAY-2001; 2001US-00849626.
10-JUL-2001; 2001US-0089991.
                                                                                                                                                                                                                                                                                               99US-00346492.
99US-0041356.
99US-0041356.
99US-0046867.
200UUS-00533077.
200UUS-00533077.
200UUS-00533077.
200UUS-00564406.
200UUS-00664124.
200UUS-00664124.
200UUS-0061353.
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28-MAR-2002; 2002US-00113872
                                  66.7%;
69.2%;
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| ASASASSAASA 14
                                                                                                                                                                     (first entry)
                                                                     1 ASMSAASAASMAA 13
                                 Query Match
Best Local Similarity 69.2
Matches 9; Conservative
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Johnson JC, Retter MW,
Bangur CS, Mcnabb A;
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                                                                                                                                                                                                                                            US2003211510-A1
                 Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                               27-APR-2000;
05-JUN-2000;
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10-APR-2000;
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17-DEC-1999;
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                                                                                                                                                    ADJ21502;
                                                                                                                   RESULT 32
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SXS
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cells isolated from a patient with at least one component chosen from a polypeptide, polynucleotide or antigen presenting cell (APC) of the invention and administering an effective amount of the proliferated T cells to the patient. The current sequence is that of the human lung cancer-related peptide of the invention. The current sequence is not shown in the specification per se but is available on the USPTO web-site http:seqdata.uspto.gov/sequence.html?DocID=20030211510.
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                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human lung cancer-related L978P peptide fragment - SEQ ID 2065.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lung tumour; cytostatic; lung cancer; human; L978P.
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Durham M, Carter D,
                                                                                                                                                                                                                                                     Score 36; DB 8;
Pred. No. 31;
2; Mismatches
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22-MAR-2000; 2000US-00519642.
27-APR-2000; 2000US-00546259.
27-APR-2000; 2000US-00546259.
11-JUN-2000; 2000US-00560184.
11-JUN-2000; 2000US-00561124.
29-AUG-2000; 2000US-00651153.
08-SEP-2000; 2000US-006511325.
26-SEP-2000; 2000US-006711325.
30-OCT-2000; 2000US-006771325.
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99US-00466867.
99US-00476300.
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10-JUL-2001; 2001US-00902941
29-OCT-2001; 2001US-00017754
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Johnson JC, Retter MW,
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Sequence 148 AA;

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The invention relates to a novel isolated polynucleotide comprising a sequence chosen from any one of 40 lung tumour polypeptides or its complements, fragments or degenerate variants. The method of the invention has cytostatic applications and may be useful for detecting and treating lung cancer in a patient, as well as for inhibiting the development of lung cancer in a patient via incubating CD4+ and/or CD8+ rells isolated from a patient with at least one component chosen from a polypeptide, polynucleotide or antigen presenting cell (APC) of the invention and administering an effective amount of the proliferated related related peptide of the invention. The current sequence is that of the human lung cancer-related peptide of the invention. The current sequence is not shown in the specification per se but is available on the USPTO web-site http:seqdata.uspto.gov/sequence.html?DocID=20030211510.
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Sequence 20 AA;

8; Length 20, 2; Indels Score 36; DB Pred. No. 31; Mismatches 2; 66.78; 69.28; 1 ASMSAASAASMAA 13 ASASSAASASA 14 8 셤

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Gaps

.. 0

RESULT 34

ABB70649 standard; protein; 148 AA. ABB70649;

developmental biology; cell signalling; insecticide; Drosophila melanogaster polypeptide SEQ ID NO 38739. Drosophila; de pharmaceutical 

(first entry)

26-MAR-2002

Drosophila melanogaster.

WO200171042-A2.

27-SEP-2001.

23-MAR-2001; 2001WO-US009231

23-MAR-2000; 2000US-0191637P. 11-JUL-2000; 2000US-00614150.

(PEKE ) PE CORP NY

Venter JC, Adams M,

Myers EW

Li PWD,

WPI; 2001-656860/75. N-PSDB; ABL14752.

New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.

18 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176) and the encoded proteins (ABBS70777-ABB72072). The sequence data for this patent did not form part of printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences Disclosure; SEQ ID NO 38739; 21pp + Sequence Listing; English.

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                                                                                                                                        Plant; transgenic; cold tolerance; growth rate; drought tolerance; disease resistance; galactomannan production; plant growth regulator; heat tolerance; herbicide tolerance; lignin production; extreme osmotic condition tolerance; pathogens resistance; pest resistance; yield improvement; seed oil yield; seed protein yield.
              Gaps
              ö
Length 148;
Score 36; DB 4; Length 148
Pred. No. 2.6e+02;
); Mismatches 3; Indels
                                                                                 ADT59595 standard; protein; 250 AA.
              .;
0
                                                                                                                            Plant polypeptide, SEQ ID 9672.
66.78;
       76.98;
                                                                                                              13-JAN-2005 (first entry)
                             1 ASMSAASAASMAA 13
                                            50 ASASAAVAASAAA 62
                Conservative
      Best Local Similarity
Matches 10; Conserv
                                                                                               ADT59595;
 Query Match
                                                                  RESULT 35
                                                                          ADT59595
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28-APR-2003; 2003US-00424599. 28-APR-2003; 2003US-00425115. 18-DEC-2003; 2003US-00739930. (KOVA/) KOVALIC D K. Kovalic DK;

US2004216190-A1. Viridiplantae.

28-OCT-2004.

new recombinant DNA constructs useful in the field of biochemistry and genetics, and in particular for producing transgenic plants with improved biological characteristics.

WPI; 2004-757369/74.

Claim 2; SEQ ID NO 9672; 14pp; English.

The invention relates a recombinant DNA construct comprising a polymucleotide having any of 5544 nucleotide sequences (CDNAs SEQ ID NO: 5244) and encoding a polypeptide with any of 5544 amino acid sequences [-5544) and encoding a polypeptide with any of 5544 amino acid sequences [-5544] and encoding a polypeptide with any of 5544 amino acid sequences of 545-11088. The CDNAs and proteins are from corn, soybean, arbaidopsis, wheat and rape but the specification does not indicate which sequences is derived from which organism. Also included is a method of producing a plant having an improved property, comprising transforming a plant with a recombinant DNA construct comprising a promoter region functional in a plant cell operably joined to a polynucleotide encoding a plant. The property is selected from improving plant cold tolerance, for plant. The property is selected from improving plant cold toleransformed plant. The property is selected from improving plant cold tolerance, for providing increased cresistance to plant disease, for galactomannan production, for improving plant tolerance to herbicides, for increasing the rate of improving plant tolerance to herbicides, for increasing the rate of improving plant tolerance to extreme osmotic conditions, for improving plant tolerance to pathogens or pests, for modifying seed oil yield improvement by modification of carbohydrate, nitrogen or phosphorus use and/or uptake and for yield improvement by modification of carbohydrate, nitrogen or phosphorus use and/or uptake and for yield improvement by providing improved plant growth and

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
          also encode a plant transcription factor. The methods and compositions of the present invention are useful in the field of biochemistry and genetics, in particular for producing transgenic plants with improved biological characteristics such as increased yield, improved nitrogen flow, increasing plant tolerance to cold or heat, improving plant tolerance to extreme osmotic and drought conditions, and improving plant tolerance to plant pesters or pathogens. They can also be used in physical arrays of molecules, plant beceding markers, computer-based storage and analysis systems. The present sequence is one of the 5544 plant protein of form part of the invention. Note: The sequence data for this patent did electronic format directly from USPPTO at sequence in uspto.gov/sequence.html?DocID=20040216190.
  The polynucleotide may
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to Pseudomonas aeruginosa polypeptides and the
                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                       Score 36; DB 8; Length 250;
Pred. No. 4.6e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nolling J, Deloughery C, Bush D;
  development under at least one stress condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 31998; 455pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa polypeptide #15427.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABO83252 standard; protein; 268 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-00252991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0074788P.
                                                                                                                                                                                                                                                                                                                                         66.7%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                       3 MSAASAASMA 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-615309/58.
N-PSDB; ABD16823.
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                  Sequence 250 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rubenfield MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US6551795-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-JUL-1998;
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The invention relates to a new isolated lung specific nucleic acid
molecule (I) comprising any of 113 fully defined nucleotide sequences
given in the specification, their encoded protein sequences, sequences
given in the specification, their encoded protein sequences
calculusly hybridizing to the nucleotide sequences. The methods and
cat least 60% identity to the nucleotide sequences. The methods and
cannitoring of the present invention are useful for identifying,
cannecrous diseases of the lung. They are also used for identifying lung
cannecrous diseases of the lung. They are also used for identifying lung
cannecrous diseases of the invention, gene therapy, production of transgenic
minals and production of engineered lung tissue for treatment and
canneals of gene expression data in the LIFESEQ Gold database using the
data mining software package candidate lead automatic search program
(CLASP). Genes were grouped into gene bins where each bin is a cluster of
c sequences grouped together where they share a common contig.
Differentially expressed tissue-specific genes were selected based on the
                                                                                                                                                                                          ö
of Pseudomonas species using biochip technology. Sequences ABO67826-
BAD64396 represent P. aeruginosa polypeptides of the invention. Note: The
Sequence data for this patent did not form part of the printed
specification but was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         identifying, diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous diseases of the lung.
                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytostatic; gene therapy; vaccine; lung; diagnosis; cancer; non-cancerous lung disease; lung tissue; antagonist; gene therapy; transgenic animal; splice variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated human lung specific nucleic acid molecule, useful for
                                                                                                                                                                                          ö
                                                                                                                                                  66.7%; Score 36; DB 7; Length 268; 81.8%; Pred. No. 4.9e+02;
                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lung specific gene splice variant encoded protein #89.
                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu
                                                                                                                                                                                                                                                                                                                                                              ADR98917 standard; protein; 278 AA.
                                                                              seqdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sun Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-DEC-2002; 2002US-0431307P.
06-DEC-2002; 2002US-0431510P.
06-DEC-2002; 2002US-0431516P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-DEC-2003; 2003WO-US038896.
                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                          9; Conservative
                                                                                                                                                                                                                                                                  152 MSPARAASMAA 162
                                                                                                                                                                                                                             3 MSAASAASMAA 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (DIAD-) DIADEXUS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-635553/61.
                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                 Sequence 268 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                        18-NOV-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Macina RA,
                                                                                                                                                                                                                                                                                                                                                                                                     ADR98917;
                                                                                                                                                                                                                                                                                                                     RESULT 37
ADR98917
ID ADR989
                                                                                                                                                                                          Matches
 88888888
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Human; primer; detection; diagnosis; antisense therapy; gene therapy

Homo sapiens, EP1074617-A2 27-AUG-1999; 99JP-00300253. 11-JAA-2000; 2000JP-00118776. 02-MAY-2000; 2000JP-00183767. 09-JUN-2000; 2000JP-00241899.

(HELI-) HELIX RES INST.

28-JUL-2000; 2000EP-00116126

29-JUL-1999;

Human protein sequence SEQ ID NO:14226.

26-JUN-2001 (first entry)

AAB94055;

AAB94055 standard; protein; 327 AA.

AAB94055 ID AAB9

214 ASTSAAAAAAAA 226

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percentage level in the targeted tissue versus all the other tissues. The expression levels for each gene in libraries of normal tissues or non-tumour tissues from cancer patients were compared with the expression levels in tissue libraries associated with tumour or disease. This sequence represents a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA asquences (ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 27588; 21pp + Sequence Listing; English.
                                                                                                                               Length 278
                                                                                                                          Score 36; DB 8; Length 278
Pred. No. 5.1e+02;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster polypeptide SEQ ID NO 27588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Myers EW;
                                                                                                                                                                                                                                                                                                                ABB66932 standard; protein; 327 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAR-2001; 2001WO-US009231
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11-JUL-2000; 2000US-00614150.
                                                                                                                                 66.7%;
                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                  8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PEKE ) PE CORP NY
                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ABL11035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 327 AA;
                                                                                                   Sequence 278 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             pharmaceutical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-SEP-2001
                                                                                                                                                                                                                                                                                                                                               ABB66932;
                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                RESULT 38
ABB66932
                                                                                                                                                                    Matches
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The present invention describes primer sets for synthesising 5602 full-
complementary strand of a polynucleotide complementary to the
complementary strand of a polynucleotide which comprises one of the 5602
complementary strand of a polynucleotide which comprises one of the 5602
complementary strand of a polynucleotide which comprises one of the 5602
complementary strand of a polynucleotide which complementary to the
complementary strand of a polynucleotide complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide which complementary to the
complementary strand of a polynucleotide complementary to the
complementary strand of a polynucleotide comprises a 1'-end sequence complementary to a
polynucleotide which comprises a 1'-end sequence complementary to a
coligonucleotide comprises a 1-end sequence, where the
coligonucleotide comprises as the selected from those defined in the
coligonucleotide comprises of the sequence, where the
coligonucleotide comprises of the primers also useful for the
collagonate collagnosis of the abnormality of the proteins encoded by
the full-length cDNAs. The primers also useful for the
collagonate collagnosis of the abnormality of the proteins encoded by
the full-length cDNAs. The primers also wseful for the
collagonate collagnosis of the abnormality of the primers also
collagonate collagnosis of the abnormality of the primers also
collagonateleotides, all of which are used in the exemplification of the
collagonateleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer sets for synthesizing polynucleotides, particularly the 5602 full length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; SEQ ID NO 14226; 2537pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.7%; Score 36; DB 4; Length 327; 69.2%; Pred. No. 6.1e+02; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saito K, Ya
, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hikawa T, Hayashi K, S
Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ota T, Isogai T, Nishikawa
Ishii S, Sugiyama T, Wakama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-318749/34.
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9; Conservative

Matches

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Gaps

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Score 36; DB 4; Length 327; Pred. No. 6.1e+02; 2; Mismatches 2; Indels

66.7%;

Query Match Best Local Similarity

2; Mismatches

9; Conservative

Matches

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1 ASMSAASAASMAA 13

Query Match Best Local Similarity

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Gaps

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2 ASMAAAIAASRSA 14

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New Stomach cancer-associated genes, useful as markers in blood tests for screening for the early stages of the disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to stomach cancer-expressed genes (AAI93842-AAI93917) and the encoded proteins (AAW93967-AAM94039). The genes can be used as markers in blood tests for screening for the early stages of the disease. The proteins and peptides can be used as targets for screening for compounds to treat the disease. They can also be used for predicting micro-metastases. The gene can predict peritoneal dissemination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Aburatani H;
Kodama T, Midorikawa Y;
                                                                                                                                            Human; stomach cancer; marker; screening; micro-metastasis; peritoneal dissemination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 66.7%; Score 36; DB 4; Length 327; Best Local Similarity 69.2%; Pred. No. 6.1e+02; Matches 9; Conservative 2; Mismatches 2; Indels
                                                                                                              Human stomach cancer expressed polypeptide SEQ ID NO 49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 119-120; 242pp; Japanese.
             AAM93990 standard; protein; 327 AA.
                                                                                                                                                                                                                                                                                                                             29-JUL-1999; 99JP-00248036.
27-AUG-1999; 99JP-00300253.
18-OCT-1999; 99US-0159590P.
11-JAN-2000; 2000JP-00118776.
17-FEB-22000; 2000JP-00183322P.
02-MAY-2000; 2000JP-00189957.
                                                                                                                                                                                                                                                                                              28-JUL-2000; 2000WO-JP005063
                                                                              13-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-570287/64.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 327 AA;
                                                                                                                                                                                                                              WO200109317-A1
                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                              08-FEB-2001
                                             AAM93990;
AAM93990
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Gaps ö

Search completed: September 9, 2006, 22:48:03 Job time : 103.418 secs

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hypothetical prote
finger of Chinese
finger protein es
homeotic protein c
polyA binding prot
segmentation prote
homeotic protein
glucan 1,4-alpha-q
serine-rich protein
parallel sister ch
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tegument protein -
tegument protein -
homeotic protein B
homeotic protein B
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hypothetical prote
BIR repeat contain
microtubule-associ
homeotic protein a
antifreeze protein
antifreeze protein
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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SUMMARIES

Query Match Length DB

Score

Result No.

138558 138558 138558 109071 109071 109071 10527 10559 10559 10559 10557

892 1533 2038 451 150 220 233 238

Total number of hits satisfying chosen parameters:

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Minimum DB Maximum DB

Minimum Match 0% Maximum Match 100% Listing first 100 summaries

Post-processing:

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Database

283416 segs, 96216763 residues

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

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Perfect score:

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Gaps

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abdominal segment formation protein pumilio - fruit fly (Drosophila melanogaster)
C; Species: Drosophila melanogaster
C; Spaces: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C; Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C; Date: 21-Sep-1993
R; Result Drosophila R. (C; Moore, J.; Dickinson, L.K.; Lehmann, R. Genes Dev. 6, 2312-2326, 1992
Genes Dev. 6, 2312-2326, 1992
A; Title: Pumilio is essential for function but not for distribution of the Drosophila ak A; Reference number: A46221; MUID:93093466; PMID:1459455
A; Contents: embryo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P25822; UNIPARC:UP1000016BD14; GB:L07943; NID:g158190; PID:g
A;Note: sequence extracted from NCBI backbone (NCBIN:120203, NCBIP:120204)
R;Macdonald, P.M.
Rubmitted to the EMBL Data Library, October 1991
A;Reference number: S22026
A;Accession: S22026
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A;Molecule type: mRNA
A;Residues: 1-361,'A',363-1102,'R',1104-1405,'KN',1408-1495,'V',1497-1518,'S',1520-1533
A;Cross-references: UNIPARC:UPI00001329FD; EMBL:X62589; NID:98393; PID:98394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:070254; UNIPARC:UP10000027BF6; EMBL:AF030131; NID:g3002587; A;Experimental source: cell line Ras-transformed NIH 3T3 cells
A;Note: activates JNK/SAPK cascade; Rac-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                             SH3 domains-containing protein POSH - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
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Pred. No. 22;
1; Mismatches 0; Indels
                                                                                                     Length 577;
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K;Tapon, N.; Nagata, K.; Lamarche, N.; Hall, A.
EMBO J. 17, 1395-1404, 1998
A;Reference number: Z16552; MUID:98151363; PMID:9482736
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-892 <TAP>
                                                                                               Score 49; DB 2
Pred. No. 16;
1; Mismatches
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F;8-58/Domain: RING finger homology <RRN>
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A,Cross-references: FlyBase:FBgn0003165
              A;Cross-references: FlyBase:FBgn0004892
C;Keywords: zinc finger
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A;Residues: 1-1533 <BAR>
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A;Gene: sob
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finger protein sob - fruit fly (Drosophila melanogaster)

() Species: Drosophila melanogaster

C) Accession: S7227

R; Hart, M.C.; Wang, L.; Coulter, D.E.

Genetics 144, 171-182, 1996

A; Fitle: Comparison of the structure and expression of odd-skipped and two related genes A; Reference number: S7227; MUD:97032935; PMID:8878683

A; Accession: S7227

A; Status: preliminary

A; Hosiques: 1-577 - HARA

A; Residues: 1-577 - HARA

A; Residues: 1-577 - HARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mi-2 autoantigen 240 kDa protein - human (fragment)
CjSpecies: Homo sapiens (man)
CjSpecies: Homo sapiens (man)
CjAccession: 138558
CjAccession: I38558
RjGe, Q.; Nilasena, D.S.; O'Brien, C.A.; Frank, M.B.; Targoff, I.N.
A;Title: Molecular analysis of a major antigenic region of the 240-kD protein of Mi-2 au A;Reference number: 138558; MUID:96013633; PMID:7560664
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A;Molecule type: mRNA
A;Residues: 1-530 <RES>
A;Residues: 1-530 <RES>
A;Cross-references: UNIPARC:UPI000016A09A; EMBL:U08379; NID:g761717; PIDN:AAC50228.1; PI
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                                                                                                                               heat shock transcription factor homolog TSC23.90 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04213
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, submitted to the Protein Sequence Database, March 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: UNIPROT:Q24571; UNIPARC:UPI000007A28D; EMBL:U62004; NID:g1480193;
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A;Experimental source: cultivar Columbia; BAC clone T5C23
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F;60-155/Domain: HSF DNA-binding domain homology <HSF>
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87 AAVAAAAAAAA 99
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Matches 12; Conservative
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A,Molecule type: DNA
A,Residues: 1-377 <BEV>
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C;Accession: JC5954
R;Tanaka, M.; Tanaka, T.; Harata, M.; Suzuki, T.; Mitsui, Y.
Biochem. Biophys. Res. Commun. 243, 531-537, 1998
A;Title: Triplet repeat-containing ribosomal protein L14 gene in immortalized human end A;Reference number: JC5954; MUID:98153799; PMID:9480843
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C.Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C.Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C.Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
R.Johnson, J.E.; Birren, S.J.; Anderson, D.J.
Nature 346, 858-861, 1990
A;Title: Two rat homologues of Drosophila achaete-scute specifically expressed in neuro A;Reference number: S11562; MUID:90363294; PMID:2392153
A;Accession: 811563
A;Status: preliminary; nucleic acid sequence not shown
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A;Residues: 1-233 <JOH>
A;Cross-references: UNIPROT:P19359; UNIPARC:UPI0000047567; EMBL:X53725; NID:956630; PID
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*Residues: 1-220 cTAN>
A;Cross-references: UNIPARC:UPI000004E622; DDBJ:D87735; NID:g1620021; PIDN:BAA13443.1;
C;Superfamily: rat ribosomal protein L14
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                                                                                                                                                                                                                                                       hypothetical protein DKFZp586E1621.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Sep-2000
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R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, submitted to the Protein Sequence Database, June 1999
A;Reference number: 217528
A;Accession: T12547
A;Status: preliminary
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A;Residues: 1-150 <OTT>
A;Cross-references: UNIPROT:Q9Y4M1; UNIPARC:UP10000071DDD; EMBL:AL080235
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Pred. No. 10;
0; Mismatches
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Pred. No. 14;
0; Mismatches
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92.3%;
                                                                              303 AAQAAAAAAAA 315
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129 AAAAAAAAAAA 141
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Best Local Similarity 92.3
Matches 12; Conservative
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Best Local Similarity
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #text_change 09-Jul-2004
C;Accession: D88395
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUID: 99069613; PMID: 9851916
A;Reference see websites genome. Wustl.edu/gsc/C elegans/ and www. sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Status: preliminary
A;Residues: 1-451 cSTO>
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                        female sterile homeotic protein, 205K - fruit fly (Drosophila melanogaster)
N;Alternate names: membrane protein fsh, 205K
N;Contains: female sterile homeotic protein, 110K
C;Species: Drosophila melanogaster
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 31-Dec-2004
C;Accession: A43742; B43742
C;Accession: A43742; B43742
Bay Batia-Dey, N.; Dawid, I.B.
A;Title: The Drosophila fsh locus, a maternal effect homeotic gene, encodes apparent A;Reference number: A43742; MUID:89276730; PMID:2567251
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F;1-2038/Product: female sterile homeoric protein, 205K #status predicted <MA2>
F;1-1106/Product: female sterile homeoric protein, 110K #status predicted <MAT>
F;59-116/Domain: bromodomain homology <BRO1>
F;503-560/Domain: bromodomain homology <BRO2>
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A;Cross-references: UNIPARC:UPI000017A10F; EMBL:M23222
C;Genetics:
A;Gene: fsh
A;Cross-references: FlyBase:FBgn0004656
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Pred. No. 18;
0; Mismatches
   Pred. No. 33;
1; Mismatches
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1; Mismatches
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92.3%;
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Best Local Similarity 92.3
Matches 12; Conservative
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Matches 12, Conservative
Best Local Similarity 92.3
Matches 12, Conservative
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A; Residues: 1-2038 <HAY>
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A; Cross-references: UNIPARC: UP10000024E69; GB:S79041; NID: 91042008; PIDN: AAB34947.1; PID
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C;Species: Homo sapiens (man)

C;Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 05-Oct-2004

C;Accession: JG5273

R;Yokoyama, M.; Nishi, Y.; Yoshii, J.; Okubo, K.; Matsubara, K.

B)NA Res. 3, 311-320, 1996

A;Title: Identification and cloning of neuroblastoma-specific and nerve tissue-specific

A;Reference number: JG5272; MUID:97191543; PMID:9039501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:099453; UNIPARC:UPI0000131D16; DDBJ:DBJ344; NID:91841337; PIC;Comment: This protein is a transcriptional repressor involved in regulating gene expre C;Keywords: DNA binding; homeobox; nucleus; transcription regulation F;99-155/Domain: homeobox homology <HOX>
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NyAlternate names: homeotic protein Hoxd-11

(Species: Mus musculus (house mouse)

C,Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 05-Oct-2004

C,Accession: 816318; 846403; 857443

R,Izpisua-Belmonte, J.C.; Falkenstein, H.; Dolle, P.; Renucci, A.; Duboule, D.

R,Izpisua-Belmonte, Journal of the Brosophila AbdB homeotic gene are sequentially expx
A,Title: Murine genes related to the Drosophila AbdB homeotic gene are sequentially expx
A,Reference number: 816317; MUID:91293104; PMID:1676674
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A,Residues: 1-323 <12Ep.
A,Gross-references: UNIPROT:P23813; UNIPARC:UPI0000029F10; EMBL:X60761; NID:951420; PIDN
R,Gerard, M.; Duboule, D.; Zakany, J.
EMBO J. 12, 353-3556, 1993
A,Title: Structure and activity of regulatory elements involved in the activation of the
A,Reference number: S40403; MUID:94074553; PMID:7902810
A;Title: Gsh-2, a murine homeobox gene expressed in the developing brain. A;Reference number: I57039; MUID:95344993; PMID:7619729
A;Accession: I57039
A;Acture preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-305 <RES>
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Pred. No. 18;
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Pred. No. 18;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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A;Molecule type: mRNA
A;Residues: 1-314 <YOK>
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Best Local Similarity
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Best Local Similarity
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homeotic protein Hox D8 - mouse

homeotic protein Hox 4.3

C;Species: Mus musculus (house mouse)

C;Species: Mus musculus (house mouse)

C;Species: Mus musculus (house mouse)

C;Accession: A43562

A;Title: Primary structure and embryonic expression pattern of the mouse Hox-4.3 homeobc

A;Title: Primary structure and embryonic expression pattern of the mouse Hox-4.3 homeobc

A;Reference number: A43562; MuID:91209232; PMID:1982431

A;Accession: A43562

A;Keference number: Drelminary; not compared with conceptual translation

A;Molecule type: DNA

A;Molecule type: DNA

A;Residues: 1-289 <1ZP>
A;Cross-references: UNIPROT:P23463; UNIPARC:UPI0000177DA6

A;Cross-references: UNIPROT:P23463; UNIPARC:UPI0000177DA6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: A48279
R;Ball, D.W.; Azzoli, C.G.; Baylin, S.B.; Chi, D.; Dou, S.; Donis-Keller, H.; Cumaraswam Proc. Natl. Acad. Sci. U.S.A. 90, 5648-5652, 1993
A;Title: Identification of a human achaete-scute homolog highly expressed in neuroendocx A;Reference number: A48279; MUID:93296195; PMID:8390674
A;Accession: A48279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: UNIPROT:P50553; UNIPARC:UP10000047566; GB:L08424; NID:g306459; PID:g
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C;Species: Mus sp. (mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Oct-2004
C;Accession: IS7039
R;Hsieh-Li, H.M.; Witte, D.P.; Szucsik, J.C.; Weinstein, M.; Li, H.; Potter, S.S.
Mech. Dev. 50, 177-186, 1995
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C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
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C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;196-252/Domain: homeobox homology <HOX>
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                                                                                   88.7%; Score 47; DB 2; Length 233; 92.3%; Pred. No. 14; ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Length 238;
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A;Molecule type: mRNA
A;Residues: 1-238 <RES>
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Matches 12; Conservative
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                                                                                                              Best Local Similarity 92.3
Matches 12; Conservative
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les 12; Conserv
                          C; Keywords: DNA binding
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A; Cross-references: UNIPARC: UP1000016A2D0; EMBL: U48250; NID: 91199656; PIDN: AAC72247.1;
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Bacte: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
C;Accession: GG2409
R;Kuroda, S.; Tokunaga, C.; Kiyohara, Y.; Konishi, H.; Kikkawa, U.
submitted to the EMBL Data Library, February 1996
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C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
C;Accession: 14818
R;Rudnick, A.; Ling, T.Y.; Odaqiri, H.; Rutter, W.J.; German, M.S.
Proc. Natl. Acad. Sci. U.S.A. 91, 12203-12207, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 47; DB 2; Length 334;
Pred. No. 19;
0; Mismatches 1; Indels
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92.3%;
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236 AAAAAAAAAAA 248
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A;Accession: G02409
                                     Query Match
Best Local Similarity
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Best Local Similarity
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Best Local Similarity
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A; Residues: 1-334 <KUR>
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Mypotheeical protein lin2792 [imported] - Listeria innocua (strain Clip11262)

C;Species: Listeria innocua

C;Species: Listeria innocua

C;Species: Listeria innocua

C;Species: Listeria innocua

C;Accession: AB1781

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker

r; Dominquez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.

D; Jones, L.M.; Karst, U.

Science 294, 849-8852, 201

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma

A;Authors: Kreft, J.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Reference number: AB1077; WuID:21537279; PMID:11679669

A;Reference number: AB1781

A;Reference number: AB1781

A;Reference number: AB1781

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             zinc-finger protein Pur-1 - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 05-Apr-1995
C;Accession: B47236
R;Kennedy, G.C.; Rutter, W.J.
Proc. Natl. Acad. Sci. U.S.A. 89, 11498-11502, 1992
A;Title: Pur-1, a zinc-finger protein that binds to purine-rich sequences, transactivate
A;Reference number: A47236; MUID:93087555; PMID:1454839
A;Cross-references: UNIPARC:UP10000029F10; EMBL:X71422; NID:g397508; PIDN:CAA50553.1; F R;Takada, S.; Cook, M.; Kramlauf, R.; McMahon, A.P. submitted to the EMBL Data Library, May 1991
A;Description: Genomic sequence of mouse Hox-4.6.
A;Reference number: S57443
A;Accession: S57443
A;Residues: 'MNDFDECGPSAAS',1-323 <TAK>
A;Residues: 'MNDFDECGPSAAS',1-323 <TAK>
A;Cross-references: UNIPARC:UP10000026A38; EMBL:X60395; NID:g871427; PIDN:CAA42943.1; I
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                                                                                                                                                                                                                                                                                                     A;Introns: 246/1
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;252-308/Domain: homeobox homology <HOX>
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                                                                                                                                                                                                                                                                                                                                                                                                                          2; Length 323;
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A,Residues: 1-331 <KEN>
A,Cross-references: UNIPARC:UPI000017C615
A,Experimental source: insulinoma cell line T
A,Note: sequence extracted from NCBI backbone (NCBIP:119832)
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 47; DB
Pred. No. 18;
0; Mismatches
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Pred. No. 19;
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Best Local Similarity 92.3
Matches 12; Conservative
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Best Local Similarity
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R,D'Esposito, M.; Morelli, F.; Acampora, D.; Migliaccio, E.; Simeone, A.; Boncinelli, E Genomics 10, 43-50, 1991
A;Title: EVX2, a human homeobox gene homologous to the even-skipped segmentation gene, A;Reference number: A39065; MUID:91257849; PMID:1675198
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                                                                                                                                                                                                                                                                                                  homeotic protein EVX2 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 31-Dec-2004
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A;Map position: 242-13-2431
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;46-102/Domain: homeobox homology <hOX>
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  Length 331;
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Pred. No. 19;
Score 47; DB
Pred. No. 19;
0; Mismatches
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A, Cross-references: UNIPARC:UP1000017A29D
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A;Cross-references: UNIPPARC:UP100016DEBB; EMBL:D49704; NID:g1805615; PIDN:BAA08554.1; P A;Experimental source: cv. Nipponbare; splice form OSH42
C;Comment: For an alternative splice form, see PIR:T03875.
                                                                                                                                          A,Gene: H45
A;Introns: 174/3; 215/1; 277/3; 321/3; 367/2
A;Introns: 174/3; 215/1; 277/3; 321/3; 367/2
C;Keywords: alternative initiators; alternative splicing; DNA binding; homeobox; nucleus F;1-375/Product: probable homeobox protein OSH45, splice form OSH44 #status predicted F;197-367/Product: probable homeobox protein OSH45, splice form OSH42 #status predicted F;291-357/Domain: homeobox homology <HOX>
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C.pate: 0.1-Dec-1991 #septimes revision 18-Nov-1994 #text_change 31-Dec-2004
C.Accession: A48423; S.13009; A26629; A24778
R.Logan, C.; Hanks, M.C.; Noble-Topham, S.; Nallainathan, D.; Provart, N.J.; Joyner, A.I Dev, Genet. 13, 346-358, 1992
A.Title: Cloning and sequence comparison of the mouse, human, and chicken engrailed gent A.Reference number: A48423; MUID:93185339; PMID:1363401
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A;Experimental source: CD-1, embryo
A;Note: sequence extracted from NCB1 backbone (NCB1P:126620)
R;Holland, P.W.H.; Williams, N.A.
FEBS Lett. 277, 250-252, 199
A;Title: Conservation of engrailed-like homeobox sequences during vertebrate evolution.
A;Reference number: S13009; MUID:91099509; PMID:1980115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Drosophila virilis
C;Species: Drosophila virilis
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 02-Jul-1998
C;Accession: A44443
R;Mainwright, S.M.; Ish-Horowicz, D.
Mol. Cell. Biol. 12, 2475-2483, 1992
Mol. Cell. Biol. 12, 2475-2483, 1992
A;Title: Point mutations in the Drosophila hairy gene demonstrate in vivo requirements
A;Reference number: A44443; MUID:92269819; PMID:1588951
A;Accession: A44443
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basic helix-loop-helix transcription repressor H - fruit fly (Drosophila virilis)
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A;Residues: 1-401 <LOG>
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Pred. No. 21;
0; Mismatches
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0; Mismatches
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Pred. No. 2
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Best Local Similarity 92.3
Matches 12; Conservative
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Best Local Similarity
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A;Molecule type: mRNA
A;Residues: 1-378 <WAI>
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probable homeobox protein OSH45, splice form OSH42
C; Species: Oryza sativa (rice)
C; Species: Oryza sativa (rice)
C; Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-Oct-2004
C; Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-Oct-2004
C; Date: 30-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-Oct-2004
R; Tamaoki, M.; Tsugawa, H.; Minami, E.; Kayano, T.; Yamamoto, N.; Kano-Murakami, Y.; Mathant J. 7, 927-938, 1995
A; Title: Alternative RNA products from a rice homeobox gene.
A; Reference number: 215126; MUID:95322999; PMID:7599652
A; Accession: T03874
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-375 cTpAN1>
A; Cross-references: UNIPPORDSJ4; UNIPPARC:UPIO000AA5D5; EMBL:D49704; NID:g1805615; PI
A; A; Accession: T03876
A; Accession: T03876
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C;Keywords: alternative initiators; alternative splicing; DNA binding; homeobox; nucleus
F;291-352/Domain: homeobox homology <HOX>
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                                                    A;Accession: I48188
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRS>
A;Cross-references: UNIPROT:Q60554; UNIPARC:UPI00001301FA; EMBL:X81409; NID:g587466; PID
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A;Molecule type: DNA
A;Residues: 1-374 <TAM>
A;Residues: UNIPROT:P93423; UNIPARC:UPI00000AB610; EMBL:D49704; NID:g1805615; Commental source: cv. Nippombare
C;Comment: For alternative splice forms, see PIR:T03874.
C;Genetics:
A;Gene: H45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable homeobox protein OSH45, splice form OSH45 [similarity] - rice C;Species: Oryza sativa (rice)
C;Species: Oryza sativa (rice)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-Oct-2004
C;Accession: T03875
R;Tamaoki, M.; Tsugawa, H.; Minami, E.; Kayano, T.; Yamamoto, N.; Kano-Murakami, Y.; Plant, J., 927-938, 1995
A;Title: Alternative RNA products from a rice homeobox gene.
A;Reference number: Z15126; MUID:95322999; PMID:7599652
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A,Title: Pancreatic beta cells express a diverse set of homeobox genes.
A,Reference number: 148185, MUID:95083670; PMID:7991607
                                                                                                                                                                                                                                          A;Gene: NKx6.1
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;237-293/Domain: homeobox homology <HOX>
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A;Molecule type: DNA
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Pred. No. 20;
0; Mismatches
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Pred. No. 3
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Local Similarity 92.3%;
nes 12; Conservative
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Matches 12; Conservative
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Matches
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C;Accession: T14911
R;Kircher, S.; Ledger, S.; Hayashi, H.; Weisshaar, B.; Schafer, E.; Frohnmeyer, H.
Mol. Gen. Genet. 257, 595-605, 1998
A;Title: CPRF4a, a novel plant bZIP protein of the CPRF family: comparative analysis of
A;Reference number: Z18261; MUID:98265918; PMID:9604882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Rebidues: 1-443 <STE1>
A;Cross.references: UNIPROT:P41225; UNIPARC:UPI000003F546; EMBL:X71135; NID:g468790; PII
A;Accession: 138242
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A;Molecule type: mRNA
A;Residues: 143-158, Pr,160-218 <STE2>
A;Cross-references: UNIPARC:UPI0000071C8C; EMBL:X71137; NID:9468793; PIDN:CAA50467.1; P
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NyAlternate names: mesodernal cell dorsoventral fates determinator Evx-2
C;Species: Mouse musculus (house mouse)
C;Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004
C;Accession: A43915
E;Dush, M.K.; Martin, G.R.
Dev. Biol. 151, 273-287, 1992
A;Title: Analysis of mouse Evx genes: Evx-1 displays graded expression in the primitive A;Reference number: A43915; MUID:92249649; PMID:1349539
                                                                                                                                       A, Accession: T14911
A, Status: preliminary, translated from GB/EMBL/DDBJ
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Residues: 1.420 «KIR»
A, Festiques: UNIPROT: O82037; UNIPARC: UPI00000A12C8; EMBL: Y10810; NID: 93336904;
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                                                                                                                                                                                                                                                                                                       A,Note: CPRF4b
C,Superfamily: BZIP G-box-binding protein; fos/jun DNA-binding domain homology
C,Keywords: DNA binding; leucine zipper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transcription factor SOX3 - human
NyAletrante names: SRX (sex determining region Y)-box 3
Aletrante names: SRX (sex determining region Y)-box 3
C;Species: Homo sapien (man)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: 138239; 138242; SG7816
R;Stevanovio: M; Lovell-Badge, R; Collignon, J; Goodfellow, P.N.
R;Stevanovio: X, 2013-2018, 1993
A;Title: SOX3 is an X-linked gene related to SRY.
A;Reference number: 138239; MUID:94154672; PMID:8111369
A;Accession: 138239
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C,Genetics:
A,Gene: GDB:SOX3; SOX-3; SOXB
A,Cross-references: GDB:250376; OMIM:313430
A,Amap position: Xq26-Xq27
C,Superfamily: human SOX3 protein; HMG box homology
F;136-211/Domain: HMG box homology <HMG>
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Pred. No. 23;
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Pred. No. 22;
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ilarity 92.3%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 92..
Loca 12; Conservative
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                                           A; Modecule type: nucleic acid
A; Residues: 321-380 «HOL»
A; Residues: 321-380 «HOL»
A; Residues: 321-380 «HOL»
A; Cooper, A.L.; Martin, G.R.
R; Joyner, A.L.; Martin, G.R.
Genes Dev. 1, 29-38, 1987.
A; Title: En-1 and En-2, two mouse genes with sequence homology to the Drosophila engrail
A; Reference number: A5629
A; Molecule type: DNA; mRNA
A; Residues: 278-401 «JOY»
A; Cross-references: UNIPARC: UP1000016CA7C; GB: Y00201; GB: M11987; NID: 949587; PIDN: CAA683
A; Title: Expression during embryogenesis of a mouse gene with sequence homology to the D
A; Recerence number: A24778; MUID: 86079501; PMID: 2416459
A; Rocession: A24778
A; Molecule type: DNA
A; Residues: 311-401 «JOS»
A; Ross-references: UNIPARC: UP1000017A2B0
C; Genetics:
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C;Species: Homo sapiens (man)
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 31-Dec-2004
C;Accession: A53662
R;Harrison, K.A.; Druey, K.M.; Deguchi, Y.; Tuscano, J.M.; Kehrl, J.H.
A;Title: A novel human homeobox gene distantly related to proboscipedia is expressed in A;Reference number: A53662; MUID:94327547; PMID:7914194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-403 <HAR>
A;Cross-references: UNIPARC:UPI000017A29E; GB:U07663
A;Note: the nucleotide sequence and conceptual translation as given are self-consistent
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b2TP DNA-binding protein - parsley
C;Species: Petroselinum crispum (parsley)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 31-Dec-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 1
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;313-369/Domain: homeobox homology <HOX>
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C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;244-300/Domain: homeobox homology <HOX>
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A,Status: preliminary, not compared with conceptual translation
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Pred. No. 22;
0; Mismatches
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nes 12; Conservative
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Matches
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Score 47; DB 2; Length 494;
Pred. No. 25;
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92.3%;
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F,174-183/Region: alanine-rich
F,207-230/Region: zinc finger
F,324-346/Region: zinc finger
F,324-346/Region: zinc finger
F,353-368/Region: zinc finger
                                                                              396 AAAAAAAAAAA 408
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F,452-468/Region: alanine-rich
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Matches 12; Conservative
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A; Residues: 1-494 < PYR>
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CiSpecies: Mus musculus (house mouse)
CiSpecies: Mus musculus (house mouse)
CiSpecies: Mus musculus (house mouse)
CiAccession: A47236
Rikennedy, G.C.; Rutter, W.J.
Proc. Natl. Acad. Sci. U.S.A. 89, 11498-11502, 1992
Airtle: Pur-1, a zinc-finger protein that binds to purine-rich sequences, transactivate A; Title: Pur-1, a zinc-finger protein that binds to purine-rich sequences, transactivate A; Reference number: A47236
Airtle: Pur-1, a zinc-finger protein that binds to purine-rich sequences, transactivate A; Reference number: A47236
A; Reference number: A47236
A; Residues: 1-477
A;
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Dasic helix-loop-helix protein, DEC2 - human

Lispecies: Homo sapiens (man)

Cjoscies: Homo sapiens (man)

Cjoscies: Homo sapiens (man)

Cjoscies: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004

Cjosciesion: JC7583

RjFujimoto, K.; Shen, M.; Noshiro, M.; Matsubara, K.; Shingu, S.; Honda, K.; Yoshida, E.

Biochem Biophys. Res. Commun. 280, 164-171, 2001

A;Title: Molecular cloning and characterization of DEC2, a new member of basic helix-loc

A;Reference number: JC7583; MUID:21092582; PMID:11162494
                                                                      A;Cross-references: UNIPROT:P49749; UNIPARC:UPI000020BC6; GB:S34322; NID:g249137; PIDN:A;Note: sequence extracted from NCBI backbone (NCBIN:100478, NCBIN:100480, NCBIN:100482, C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q9C0J9; UNIPARC:UPI0000052B52; DDBJ:AB044088
C;Comment: This protein, a novel member of the DEC subfamily of basic helix-loop-helix
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C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;192-248/Domain: homeobox homology <HOX>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 47; DB 2; Length 477;
Pred. No. 25;
0; Mismatches 1; Indels
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C;Keywords: transcription factor
F;1-13/Region: highly conserved #status predicted
F:130-173/Domain: Orange #status predicted <ORA>
F;286-411/Region: alanine and glycine-rich #status predicted
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Pred. No. 24;
0; Mismatches
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Best Local Similarity 92.3%;
Matches 12; Conservative (
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96 AAAAAAAAAAA 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Conservative
A;Status: preliminary
A;Molecule type: DNA; mRNA
A;Residues: 1-475 <DUS>
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Matches 12; Conserv
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A; Residues: 1-482 <FU
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phosphatidylinositol 3-kinase - Chlamydomonas reinhardtii (fragment)

C,Species: Chlamydomonas reinhardtii
C,Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C,Accession: T09084
R,Molendijk, A.J; Irvine, R.F.
Plant Mol. Biol. 37, 53-66, 1998
A,Title: Inositide signalling in Chlamydomonas: Characterization of a phosphatidylinosit A,Reference number: 216411; MUID:98281574; PMID:9620264
A,Accession: T09084
A,Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-490 <MOL>
A;Cross-references: UNIPROT:004270; UNIPARC:UPI00009C6FA; EMBL:U97663; NID:g2109290; PI
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Biochemistry 31, 4102-4110, 1992
A,Title: Isolation of a novel cDNA encoding a zinc-finger protein that binds to two site
A,Reference number: A42170; MUID:92232709; PMID:1567856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ajross-references: UNIPROT: P56270; UNIPARC:UPI000017C427; GB:J05371
A,Note: it is uncertain whether Met-18 is the initiator or whether translation is initia
R,Bossone, S.A.; Asselin, C.; Patel, A.J.; Marcu, K.B.
Proc. Natl. Acad. Sci. U.S.A. 89, 7452-7456, 1992
A,Title: MAZ, a zinc finger protein, binds to C. MYC and C2 gene sequences regulating tra
A,Reference number: A46153; MUID:92366479; PMID:1502157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          zinc finger protein MAZ - human (fragment)
N;Alternate names: MYC-associated zinc finger protein ZF87
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004
C;Accession: A42170; A46153
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A; Note: sequence extracted from NCBI backbone (NCBIN:110666, NCBIP:110667)
C; Keywords; DNA binding: zinc finger
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A;Residues: 18-417,'L',419-494 <BOS>
A;Cross-references: UNIPARC:UPI000012ECF8; GB:M94046
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Pred. No. 25;
0; Mismatches
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polyomavirus enhancer-binding protein 2 alpha chain type 1 - mouse
NiAlternate names: PEA2 alpha chain type 1; PEA2 alpha chain type 2; PEBP2 alpha chain
C;Species: Mus musculus (house mouse)
C;Date: 26-May-1994 #lesquence_revision 26-May-1994 #text_change 09-Jul-2004
C;Accession: A48233; B48233
E;Ogawa, B.; Martyama, M.; Kagoshima, H.; Inuzuka, M.; Lu, J.; Satake, M.; Shigesada, K
Proc. Natl. Acad. Sci. U.S.A. 90, 6859-6863, 1993
A;Title: PEBP2/PEA2 represents a family of transcription factors homologous to the prod
                                                                                                                                                                                                                                                                                                                                                                                                              A,Molecule type: mRNÅ
A,Residues: 1-513 <CGA>
A;Cross-references: UNIPROT:Q08775; UNIPARC:UPI000002B2F8; GB:D14636; NID:g391766; PIDN
A;Accession: B48233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-304,'L',306 <OG2>
A;Cross-references: UNIPARC:UPI000002B2F9; GB:D14637; NID:g391768; PIDN:BAA03486.1; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Gene: PEBP2alphaA
C,Superfamily: transcription factor CBF alpha 2
C,Keywords: alternative splicing; DNA binding; T-cell; transcription factor; transcript:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               zinc finger protein noch - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Os-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004
C;Accession: A55529
R;Cheah, P.Y.; Meng, Y.B.; Yang, X.; Kimbrell, D.; Ashburner, M.; Chia, W.
Mol. Cell. Biol. 14, 1487-1499, 1994
A;Titler: The Drosophila 1(2)35Ba/nocA gene encodes a putative Zn finger protein involved A;Reference number: A55929; MUID:94119100; PMID:8289824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: UNIPROT: Q24423; UNIPARC: UPI000007B356; GB: L14009; NID: g431289; PID:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Pred. No. 27;
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Pred. No. 26;
0; Mismatches
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92.3%;
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Matches 12, Conservative
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Best Local Similarity
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A; Residues: 1-537 < CHE>
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Matches
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NyAlternate names: MAZ protein
NyAlternate names: MAZ protein
Cippecies: Homo sapiens (man)
Cipate: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 05-Nov-1999
Cipate: 31-Jan-1997 #sex Commun. 226, 801-809, 1996
Biochem. Biophys. Res. Commun. 226, 801-809, 1996
Airtle: Members of the MAZ family: A novel colbA clone for MAZ from human pancreatic isl
Airtle: Members of the MAZ family: PMID:96428591; PMID:8831693
Airtle: MANPAR:UPI0000163B39; DDBJ:DBS:085131; NID:91752741; PIDN:BAA12728.1; FA; Cross references: UNIPARC:UPI000163B39; DDBJ:DBS:131; NID:91752741; PIDN:BAA12728.1; FA; Experimental source: pancreatic islet
Cicomment: This protein plays a role in the control of transcriptional initiation of genand between the introns of the mouse gene for immunoglobulin M-D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-495 <HAR>
A;Cross-references: UNIPROT:P31361; UNIPARC:UP10000029AAF; EMBL:M88299; NID:g200444; PIL C;Superfamily: transcription factor Brn-1; homeobox homology; POU domain homology C;Keywords: DNA binding; homeobox; nucleus; transcription regulation F;27-49/Region: glycine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Keywords: phosphoprotein; zinc finger
F;146,204,480/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status pre
F;349/Binding site: phosphate (Tyr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                     R;Hara, Y.; Rovescalli, A.C.; Kim, Y.; Nirenberg, M.
Proc. Natl. Acad. Sci. U.S.A. 89, 3280-3284, 1992
A;Title: Structure and evolution of four POU domain genes expressed in mouse brain.
A;Reference number: S31223; MUID:92228768; PMID:1565620
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                                                                                                                                                                                                                                                       transcription factor Brn-1 - mouse
N;Alternate names: class III POU domain protein brain-1
C;Species: Wus musculus (house mouse)
C;Date: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S31223
      Gaps
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Pred. No. 25;
0; Mismatches 1; Indels
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Pred. No. 25;
0; Mismatches 1; Indels
      Indels
      ä
   Mismatches
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Fi316-383/Domain: POU domain homology <POU>F;402-458/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;101-112/Region: alanine-rich
F;162-180/Region: histidine/proline-rich
F;186-201/Region: alanine-rich
F;236-247/Region: glycine-rich
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A; Status: preliminary
A; Molecule type: DNA
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Length 627;

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C;Accession: $40382
R;Abel, T.; Michelson, A.M.; Maniatis, T.
Pevelopment 119, 623-633, 1993, member that binds to Adh regulatory sequences is expre
A;Title: A Drosophila GATA family member that binds to Adh regulatory sequences is expre
A;Reference number: $40382; MUID:94244465; PMID:8187633
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A,Residues: 1-779 cABE.
A,Croms-references: UNIPROT:P52172; UNIPARC:UPI0000135F5F; EMBL:X76217; NID:9441491; PII
C,Coment: This transcriptional activator is the earliest known marker of the developing
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A,Cross-references: FlyBase:FBgn0003507
C;Superfamily: box A-binding factor; GATA-type zinc finger homology
C;Keywords: DNA binding; nucleus; transcription factor; transcription regulation; zinc
F;316-369/Domain: GATA-type zinc finger homology <GZF>
                      A,Molecule type: DNA
A,Residues: 1-627 <STO>
A,Cross-references: UNIPARC:UPI000017885F; GB:AE002093; NID:93413700; PIDN:AAC31223.1;
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R,Wimmer, B.A.; Jaeckle, H.; Pfeifle, C.; Cohen, S.M.
Nature 366, 690-694, 1993
A,Title: A Drosophila homologue of human Spl is a head-specific segmentation gene.
A,Reference number: S39356; MUID:94081952; PMID:8259212
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A;Modecule type: DNA
A;Modecule type: DNA
A;Rossiques: 1-644 <WIM>
A;Cross-references: UNIPARC:UPI0000124C17; EMBL:Z29361; NID:9441283; PID:9441284
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N;Alternate names: ABF; transcription factor dGATAb
C;Species: Drosophila melanogaster
C;Species: Jan-1995 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C;Accession: S40382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transcription factor btd - fruit fly (Drosophila sp.)
C;Species: Drosophila sp.
C;Date: 18-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 07-May-1999
                                                                                                                                                                                                                      A;Map position: 2
A;Introns: 40/1; 119/1; 160/3; 319/3
C;Superfamily: FtsH/SEC18/CDC48-type ATP-binding domain homology
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Matches 12; Conservative 0; Mismatc
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A,Gene: T19L18.5, At2g26140
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A, Molecule type: DNA
A, Residues: 47-485, E, 487-518, WH' <FJO>
A, Residues: 47-485, E, 487-518, WH' <FJO>
A, Cross-references: UNIPARC:UPI00001745BF; GB:X01765; GB:X03059; NID:g8084; PIDN:CAA2590
A, Note: the translation of the nucleotide sequence from Fig. 5 is shown, not the translation of the nucleotide sequence from Fig. 5 is shown, not the translation of the nucleotide sequence from Fig. 5 is shown, not the translation of the sequence or servation in the protein coding and intron regions of the engrailed A, Title: Sequence conservation in the protein coding and intron regions of the engrailed A, Reference number: A91059; MUID:87161768; PMID:2881781
A, Contents: annotation; intron locations and sequences R, Gay, N.J.; Poole, S.J.; Kornberg, T.B.
Nucle A, Reference number: 803677, MUID:88289425; PMID:2899884
A, Contents: annotation; potential phosphorylation sites; homeobox domain C, Comment: This protein specifies the body segmentation pattern.
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A, Rolecule type: DNA
A, Rolecule type: DNA
A, Rolecule type: DNA
A, Residues: 1-627 <ROUS
A, Gross-references: UNIPROT: 080983; UNIPARC: UPI000017885F; EMBL: AC004747; NID: 93413696;
A, Experimental source: cultivar Columbia
R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUID: 20083487; PMID: 10617197
A;Title: The engrailed locus of Drosophila: structural analysis of an embryonic transcri
A;Reference number: A90862; MUID:85099327; PMID:3917855
                                                                                                             A; Molecule type: mRNA
A; Residues: 1-552 < POO>
A; Residues: 1-552 < POO>
A; Cross-references: UNIPROT: P02836; UNIPARC: UPI000012CA13; GB:M10017; NID: g157363; PIDN:
R; Fjoss, A.; McGinnis, W.J.; Gehring, W.J.
Nature 313, 284-289, 1985
A; Title: Isolation of a homoeo box-containing gene from the engrailed region of Drosophi
A; Reference number: A93354; MUID: 90114393; PMID: 2481829
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N;Alternate names: YTA11 protein homolog T19L18.5
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 2-4-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 31-Dec-2004
C;Accession: T02610; H84656
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, August 1998
A;Bescription: Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence.
A;Reference number: Z14681
A;Accession: T02610
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A,Gene: en
A,Cross-references: FlyBase:FBgn0000577
A,Map position: 2R,62.0 (48A1-4)
A,Introns: 438/1; 470/3
C,Superfamily: engrailed homeotic protein; P
C,Seywords: DNA binding; embryo; homeobox; 1
F,26-53/Region: glutamine-rich
F,68-87/Region: alanine-rich
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F;320-368/Region: serine-rich
F;455-511/Domain: homeobox homology <HOX>
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Q86110 mus musculu Q3us18 m 16 days e Q5249 or yza sativ Q4pei8 ustilago ma Q7sbk2 neurospora gycod3 arabidopsis O9rxd6 homo sapien Q80us0 mus musculu Q8bkc1 m 0 day neo Q3ts94 mus musculu Q5vyv0 homo sapien Q5vyv0 homo sapien Q5cyv0 homo sapien Q5cyv0 homo sapien Q5pg20 ustilago ma Q7pps0 anopheles g Q9rxd homo sapien Q7pps0 anopheles g Q9rxd homo sapien Q9byz drosophila Q9vws drosophila Q9ves drosophila Q9ves
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             GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
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Q4SPHO TETNO
PYGO DROWE
Q3UG42 MOUSI
Q9VE88 DROM
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Q69Z11 MOUSI
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Gapop 10.0 , Gapext
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RIABLES, Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Alteshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,
Alteshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,
Backlin R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
A biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Godres M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., Usdin T.B., Tobhiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Robask S.A., Morkernan K.J., Malek J.A., Gunaratne P.H.,
A Hitlon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Witting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman M., Maram M., Marra M.A.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
A Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWART, SWO0355; Znr Land Research SWART; SWO0355; Znr Land Research PROSITE; PS50097; BTB; 1. PROSITE; PS0028; ZINC FINGER C2H2 1; 1. PROSITE; PS0157; ZINC FINGER C2H2 2; 2. PROSITE; PS50157; ZINC FINGER CAPE 2; 2. DNA-binding; Metal-binding; Nuclear protein; Repeat; Transcription; DNA-binding; Metal-binding; Nuclear protein; Repeat Transcription; Zinc, Zinc-finger and BTB domain-containing Zinc finger and BTB domain-containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse CDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: May be involved in transcriptional regulation.
-!- SUBCELIULAR LOCATION: Nucleus (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .49 Ala-rich.
53387 MW; B4FF082555B0CAIA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Contains 1 BTB (POZ) domain.
                                                                                                integrated into UniProtKB/Swiss-Prot.
                                                                                                                                          07-MAR-2006, entry version 22.
Zinc finger and BTB domain-containing protein 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ensembl; ENSMUSG0000048485; Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C2H2-type 1.
C2H2-type 2.
                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; BC023839; AAH23839.1; -; mRNA.
                                                            PRT;
                                                                                                                    01-MAR-2003, sequence version 1.
07-MAR-2006, entry version 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGI; MGI:2387181; Zbtb8.
InterPro; IPR000210; BTB.
InterPro; IPR013069; BTB POZ.
InterPro; IPR007087; Znf_C2H2.
Pfam; PF00651; BTB; 1.
Pfam; PF00661; Zf-C2H2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probom; PD000003; Znf C2H2; 1.
SMART; SM00225; BTB; 1.
SMART; SM00355; Znf C2H2; 2.
                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92
353
382
149
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                                                                                                  26-APR-2004,
                                                            ZBTB8 MOUSE
QBCII0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPBIAS
SEQUENCE
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ZN_FING
ZN_FING
                          RESULT 1
ZBTB8_MOU
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Length 484;

DB 1;

Score 53;

100.08;

Query Match

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RD STRAIN-CSTEL/64) TISSUB-Cerebellum, and Head;

RR VELCOTIDE STOURCE.

RA CATRINGOPTIDE STOURCE.

RA CATRINGOPTIDE STOURCE.

RA CATRINGOPTIDE STOURCE.

RA CATRINGOPTIDE STOURCE.

RA DAVIS N. RAVABA T. LEMBLE C., ROGZUB R., SHIMOKAWA K., RADAR R., RAVABA T., LEMBLE C., ROGZUB R., SAVOLAN M., BADIC V. B., BETCHNET S. A., ANDINGOPTION S., FORTEST A.R., ZAVOLAN M., ADAIGN M., MITMING L.G., Addinis V., Allen J.E.,

RA DAVIS M.J., WILMING L.G., Addinis V., Allen J.E.,

RA DAMBERI M., BARKET L., Beisel K.W., BETSAND T., BONO H., Chalk A.M.,

RA CHIU K.P., CHOUGHARY V., CHISTOFFER A., FAULTETOUCK D.R.,

A DEFURACO D., DOWN T., ENGSTROM P., PAGIOLINI M., FAULKE G.,

RA PIECCHET C.F., PUKUSHIMA T., BIGSTROM P., PAGIOLINI M., FAULKI G.,

RA PIECCHET C.F., PUKUSHIMA T., BIGSTROM P., PAGIOLINI M., FAULKI G.,

RA GUSTIL-HUMINICAL L., LAGORON M., TREOK K., HINCKAWA N.,

HILD D., HUMINICAL L., RACON M., RAWASAWA Y., RES. G.,

GUSTINICH S., HATDERS M., HAYASHI Y., HENSCH T.K., HINCKAWA N.,

RA KITANO H., KAOLINI S., MACH M., KAWASAWA Y., KARDON T.K., MINCHEN S., MORTIS K.,

MATCHON I. V. LARCAU L.F., LAZATEVIC D., LIPOTICH J., LIU J.,

LIUNI S., MORVILLAM S., MIKH H., MIGHORE F., MYAKE S., MORTIS K.,

MATCHOL T., SHIMGHER S., NIGHTHAWA S., NORTIS K.,

MALSARI Y., OLIABAR S., MULGER N., NARANO N., NAKAUCH H., KING P.,

RA ROST B., RUMM Y., SALDEDER S., NORTIS K.,

RA ROST B., RUMM Y., SALDEDER S., L., SANGEL B., SCHNEIGHER C.,

SCHOOLOCK, SCHIGUCHI K., SEMPLE C.A., SENG S., SESSA L., SHORY A.,

RADICAL S., TANG S., HUMBER K., SILLAM B., TREFRER Y., TREFRER Y.,

RADICAL S., TANG S., HUMBER R., SILLAM B., TREFRER Y., TREFRER Y.,

RADICAL S., TANG S., HUMBER R., SILLAM S., TREFRER Y., TREFRER Y.,

RADICAL S., TANG S., HUMBER R., SILLAM S., TREFRER Y., TREFRER Y.,

RUMDAS S., TRABACTOR S., HUMBER R., SILLAM S., TREFRER Y.,

RUMDAS S., TRABACTOR S., HUMBER R., SILLAM S., ANDRAWAN N.,

RUMANDAR S., KANDAMONI Y., RADO T., KANDAN W., NAKAND N.,

RIGH H., NAKANDAN M., PROND S., KONDO H., NAKAND N., NAKAND N.,

RIGH H., NAKANDAN S., TON
                                                                                                                                                                                                                                                                                                                                       11-FEB-2006, entry version 7.

16 days embryo head cDNA, RIKEN full-length enriched library,
16 days embryo head cDNA, RIKEN full-length enriched library,
19 days embryo head containing 8, full
19 insert sequence (0 day neonate cereballum cDNA, RIKEN full-length
19 enriched library, clone:C230068H07 product:zinc finger and BTB domain
20 containing 8, full insert sequence) (14, 17 days embryo head cDNA,
RIKEN full-length enriched library, clone:3222401B20 product:zinc
finger and BTB domain containing 8, full insert sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CS7BE,63; TISSUB=Cerebellum, and Head;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carnino: P., Hayashizaki Y.;
High-efficiency Hayashizaki Y.;
High-efficiency 11-1ength cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                      Gaps
                                      ö
                                      Indels
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                                                                                                                                                                                                                                                                                          11-OCT-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                    484 AA.
                   42;
                Pred. No. 42;
; Mismatches
                                                                                                                                                                                                                                                    PRT;
100.08;
                                                                                                                                                                                                                                                                                                                       11-OCT-2005, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                 136 AAMAAAAAAAAA 148
                                                                                   1 AAMAAAAAAAA 13
                                        13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                 Q3US18 MOUSE
Q3US18;
                                           Matches
                                                                                                                                                                                                        RESULT 2
Q3US18_MO
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Mon

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CSTRAIN=C57BL/61 TISSUB=Cerebellum, and Head;

KRAIN=C57BL/62 TISSUB=Cerebellum, and Head;

KRAIN=C57BL/61 TISSUB=Cerebellum, and Head;

KRANI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arawaw T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalou S., Casavant T.,

Rieischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Rromstein M.J., Bult C., Fletcher C., Fullita M., Gariboldi M.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nurahiaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Narahiizaki Y., Wang K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Narahii V., Vandor K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
                                                                                   STRAIN=C57BL/63; TISSUB=Cerebellum, and Head;
PubMed=16141073; DOI=10.1126/science.1112009;
RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;
"Antisense Transcription in the Mammalian Transcriptome.";
Science 309:1564-1566 (2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Functional annotation of a full-length mouse cDNA collection.";
                      "The transcriptional landscape of the mammalian genome."; Science 309:1559-1563(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CS7BL/6J; TISSUE-Cerebellum, and Head;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60,770 full-length cDNAB.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 420:563-573(2002).
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                                                                      NUCLEOTIDE SEQUENCE
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Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Wormalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             ATRAIN=CSTBL/6J; TISSUE=Head;
Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
Shibata K., Ohno M., Sakazume N., Sano H., Sasaki D.,
Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
Muramatsu M., Hayashizaki Y.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CSTBL/63; TISSUB-Cerebellum; Arakwa T., Carninci P., Fukuda S., Hashizume W., Hayashida K., Arakwa T., Carninci P., Fukuda S., Hashizume W., Kanagawa S., Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N., Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D., Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A., Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                       MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibatea K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M., Yoneda Y., Ishikama T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Kokazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50097; BTB; 1.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.
Metal-binding; Nuclear protein; Repeat; Zinc, Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     484 AA; 53414 MW; ACABID5402A2E7F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AK140914; BAE24519.1; -; mRNA.
EMBL; AK163930; BAE37541.1; -; mRNA.
EMBL; AK132152; BAE20999.1; -; mRNA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0046872; F:metal ion binding; IEA.
GO; GO:0008776; F:nucleic acid binding; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
InterPro; IPR00210; BTB.
InterPro; IPR00310; BTB.
InterPro; IPR013069; BTB.
InterPro; IPR013069; BTB.
InterPro; IPR013069; BTB.
                                                                                                                                                                                                                                                                                                                                                                                    Genome Res. 10:1757-1771 (2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00096; zf-C2H2; 2. ProDom; PD000003; Znf_C2H2; 1 SMART; SM00225; BTB; 1. SMART; SM00355; ZnF_C2H2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 AAMAAAAAAAAA 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00651; BTB; 1.
                                                                                                                                 NUCLEOTIDE SEQUENCE
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NUCLEOTIDE SEQUENCE
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RESULT 3 Q6Z8T9\_OR

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RA Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N., Ratous S., Camarate J., Campoo, K., Chang J., Cheshatsang Y., Cutroen M., Collymore A., Campoo, K., Chang J., Chossattsang Y., Cutroen M., Collymore A., Considing J., Chock P., Cooke P., Cotum B., Cutroen M., David R., Elkins T., Rackler H., Engels R., Erickeon J., Razina A., Faro S., Ferreira P., Fischer H., Ragols R., Erickeon J., Razina A., Faro S., Ferreira P., Fischer H., Radols R., Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H., Hagopian D., Hagos B., Hall J., Hatcher B., Haller M., Hagins H., Hadden T., Hour A., Hudde N., Huddes L., Hulme W., Haby E., Illav I., Ra Lindblad-Toh K., Liu X., Legar J., Levine S., Lewis D., Lewis T., Labutti R., Lindblad-Toh K., Liu X., Ledyir R., MacDonald J., MacLean C., Major J., Maning J., Marabella R., Maclu R., Machen C., Mayor C., Mayor D., Mabbitt R., Machon G., Mayor N., Mihalev A., Mihor Y., Marton G., Naylor J., Nachella R., Nicale R., Nicales C., Nalizari M., Norbu R., Norbu N., O'Donnell P., Olocawo D., O'Leary S., Omotosho B., Norbu N., O'Donnell P., Nicol R., Nieles C., Raditud J., Radungka T., Ramasamy U., Rameu R., Radyor J., Ramasamy U., Rameu R., Radyor S., Radith C., Stone S., Stubbs M., Talamas J., Trohinga P., Rutran M., Schupbach R., Seamen C., Settipalis S., Sharpe T., Spence I. Stanker J., Stone S., Stubbs M., Talamas J., Trohinga P., Rutran M., Schupbach R., Seamen C., Stone S., Stubbs M., Talamas J., Trohing P., Treining P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Bukaryota; Fungl; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordarlaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=74-0R23-1A / FGSC 987;
MEDLINE=22598136; PubMed=12712197; DOI=10.1038/nature01554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 361 AA; 39615 MW; 038F774408202041 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AACP01000053; EAK82242.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 49; DB 2;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-2003, integrated into UniProtKB/TrEMBL.
15-DEC-2003, sequence version 1.
07-FEB-2006, entry version 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     368 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q7SBK2_NEUCR PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 AAIAAAAAAAAA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AAMAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 92.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Predicted protein.
ORFNames=NCU08548.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEUCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution.NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN: The RING-type zinc finger domain is essential for ubiquitin ligase activity. It coordinates an additional third zinc
                                                                                                                                                                                                                                                                       Zinc finger protein family-like.
Name=P0686H11.17;
Oryza sativa (japonica cultivar-group). Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; BEP clade;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Ustilaginomycetidae, Ustilaginales, Ustilaginaceae, Ustilago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gramene; QG28T9; ...
GG; GO:000554; C:nucleus; IEA.
GG; GO:000151; C:ubiquitin ligase complex; IEA.
GG; GO:000151; C:ubiquitin ligase complex; IEA.
GG; GO:00046872; F:metal ion binding; IEA.
GG; GO:0004682; F:mbiquitin-protein ligase activity; IEA.
GG; GG:0001567; F:protein ubiquitination; IEA.
InterPro; IPR011016; RINGV.
InterPro; IPR011016; RINGV.
InterPro; IPR011016; RINGV.
INTERPRO; IPR001841; Znf_RING.
SWART; SW0014; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 49; DB 2; Length 167;
Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sasaki T., Matsumoto T., Yamamoto K.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSTITE: PESSONS, ZEF. RING 2; 1.
Metal-binding; Nuclear protein; Zinc; Zinc-finger.
SEQUENCE 167 AA; 17664 MW; 4729ACE00A901AE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ion (By similarity).
SIMILARITY: Contains 1 RING-type zinc finger.
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19-JUL-2005, sequence version 1.
07-FEB-2006, entry version 3.
Hypothetical protein.
                                                                                                                                                                                     Uni Prot KB/TrEMBL.
                                                                                                                      167 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY; PRT; 361 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AP004762; BAD10011.1; -; Genomic_DNA.
                                                                                                                   PRT;
                                                                                                                                                                                 05-JUL-2004, integrated into Unit
05-JUL-2004, sequence version 1.
07-FEB-2006, entry version 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92.5%;
                                                                                                                   QEZBT9 ORYSA PRELIMINARY;
QEZBT9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 92.3
Marches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AAMAAAAAAAA 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q4PEI8_USTWA PACTOR OF PEIR USTWA PAC Q4PEI8_USTWA PAC Q4PEI8_TO PACTOR OF P
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Gaps .

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Length 361; 0; Indels

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Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D., Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M., Qui D., Ianakiev P., Bell-Pedersen D., Nelson M.A., Braun E.L., A Zelter A., Schulte U., Kothe G.O., Jedd G., Mewes H.-W., Staben C., Marcotte E., Greenberg D., Roy A., Foley K., Naylor J., Stange-Thoman N., Barrett R., Gnerre S., Kamal M., Kamvysselis M., A Maucell E., Bielke C., Rudd S., Frishman D., Krystofova S., Cogoni C., Macino G., Catcheside D.E.A., Li W., Pratt R.J., Osmani S.A., DeSouza C.P.C., Glass N.L., Orbach M.J., Berglund J.A., Voelker R., Parden O., Plamann M., Seiler S., Dunlap J.C., Radford A., Aramayo R., Arte G.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M., Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.W.; The genome sequence of the filamentous fungus Neurospora crassa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   091003; 09SCW3; 01-0010 UniProtKB/Swiss-Prot. 01-DEC-2000, integrated into UniProtKB/Swiss-Prot. 01-MAY-2000, sequence version 1. 07-MAX-2006, entry version 37. Heat shock factor protein 7 (HSF 7) (Heat shock transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Makaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; eudicotyledons; core eudicotyledons; cosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 422:859-868(2003).
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 92.5%; Score 49; DB 2; Length 368; 1. Similarity 100.0%; Pred. No. 1.1e+02; 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=HSF7; OrderedLocusNames=At4g11660; ORFNames=T5C23.90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AABX01000166; EAA33794.1; -; Genomic DNA.
SEQUENCE 368 AA; 35691 MW; 7AB0F69255969DD2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=cv. Columbia;
MEDLINE=20083488; PubMed=10617198; DOI=10.1038/47134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preliminary data.
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PRESENCE D. RICHARD M., PRINCE A. Schaefer M., Masller-Naur S., Adjellor M., Pater M., Massers A.C., Schaefer M., Masller-Naur S., Adjellor M., Pater M., Massers A.C., Schaefer M., Masller M., Pater M., Massers C.D., Herzi A., Manner S., Adjellor M., Vitale D., Liguori R., Pater M., Pater M., Pater M., Massers C.D., Herzi A., Ribber R., Schael D., Liguori R., Pater M., Pater M., Falber R., Schael D., Massers C., Addong S., Manner S., Manner C., Oldjely F., Chabaud G. Wanneller A., Falber R., Schael S., Haller R., Schael M., Manner M., Pater S., Pater
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RX STRAIN=C57BL/6; TISSUE=Mouse:

RX STRAIN=C57BL/6; TISSUE=Mouse:

RX Strausberg R.L. Feingold E.A., Grouse L.H., Derge J.G.,

RISDLINE=22388625; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Klausberg R.L. Feingold E.A., Grouse L.H., Derge J.G.,

RISDLINE=22388625; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Klausberg R.L. Feingold E.A., Grouse L.H., Derge J.G.,

RA Altechul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

RA Altechnon L., Maruahna K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Robards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Fahby J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting W. Nadan A., Young A.C., Shevchenko Y., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003, sequence version 1.
07-FEB-2006, entry version 22.
0 day neonate eyeball cDNA, RIKEN full-length enriched library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.5%; Score 49; DB 2; Length 395
92.3%; Pred. No. 1.1e+02;
Virmarrhes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF03171; 20G-FeII Oxy; T.
Hypothetical protein; Iron; Oxidoreductase.
SEQUENCE 395 AA; 44410 MW; 4CE25B4FB5B04DEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; BC052076; AAH52076.1; -; mRNA.
Ensembl; ENSWUSG0000042656; Mus musculus.
MGI: MGI:2144489; AW050020.
GO; GO:0005506; F:irron ion binding; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
InterPro; IPRO6513; 20G-FeII Oase.
Pfan. PRO3171; 20G-FeII Oxv: 1.
                                                  01-JUN-2003, integrated into UniProtXB/TrEMBL
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           395 AA
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           PRT;
                                                                        sequence version 1. entry version 20.
                                                                                                                                                                                                                    Muroidea; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6; TISSUE=Mouse;
           PRELIMINARY;
                                                                      01-JUN-2003, sequence versi
07-FEB-2006, entry version
Hypothetical protein Ofoxd
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Matches 12, Conservative
                                                                                                                                                               Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH MGC Project;
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Q8BKC1;
           Q80USO_MOUSE
Q80USO;
                                                                                                                                             Name=Ofoxd;
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             EHAHAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                     PROSITE; PS00434; HSF_DOMAIN; 1.
Activator; DNA-binding; Heat shock; Nuclear protein; Phosphorylation; Transcription; Transcription regulation.
Transcription; Transcription regulation.
1 377 Heat shock factor protein 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 49; DB 1; Length 377;
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Heat shock factor protein 7.
/FIIG=PRO 0000124588.
By similarity.
Poly-Gly.
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Mismatches 0; Indels
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FD1D5E595B7FC584 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ensembl; ENSG0000091542; Homo sapiens.
GO; GO:0005506; F:iron ion binding; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
InterPro; IRF00513; 20G-FeII Oase.
Fran; PF03171; 20G-FeII Oxy; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000, integrated into UniProtKB/TrEMBL.
01-OCT-2000, sequence version 1.
07-FEB-2006, entry version 18.
Hypothetical protein FLJ20308.
Home sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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Poly-Ala.
                                 InterPro; IPR00023; HSF DNA bd.
InterPro; IPR002341; HSF ETS_DNA_bd.
InterPro; IPR011991; Wing hlx DNA_bd.
PEdm, PF00447; HSF DNA-bind; I.
PRINTS; PR0045; HSFDOMAIN.
PRODOM; P0001788; HSF DNA_bind; 1.
SWART; SM00415; HSF; I.
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14 21 PO
32 22 PO
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20 207 PO
50 50 G
377 AA; 39705 MW;
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100.0%;
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Q9NXD6;
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Best Local Similarity 92.3%;
Matches 12; Conservative
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Local 12; Conserve
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                   FAIR; At4g11660;
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GeneFarm; 4072;
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SOUR PRESENTATION OF THE PROPERTY OF THE PROPE

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Length 395;

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RC STRAIN-657BL/60; TISSUE-Egg, and Eyeball;
RD Pubbed=1641072; DOI=10.1126/science.1112014;
RA STRAIN-657BL/61; TISSUE-Egg, and Eyeball;
RA RAIN-657BL/61; TISSUE-Egg, and Eyeball;
RA Bajic V. B., Berner S. B., Betalvo S., Forrest A.R., Zavolan M.,
RA Bajic V. B., Brenner S. B., Raidnis V., Allen J.E.,
Ambeai-Impiombato A., Apweller R., Aturaliya R.N., Bailey T.L.,
Banaal M., Baxter L., Beisel K.W., Allen J.E.,
Anderi-Impiombato A., Apweller R., Aturaliya R.N., Bailey T.L.,
Banaal M., Baxter L., Beisel K.W., Putaki S., Caribod R.N.,
A Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
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A Thomas R. Bernard D., Bown T., Engetrom P., Regiolini M., Faulkner G.,
RA Georgii-Hemming P. Gingeres T.R., Golobori T., Galla Gate G.,
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Bantanishi H., Zabarovsky B., Ziuu S., Liuu B.T., Ramer J., Hide W., Bult C.,
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Berlando S., Stupka E., Suguiura K., Sultana R., Takenaka Y.,
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Rida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawasani J.,
Rida J., Imamura K., Itoh M., Rato T., Kawai, J., Kawashima T., Kolima M., Plessy C., Shibacta X., Sultana S., Stuki H., Sakashima T., Suluki H., Rayashinaki Y., Suluki H., Rayashinaki Y., Suluki H., Rayas
clone:E130207K11 product:hypothetical Alanine-rich region/Type I antifreeze protein/20G-Fe(II) oxygenase superfamily containing protein, full insert sequence (2 cells egg cDNA, RIKEN full-length enriched library, clone:B020011005 product:Hypothetical alanine-rich region/type I antifreeze protein/20G-Fe, full insert sequence) (Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Egg, and Eyeball;
MEDLINE=99279253; Pubmed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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PubMed=16141073; DOI=10.1126/science.1112009;
                                                                                                                                                                                                                                     Name=AW050020; ORFNames=RP23-331121.1-001;
                                                                                                                                                                                                                                                                                                                                                                                           Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                musculus (Mouse).
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"Antisense Transcription in the Mammalian Transcriptome.";

STRAIN=C57BL/6J; TISSUE=Egg, and Eyeball;

NUCLEOTIDE SEQUENCE.

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RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Saldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Schriml I.M., Kanapin A., Matsuda H., Batalov S., Belsel K.W.,

RA Balake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,

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Ranai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

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Ranagott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

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Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

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RA Miyazaki T., Waki K., Kawai J., Aizawa R., Shibata R., Shibata R., Shibata R.,

Marazaki T., Waki K., Sakaki D., Shibata K., Shibata R.,

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Manazaki A., Sakai K., Sakai D., Shibata K., Shibata K., Shibata K.,

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Sanada K., Shibata K., Shibata K., Shibata K.,

Sanada K., Shibata K., Shibata K., Shibata K., Shibata K.,

Sanada K., Shibata K.
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RAYARNA-CT-SELO SUCKENCE.

RAYARNA-CT-SELO SEGOO, PUDDMEd=11217851; DOI=10.1038/35055500;

RAYARNA-CT-SELO SEGOO, PUDDMEd=11217851; DOI=10.1038/35055500;

RAYARNA-CT-SELO SEGOO, PUDDMED-11217851; DOI=10.1038/35055500;

RAYARNA-CT-SELO SEGOO, PUDDMED-NOTE SERONALY.

RAYARNA-CT-SERO SELO SERONALY.

RAYARNA-CT-SERO SERONALY.

RAYARNA-CT-SERONALY.

RAYARNA-CT-SERO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y., "Analysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Muramatsu M., Hayashizaki Y.; Itoh M., Wormalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA lbraries for rapid discovery of new genes."; Genome Res. 10:1617-1630 (2000).
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STRAIN=C57BL/6J; TISSUB=Egg, and Eyeball;
MEDLINE=20530913; PubMed=110.76861; DOI=10.1101/gr.152600;
MEDLINE=20530913; PubMed=110.76861; DOI=10.1101/gr.152600;
MEDLINE=20530913; PubMed=110.76861; Magaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishlii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
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MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
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NCBI_TaxID=10090;
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                                                                                                                                                                                                      Adachi J., Aizawa K., Akinura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayabu N., Hiranoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saitoh H., Sakai K., Sakai 
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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STRAIN=C57BL/6J; TISSUB=Egg;
Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
Hori F., Iida J., Immaura K., Imocani K., Itoh M., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
Muramatsu M., Hayashizaki Y.;
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7-MAR-2006, entry version 6.
In vitro fertilized eggs cDNA, RIKEN full-length enriched library clone:7420402E17 product:Hypothetical alanine-rich region/type I
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   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., "RIKRN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000).
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Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Muramatsu M., Hayashizaki Y.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0016491; F.oxidoreductase activity; IEA.
InterPro; IRR005123; 2OG-FeII Oase.
Pfam; PF03171; 2OG-FeII Oxy; I.
Hypothetical protein; Iron; Oxidoreductase.
SEQUENCE 395 AA; 44411 MW; 2822BF4BFFFEETFF CRC64;
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Name-AW050020;
Mus musculus (Mouse).
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QJTSG4;
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EMBL; AKK62394; BAS37281.1; -; mRNN.
EMBL; AL596386; CAI35332.1; -; Genom.
Ensembl; BNSMUSG00000042650; Mus musculus.
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GO; GO:0005506; F:iron ion k
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Ronagays A., Wiscocking I.V., Lew Y., Lew R., Thombard B., Lyone P.M., Magnashina T., Marcocking I.V., Lew Y., The Magnashina T., Managashina M., Managashina M., Managashina T., Managashina M., Managashina T., Managashina M., Managashina T., Managashina T., Managashina T., Managashina M., Managashina T., Managashina T., Managashina T., Managashina M., Managashina T., Managashina M., Managashina
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RC STRAIN-CSTBL/67; TISSUE-Eyeball;
RA Garninci P., Kasukwa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Garninci P., Kasukwa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Garninci P., Kasukwa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Ambesi-Impiombato A., Apweiler R., Alten J.E.,
RA Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Balley T.L.,
RA Ambesi-Impiombaty V., Christoffels A., Clutterbuck D.R.,
Crowe M.L., Dalla E., Dallarymple B.P., de Bono B., Della Gatta G.,
RA Crowe M.L., Dalla E., Dallarymple B.P., de Bono B., Della Gatta G.,
RA Growe M.L., Dallar E., Dallarymple B.P., de Bono B., Della Gatta G.,
RA Growe M.L., Dallar B., Dallayamia T., Furuno M., Futaki S., Gariboldi M.,
RI Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa T.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa T.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
Rucchkin I.V., Lareau Babu M., Madera M., Marchiani L.,
RA Matsuda H., Matsuzawa S., Maki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakauchi H., Ng P., Ohara O.,
                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J; TISSUB=Eyeball; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninol P., Hayashlaski Y.; Hayashlaski Y.; Hitch-efficiency Full-length CDNA cloning."; Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                    Gaps
Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A., Muramatsu M., Hayashizaki Y.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003, sequence version 1.
07-MAR-2006, entry version 24.
0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:E130210021 product:hypothetical Alanine-rich region/Type antifreeze protein/20G-Fe(II) oxygenase superfamily containing protein, full insert sequence.
Name=AW050020;
                                                                                                                                                                                                                                                                                                                                                                    ·;
                                                                                                                                                                                                                                                                                                                        92.5%; Score 49; DB 2; Length 395; 92.3%; Pred. No. 1.1e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                               EMBL; AK162072; BAE36711.1; -; mRNA.
MGI; MGI:2144489; AW050020.
GO; GO:0005506; F:iron ion binding; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
InterPro; IPR05123; 20G-FeII ase.
Pfam; PF03171; 20G-FeII_Oxy; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003, integrated into UniProtXB/TrEMBL
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                                                                                                                                                                                                                                                                                                                                                                    12; Conservative
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NUCLEOTIDE SEQUENCE,
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Qebkb9;
                                                                                                                                                                                                                                                               Hypothetical
SEQUENCE 39
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Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G., Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M., Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Schneider C., Schimada H., Shimada K., Singlain B., Schneider C., Shimada H., Shimada K., Silva D., Sinclair B., Sperling S., Stupka E., Sugiura K., Silva D., Sinclair B., Sperling S., Stupka E., Sugiura K., Silva D., Sinclair B., Sperling S., Stupka E., Valva M., Takenaka Y., Takenaka M., Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C., & Grimmond S. M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J., Mahlestedt C., Mattick J.S., Hume D.A., Kaal C., Sasaki D., Tomaru Y., A. Hida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N., Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N., Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki H., Kawai J., Hayashizaki Y.; ARDINES-21354683; PubMed=12466851; DOI=10.1038/nature01266;

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A Okazaki Y., Furuno M., Kaivakawa T., Adachi J., Bono H., Kondo S.,
A Nikaido II., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
A Badarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
A Badarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
A Schriml L.M., Kanapin A., Fletcher C.F., Forrest A., Frazer K.S.,
B Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
A Balla E., Dragani T.A., Fletcher C.F., Forrest A., Gough J.,
A Gariboldi M., Gissi C., Godzik A., Gough J.,
A Kawaji H., Kawasawa Y., Kedzierski R.N., King B.L.,
A Kanai A., Kawaji H., Kawasawa Y., Kedzierski R., Lyons P.A.,
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A Mangott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
A Magashima T., Numara K., Okido T., Pavan W.J., Pertea G., Pesole G.,
A Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
A Sandelin A., Schneider C., Semple C.A., Setou M., Shimdad K.,
A Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
A Verardo R., Mapner L., Wahlestedt C., Wang Y., Watanabe Y., Wang I.,
A Nilming L.G., Wynbaw-Boris A., Yanagiasawa M., Yang I.,
A Nilming L.G., Wynbaw-Boris A., Yanagiasawa M., Yang I.,
A Nilming L.G., Wynbaw-Boris A., Yanagiasawa M., Yang I.,
A Nilming L.G., Wynbaw-Boris A., Yanagiasawa T., Putuda S.,
A Shiraki T., Waki K., Kawa J., Alaxawa T., Putuda S.,
A Hara A., Hashizume W., Imotani K., Ishii Y., Iloh M., Kagawa I.,
A Wiyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
A Hara A., Hashizume W., Imotani K., Ishii Y., Iloh M., Kagawa I.,
A Hyazahi A., Sukai Y., Sasaki D., Shibata K., Shinagawa J.,
A Hyazahi A., Shaki Y., Birney E., Hayashizaki Y., "Analysis of the mouse transcriptome based on functional annotation of MEDLINE=2108560; PubMed=11217851; DOI=10.1038/35055500; MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500; MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500; MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500; Marawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Odjobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Fleischmann W., Staubli F., Suzuki R., Tomita M., Wagner L., Washlo T., Sakai K., Okido I., Furuno M., Aono H., Baldarelli R., Barsh G., T., STRAIN=CS7BL/6J; TISSUE=Eyeball;
PubMed=16141073; DOI=10.1126/science.1112009;
RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;
"Antisense Transcription in the Mammalian Transcriptome.";
Science 309:1564-1566 (2005). "The transcriptional landscape of the mammalian genome."; Science 309:1559-1563(2005). 60,770 full-length cDNAs."; Nature 420:563-573(2002). NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE 

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C STRAIN=C57BL/6J; TISSUB=Eyeball;

MEDLINE=C5080913; PubMed=11076861; DOI=10.1101/gr.152600;

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Shibata K., Itoh M., Aizawa K., Ritsunai T., Tashiro H., Itoh M.,

A Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harda A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watchiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format

Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carninci P., Shibata Y., Hayatan N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., Shibata K., Itoh M., Hayashizaki Y., Shibata K., Itoh M., prepare in and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownetein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wingham Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tagami M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carninci P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adachi, J., Aizawa K., Julianza, T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hirzoka T., Hirozane T., Hori F., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katch H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya Ś Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito H., Saito H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Tanaka T., Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Pred. No. 1.18+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6J; TISSUE=Eyeball;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 395 AA; 44415 MW; 6D22C26B1A99EDA8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AK053700; BAC35481.1; -; mRNA.
Ensembl; ENSMUSG0000042650; Mus musculus.
MGI; MGI:2144489; AW050020.
GO; GO:000560; Fitron ion binding; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Eyeball;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                   Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 92.3
hes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                        Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOXB2_MOUSE
TO FOXB2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                       SOW RREPRENCE TO SERVE TO SERVE THE SERVE TO SERVE THE S
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428 AA.

PRT;

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QSVYVO_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00657; FORK HEAD 1; 1.
PROSITE; PS00658; FORK_HEAD 2; 1.
PROSITE; PS00658; FORK_HEAD 3; 1.
PROSITE; PS50039; FORK_HEAD 3; 1.
DN1-binding; Nuclear protein; Transcription regulation.
CHAIN 1 428 Forkhead box protein B2.
                                                                                                                                                 MEDLINE=97014266; Pubmed=8861101; DOI=10.1016/0925-4773(96)00507-2; Kaestner K.H., Schuetz G., Monaghan A.P.; "Expression of the winged helix genes fkh-4 and fkh-5 defines domains
                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                          Kaestner K.H., Lee K.H., Schloendorff J., Hiemisch H., Monaghan A.P.,
                                                                                                                                                                                                                                                                                  "Six members of the mouse forkhead gene family are developmentally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 49; DB 1; Length 428; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                            regulated.",
Proc. Natl. Acad. Sci. U.S.A. 90:7628-7631(1993).
-- SUBCELLULAR LOCATION: Nucleus.
-- DEVELODMENTAL STAGE: Expressed during embryogenesis.
-- SIMILARITY: Contains 1 fork-head DNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DESASEFDIE94AB10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Forkhead box protein B2./FTId=PRO_0000091805.
          01-NOV-1997, integrated into UniProtKB/Swiss-Prot. 01-NOV-1997, sequence version 1. 07-FEB-2006, entry version 31. Forkhead box protein B2 (Transcription factor FKH-4) Name-Poxb2; Synonyms-FkH4; Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSFAC, T02442;
Ensembl: ENSMUSG0000056829; Mus musculus.
MGI; MGI:1347468; Foxb2.
InterPro; IPR001766; TF Fork head.
InterPro; IPR011991; Wing hlx_DNA_bd.
Pfam; PF00250; Fork_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X92591; CAA63335.1; -; mRNA.
ERMB; X71942; CAA50744.1; -; Genomic_DNA.
PIR; D47746; D47746.
HSSP; Q63245; ZHDC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Poly-His.
Poly-His.
Poly-Pro.
Poly-Ala.
Poly-Ala.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00053; FORKHEAD.
ProDom; PD000425; TF Fork_head; 1.
SMART; SM00339; FH; 1.
                                                                                                                                                                                                                                              MEDLINE=93361500; PubMed=7689224;
                                                                                                                                                                                       in the central nervous system."; Mech. Dev. 55:221-230(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45170 MW;
                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE OF 4-114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.5%;
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nes 12; Conservative
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258
330
399
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153
162
172
                                                                                                                                         NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           428 AA;
                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                       Schuetz G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA BIND
COMPBIAS
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EWEL, ALSISSATY, CAH70683.1; -; Genomic_DNA,

REMEL, ALSISSATY, CAH70683.1; -; Genomic_DNA,

REMEL, ALSISSATY, CAH70683.1; -; Genomic_DNA,

RO; GO:0005350; F:transcription f transcription, DNA-dependent; IEA.

RO; GO:0006355; P:transcription; IEA.

RO; GO:0006355; P:transcription; IEA.

RIGETPC; IPR011991; Wing hlx_DNA_bd.

RIGETPC; IPR011991; Wing hlx_DNA_bd.

RIGHTPC; ROWO0425; FORK_head; 1.

RODON; PD000425; FF Fork_head; 1.

RODON; PD000425; FFF Fork_head; 1.

ROSITE; FS000659; FORK_HEAD 1; 1.

ROSITE; RS000659; FORK_HEAD 1; 1.

ROSITE; RS000659; FORK_HEAD 2; UNKNOWN_1.

ROSITE; PS500039; PORK_HEAD 2; UNKNOWN_1.

ROSITE; PS500039; PORK_HEAD 2; UNKNOWN_1.

ROSITE; RS000659; FORK_HEAD 2; UNKNOWN_1.

ROSITE; RS000659; FORK_HEAD 2; UNKNOWN_1.

ROM-binding; Nuclear protein; Transcription regulation.

SQUENCE 432 AA; 45581 MW; 9A832ACDD9A765EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                              Dukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDILINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae, Xenopodinae, Xenopus; Silurana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUL-2004, integrated into UniProtKB/TrEMBL.
19-JUL-2004, sequence version 1.
07-FBB-2006, entry version 16.
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1.
Name=smarce1-prov;
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                                                                                                                                                                                                                                                                                                                                                                                  Kimberley A.;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
                      QSVIVO;
07-DBC-2004, integrated into UniProtKB/TrEMBL.
07-DBC-2004, sequence version 1.
OT-FBB-2006, entry version 12.
OTTHUMP00000021510.
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PRT;
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QGGLG1;
PRELIMINARY;
                                                                                                                                                             ORFNames=RP11-159H20.4-001;
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Matches 12; Conservative
                                                                                                                                                                                       Homo sapiens (Human).
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NUCLEOTIDE SEQUENCE.
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Gaps

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0; Indels

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Matches

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RESULT 13

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X MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Strausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Warusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshlywiki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glabs R.A.,

Rahey J., Halton E., Ketteman M., Nadan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Hulyk S.W., Villalon D.K., Maclan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schmin J.B., Schmutz J., Myers R.M., Schmin J.B., Schmin J.B., Schmin J.B., Schmin J.B., Schmin J.B., Sones S.J.M., Marra M.A., Schmin J.B., Sones S.J.M., Marra M.A., Schmin J.B., Jones J. M. Marra M.A., Schmin J.B., Jones J. M. Marra M.A., Schmin J.B., Jones J. M. Marra M.A., Schmin J.B., Jones J. M., Mannan J. M., M., J. M., J. M., J. M., M., J. M., M., M., J. M., 
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; BC074534; AAH74534.1; -; mRNA.
Ensembl; ENSXETG0000021355; Xenopus tropicalis.
Ensembl; ENSXETG0000021355; Xenopus tropicalis.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000910; HNG 12 box.
Fram; PF00505; HNG box; 1.
FRAMI; SMART; SM00398; HNG; 1.
PROSITE; PSS0118; HNG BOX 2; 1.
SEQUENCE 435 AA; 48441 MW; 6F227ASD387A9CA2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Klein S., Gerhard D.S.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004, integrated into UniProtKB/TrEMBL. 05-JUL-2004, sequence version 1. 07-FEB-2006, entry version 16. Hypothetical protein OFOXD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 458 AA
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Q6P6C2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             318 AAVAAAAAAAAA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 92.3
Matches 12, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rissue=Embryo;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
Erezyilmaz D.F., Riddiford L.M., Truman J.W.;
"An ancestral role for a metamorphosis-determining factor in a direct-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                 Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; BC062339; AAH62339.1; -; mRNA.
Ensembl; BKSG0000091142; Home sapiens.
GO; GO:0005569; Friron ion binding; IEA.
GO; GO:0016491; Frironion binding; IEA.
InterPro; IPR05123; 20G-FeII Oase.
Pfam; PF03171; 20G-FeII Cox; I.
Hypothetical protein; Iron; Oxidoreductase.
SEQUENCE 458 AA; 51409 MW; 88ACCDA9992B5AEB CRC64;
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G0; G0:0005634; C:nucleus; IEA.
G0; G0:000516; F:nucleic acid binding; IEA.
G0; G0:0005515; F:protein binding; IEA.
G0; G0:0008270; F:zinc ion binding; IEA.
InterPro; IPR000210; BTB.
InterPro; IPR013069; BTB.PoZ.
InterPro; IPR013069; BTB.PoZ.
InterPro; IPR013069; BTB.PoZ.
InterPro; IPR01081; Znf_C2H2.
Pfam; PF00651; BTB; 1.
SMART; SM00255; BTB; 1.
SNART; SM00255; ZnP_C2H2; 2.
SNART; SN00255; ZnP_C2H2; 2.
PROSITE; PS50197; ZINC_FINGER_C2H2_1; 2.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.
Metal-binding; Nuclear_protein; Zinc; Zinc-finger.
                                                                                                                                                                          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Q3S2W8;
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21-FEB-2006, entry version 7.
BroadZ1 isoform.
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Matches 12; Conservative
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                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                          NIH MGC Project;
                                                                                                                                                                                                                                                                                                         TISSUE=Brain;
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STRAIN=PEST;
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SEQUENCE
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ZN_FING
ZN_FING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

Human chromosome 1 international sequencing consortium;

Submitted (WAY-2005) to the EMBL/denBank/DDBJ databases.

-!- FUNCTION: May be involved in transcriptional regulation.

-!- SUBCELLUIAN LOCATION: Nucleus (Potential).

-!- SIMILARITY: Contains 1 BTB (POZ) domain.

-!- SIMILARITY: Contains 2 C2H2-type zinc fingers.
                                                 Length 506;
                                                                                           Indels
  54175 MW; F4FCCA9BE6415EC0 CRC64;
                                                                                                                                                                                                                                                                                             ZBTBB HUMAN STANDARD; PRT; 512 AA. QBNAPB; QSYXRS; 26-APR-2004, integrated into UniProtKB/Swiss-Prot. 01-OCT-2002, sequence version 1. 07-MAR-2006, entry version 25. Zinc finger and BTB domain-containing protein 8.
                                               Score 49; DB 2; Ler
Pred. No. 1.4e+02;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
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                                               92.5%;
                                                                                                                                                                                   218 AAVAAAAAAAA 230
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                                                                                                                                        1 AAMAAAAAAA 13
                                        Query Match
Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
  506 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=ZBTB8;
SEQUENCE
                                                                                                                                                                                                                                                                               HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anopheles gambiae str. PEST.
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
Anophelinae; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                         The Anopheles gambiae Sequence Committee;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92.5%; Score 49; DB 1; Length 512; 92.3%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Anopheles gambiae re-annotation.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BB970D200B60CC9F CRC64;
EMBL; AL356986; CAH73355.1; -; Genomic_DNA.
EMBL; AL033529; CAH73365.1; JOINED; Genomic_DNA.
EMBL; AL033529; CAT20022.1; -; Genomic_DNA.
EMBL; AL033529; CAT20022.1; JOINED; Genomic_DNA.
EMBL; AL0356986; CAI20022.1; JOINED; Genomic_DNA.
Ensembl; ENSC00000185718; Homo sapiens.
InterPro; IPR000210; BTB.
InterPro; IPR000210; BTB.
InterPro; IPR000210; BTB.
From PF00651; BTB.
From PF006525; BTB.
From PF00655; ZnfCC2H2; I.
From PF00655; ZnfCC2H2; I.
From PF00655; ZnfCC2H2; I.
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GO; GO:0003676; F:nucleit acid binding; IEA.
GO; GO:0000166; F:nucleotide binding; IEA.
InterPro; IPR012677; a_b_plait_nuc_bd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-DEC-2003, integrated into UniProtKB/TrEMBL. 07-DEC-2004, sequence version 2. ENSANGPO0000016. entry version 16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C2H2-type 1.
C2H2-type 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 BT
363 C2
392 C2
153 Po
55562 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 AAVAAAAAAAA 148
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Birren B.W., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Fungi, Basidiomycota; Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
NCBI_TaxID=237631;
                                                                                                                                                                                                                                                                            92.5%; Score 49; DB 2; Length 521; 92.3%; Pred. No. 1.4e+02; ive 1; Mismatches 0; Indels
                                                                                              Pfam; PP00076; RRM 1; 3.
SMART; SM00360; RRM; 3.
SMART; SM00361; RRM; 3.
TIGRFAMS; TIGRO1645; half-pint; 1.
PROSITE; PS50102; RRM; 3.
SEQUENCE 521 AA; 55760 MW; 68A0C7DEA9FE24DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JUL-2005, integrated into UniProtKB/TrEMBL.
19-JUL-2005, sequence version 1.
07-FBB-2006, entry version 4.
Hypothetical protein.
ORFNames=UM05773.1;
InterPro; IPR006532; Polyu bd.
InterPro; IPR001504; RNP1_RNA_bd.
InterPro; IPR003954; RRW 1.
PANTHER; PTHR10432:SF141; Polyu_half_pint; 2.
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Q4P290;
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les 12, Conservative
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MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Holt R.A., Evans C.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaaley E.M., Ballew R.M., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Buller H., Cadieu E., Center A., Chandra I., Antis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Anderny J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Anderny J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Durnh K.J., Evangelista C.C., Ferraz C., Ferrac R., Fleischmann W., Glasser K.,
                                                                                                                                                                                                                                                                                                                                           Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
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GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000679; Znf_GATA.
Pfam; PF00220; GATA; 1.
SMART; SM00401; ZnF_GATA; 1.
PROSITE; PS50114; GATA_ZN_FINGER_2; 1.
                                                   "The genome sequence of Ustilago maydis.";
Submitted (FBE-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDB whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Canton-5; TISSUB-Embryo; MEDLINE=97032935; PubMed=8878683; Hart M.C., Wang L., Coulter D.E. (Comparison of the structure and expression of odd-skipped and related genes that encode a new family of zinc finger proteins
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01-MAY-2000, sequence version 1.
07-MAR-2006, entry version 30.
Protein sister of add and bowel.
Name=sob; ORFNames=CG3242;
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Prerygota; Nooptera; Endopterygota; Diptera; Diptera; Endopterygota; Diptera; Endopterygota; Diptera; Endopterygota; Diptera; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 49; DB 2; Length 529;
Pred. No. 1.4e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      il protein. - 53820 MW; D5ABC2C8EA96B06D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AACP01000212; EAK86012.1; -; Genomic_DNA.
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Zimmer A., Zody M., Lander E.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.5%;
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Matches 12; Conservative
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dlodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D.A., Heiman T.J., Heimandez J.R., Houck J.,
Hostin D., Houston K.A., Heiman T.J., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Re Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
Liu X., Mattei B. McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Nelson D.R., Nelson K.A., Stunders R.D.C., Scheeler F., Shen H.,
Raiazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Spier E., Siden-Kiamos I., Simpson M., Stupski M.E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Williams S.M., Woodage T., Weinstock G.M., Weissenbach J.,
Williams S.M., Woodage T., Weinstock G.M., Vang S., Zho Q., Zhong X.,
Williams S.M., Woodage T., Weinstock G.M., Vang S., Zho X., Smith H.O.,
Cheng X.H., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a transcriptional activator, depending on the stage of development and spatial restrictions (By similarity). May function redundantly with odd and drm in leg joint formation during the larval stages, acting downstream of Notch activation.
SUBCELLULAR LOCATION: Nucleus (Probable).
TISSUE SPECIFICITY: Has two temporally distinct modes of expression during early embryogenesis; expressed in seven stripes at the blastoderm stage. Also expressed in a non-periodic domain at the anterior of the embryo. During gastrulation, the seven primary stripes are supplemented by seven secondary stripes that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22930851; PubMed=14568103; DOI=10.1016/j.mod.2003.08.001; Johansen K.A., Green R.B., Iwaki D.D., Hernandez J.B., Lengyel J.A.; Johansen K.A., Green R.B., Iwaki D.D., Hernandez J.B., Lengyel J.A.; The Externing and morphogenesis."; hindgut patterning and morphogenesis."; Mech. Dev. 120:1139-1151(2003).

-! FUNCTION: Pair-rule protein that determines both the size and polarity of even-numbered as well as odd-numbered parasegments during embryogenesis. DNA-binding transcription factor that acts primarily as a transcriptional repressor but can also function as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Berkeley; TISSUE=Embryo;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R.A., Gonzalez M., Glarin H., Krommiller B., Li P.W., Liao G.,
Miranda A., Mungall C.J., Nunoo J., Pacleb J.M., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K.H., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=14597202; DOI=10.1016/j.ydbio.2003.07.011;
Hao I., Green R.B., Dunaevsky O., Lengyel J.A., Rauskolb C.;
"The odd-skipped family of zinc finger genes promotes Drosophila leg
segmentation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POSSIBLE FUNCTION, AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dev. Biol. 263:282-295(2003).
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                                                                                                                                                                                                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
appear in alternate segments. This results in the labelling of each of the 14 segments in the extended germ band. Expression is relatively weak at the blastoderm stage, gaining in intensity at gastrulation. Expressed in the invaginating stomodeum and proctodeum of the embryonic gut. By stage 13, expressed in the region that will form the proventriculus and in a wide ring at the most posterior portion of the midgut. Expression continues in the gut through the remainder of embryogenesis. Expressed in the proximal Malphighian tubules, brain and pharyngeal muscles during late embryogenesis. Expressed weakly in a segmentally repeated pattern in the leg disk at the distal edge of each presumptive leg segment except in tarsal segments 1 to 4.

SIMILARITY: Contains 5 C2H2-type zinc fingers.
                                                                                                                                                                                                                    Metal-binding; Nuclear procein; Pair-rule protein; Repeat; Repressor;
Transcription; Transcription regulation; Zinc; Zinc-finger.
CHAIN 1 578 Protein sister of odd and bowel.
Frid=PRO 0000046928.
ZN_FING 395 417 C2H2-type
                                                                                                                                                                                                                                                                                                                                                          Ensembl; G3242; Drosophila melanogaster.
FlyBase; FBG0004892; sob.
G0; G0:0005637; F:DAB binding; ISS.
G0; G0:0005677; F:DAB binding; ISS.
G0; G0:0016563; F:transcriptional activator activity; ISS.
G0; G0:0015664; F:transcriptional repressor activity; ISS.
G0; G0:0015664; F:transcriptional repressor activity; ISS.
G0; G0:0016348; F:Dastoderm segmentation; ISS.
G0; G0:0016348; P:leg joint morphogenesis (sensu Endopterygota); IMP.
G0; G0:00001366; P:periodic partition of transcription from R. .; ISG.
G0; G0:0045944; P:positive regulation of transcription from R. .; IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SW00355; ZnF CZH2; 5.
PROSITE; PS00028; ZINC FINGER C2H2]; 5.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 5.
Activator; Complete proteome; Developmental protein; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Pred. No. 1.56+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (in Ref. 1)
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P -> L (in Ref. 1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           640 AA.
                                                                                                                                                                                                                                                                          EMBL; U62004; AAC47282.1; -; mRNA.
EMBL; AE001579; AAF51087.1; -; Genomic_DNA.
EMBL; BT003205; AA024960.1; -; mRNA.
PIR; S7227; S7227.
HSSP; P07248; ZADR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C2H2-type 2.
C2H2-type 3.
C2H2-type 4.
C2H2-type 5.
Ala-rich.
Ser-rich.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S -> P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2002, sequence version 2.
21-FEB-2006, entry version 39.
CG32105-PB (RE70810p).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007087; Znf C2H2.
Pfam; PF00096; zf-C2H2; 5.
ProDom; PD000003; Znf C2H2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58455 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            274 AAVAAAAAAAAA 286
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Q9VTW5;
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COMPBIAS
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PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
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Best Local Similarity 92.3
Marches 12; Conservative
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SMART; SM00132; LIM; 2.
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                                                                                                                                                           NUCLEOTIDE SEQUENCE.
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                                                                         Lewis S.E.
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                                                                                                                    MUCLEOTIDE SEQUENCE.

RADINE-ZO196066; Publed=10731132; DOI=10.1126/science.287.5461.2185; RADINE-ZO196066; Publed=10731132; DOI=10.1126/science.287.5461.2185; RADINE-ZO196066; Publed=10731132; DOI=10.1126/science.287.5461.2185; RADINE-ZO196066; Publed=10.7181.

RADINE-ZO196066; Publed=10731132; DOI=10.1126/science.287.5461.2185; RADINE-ZONE MA. Addams M.D., Cahing O., Chen L.X., Addams M.D., Cahing O., Chen L.X., Brutcon G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Brutcon G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Brutcon G.G., Mortman J.R., An H.-J., Andrews-Frankoch C., Baldwin D., RADILLOY, Backer M. Baud M. Bau
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Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20126065; PubMed=12537568; Celliker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.B., Sacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; "Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence."; Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.
ORFNames=CG12105, Dmel CG32105;
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22426070; PubMed=12537573;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J., Park S., Wan K., Yu C., Celniker S.; Submitted (AUG-2005) to the EMBL/Genank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- SIMILARITY: Contains 2 LIM zinc-binding domains.
                                                                                                                                                                                                                                                                                                                          Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
Yu C., Rubin G.;
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B. Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                       "Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.5%; Score 49; DB 2; Length 640; 92.3%; Pred. No. 1.6e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00478; LIM_DOWAIN_1; 2.
PROSITE; PS00428; LIM_DOWAIN_2; 2.
PROSITE; PS01359; ZF FHD_1; ÜNKNOWN_1.
DNA-binding; Developmental protein; Homeobox; LIM domain; Metal-binding; Nuclear protein; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ion regulation; Zinc.
640 AA; 67760 MW; AlAlOF826018C98E CRC64;
                                                                                                                                                                                                                 systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE003541; AAF49930.2; -; Genomic_DNA.
EMBL; BT003467; AAO39470.1; -; mRNA.
HSSP; P50480; 1BW5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Flyase; FBGD052105; CG32105. GO; GO; GO:0005515; F:protein binding; IPI. GO; GO:0005515; F:protein binding; IPI. InterPro; IPR0011356; Homeodowain-rel. InterPro; IPR0012087; HOmeodowain-rel. InterPro; IPR001707; LIM homeo. InterPro; IPR001781; LIM Zn bd. InterPro; IPR001965; Znf-PHD. Pfam; PF00046; Homeodox; 1.
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Q9NVRO;
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Q9NVR0 HUM
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RESULT 23
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Rubbed-14702039; DOI=10.1038/ng1285;

Rubbed-15. Kawai Y., Isono Y., Nakamura Y., Nagahari K., Nakamoto J., Raku Y., Kodaira H., Kondo H., Sudawara M., Andracori A., Rakanbara K., Katsucta N., Sato K., Tanikawa E., Omura Y., Abe K., Kamihara K., Katsucta N., Sato K., Tanikawa M., Taniacori K., Namazaki M., Ninomiya K., Ishibashi T., Yamanhita H., Murakawa M., Taniaca N., Rusano J., An Andrabe S., Yosida M., Hotura T., Kusano J., An Andrabe S., Yosida M., Hotura T., Kusano J., An Andrabashi-Fujii A., Hara H., Taniaca T.-O., Nomura Y., Togiya S., Komai P., Hara R., Takeuchi K., Arita M., Imose N., Nasahima Y., Sato N., Andrabashi-Fujii A., Satoki N., Arita M., Imose N., Nomiyama H., Satoh N., Takani S., Terashima Y., Sano S., Nomiyama H., Satoh N., Takani S., Terashima Y., Sano S., Nomiyama H., Satoh N., Takani S., Terashima Y., Wakebe H., Nakagawa S., Senoh A., Watanabe K., Kumagai A., Itakura S., Fukurumi Y., Komiyama M., Tashico M., Ohmori Y., Yamasaki M., Watanabe K., Kumagai A., Itakura S., Fukurumi Y., Kohtuyama M., Tashico M., Ohmori Y., Sanaki M., Rawabata A., Hikiji T., Yogaki K., Hiroo M., Ohmori Y., Yamashita R., Nakajima Y., Matanabe M., Komatsu T., Matsumura K., Nakajima Y., Matanabe M., Komatsu T., Matsumi M., Hata H., Watanabe M., Komatsu T., Sugamo J., Sasaki M., Watsuhi M., Yada T., Nomura N., Kikuchi H., Wasuho Y., Yamashita R., Nakai M., Yada T., Nomura N., Kikuchi H., Wasuho Y., Yamashita R., Nomi Watai R., Yada T., Nomura N., Kikuchi H., Masuho Y., Nakasima W., Nakai W., Nakami M., Nakai W., Nakai M., Nakai M., Nakai M., 
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A klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
A ltschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
A hopkins R.F., Jordan H., Moore T., Mans J.I., Haich F.,
A biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S.W. Worley D.M., Rockernan K.J., Malek J.A., Gubaratne P.H.,
A Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Villalon D.K., Many D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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01-OCT-2000, integrated into UniprotKB/TrEMBL. 01-OCT-2000, sequence version 1. 07-MAR-2006, entry version 27. Hypothetical protein FLJ10572 (Kelch-like 11). Mane=KLH111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genet. 36:40-45(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.
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                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                          NCBI_TaxID=9606;
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Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

NUCLEOTIDE SEQUENCE.

NIH MGC Project; TISSUE=Testis;

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Carninci P., Kacukawa T., Katapama S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Aidinis V., Allen J.E., Bailey T.L., Ambest-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L., Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., Crow M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G., Pletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M., Goorgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E., A Gustincich S., Harbers M., Hayshi Y., Hensch T.K., Hirokawa T., Hall D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T., Ank M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., A. Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J., A., Liu J., Liu J., Liu J., Liu S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/63; TISSUE=Corpora quadrigemina;

MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

Carnino! P., Hayashizaki Y.;

"High-efficiency full-length cDNA cloning.";

Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone: B230201M16 product: Mi-2 autoantigen 240 kDa protein homolog (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                            92.5%; Score 49; DB 2; Length 708; 92.3%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                               80148 MW; 38733CE875172E12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-C57BL/6J; TISSUE-Corpora quadrigemina; PubMed=16141072; DOI=10.1126/science.1112014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                       Ensembl; BOSGONO0178502; Homo sapiens.
HGNC; HGNC:19008; KLHL11.
G0; G0:0005215; F:protein binding; IEA.
InterPro; IPR011705; BTB.
InterPro; IPR0100210; BTB.
InterPro; IPR010652; Kelch_rep.
Pfam; PF07707; BACK; 1.
Pfam; PF00551; BTB; 1.
Pfam; PF00551; BTB; 1.
Pfam; PF00551; BTB; 1.
PMART; SM00225; BTB; 1.
PROSITE: PS50097; BTB; 1.
                                                                   EMBL; AK001434; BAA91689.1; -; mRNA.
EMBL; BC034470; AAH34470.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2003, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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4 AAVAAAAAAAA 16
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Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                   708 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Chd3;
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8BR71;
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Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K., Makengali-Paha S., Milder M., Makanda N., Makanda H., Matsuda H., Matsuda S., Milder M., Makanda N., Makenda J., Sheeld J., Seld, J. F., Milder B., Shinayal M., Shombach C., Shinada H., Sinada H., Sinada H., Silada D., Silada E., Sheeld J., Seld, J., Shinada H., Shinada H., Shinada K., Silada D., Silada E., Sheeld J., Seld, J., Shinada H., Shinada H., Shinada K., Silada D., Silada E., Sheeld J., Seld, J., Shinada H., Shinada H., Shinada K., Shinada H., Shinada K., Shinada H., Shinada H., Shinada K., Tarkenka Y., Tarkenka Y., Shinada H., Shinada H., Shinada K., Shinada H., Shinada K., Tarkenka Y., Tarkenka Y., Tamangan M., Makanda M., Makanda K., Tarkenka Y., Tarkenka Y., Matsuda M., Makanda M., Makanda M., Makanda M., Makanda M., Makanda M., Makanda K., Tan S., Hanaga S., Taylor W.S., Tegrac J., Tanaga J., Tanaga S., Taylor W., Shinada H., Shinada H., Shinada K., Shinada H., Shinada H., Shinada M., Sondo S., Konno H., Nakano K., Ninomiya M., Makanda M., Makanda M., Makanda K., Minomiya M., Makanda M.,

Scholl P. 100 S. World P. 100 S. W. Wagner L. Washin J. S. Shall J. 100 S. World P. 100 S. World P. 100 S. World P. 100 S. World P. 100 S. World S. W. Wagner L. Washin J. S. Shall K. Wolder T. Purner M. Carrinci P. de Bonaldo M. F. Mander S. W. Wagner L. Washin J. W. Shall J. World S. W. Wagner L. Washin J. W. Shall J. W. Shall J. W. Garrinci P. de Bonaldo M. F. Mander S. W. Wagner L. Shall J. W. Wagner P. M. Wagner P. M. Wagner P. W. Wagner P. W. Wagner P. W. Wagner P. W. Wall J. W. Wagner P. Wagner P. W. Wagner P. W. Wagner P. W. Wagner P. W. Wagner P. Wagner P. W. Wagner P. W. Wagner P. Wagner P.

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Hayashizaki Y.;
    Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., A Garninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Barener S.E., Batalov S., Porrest A.R., Shimokawa K., Allon V., Wilming L.G., Aidinis V., Allon J.E., Bailey T.L., Bansei-Impiombaco A., Apweller R., Aturaliya R.N., Balley T.L., Bansei M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., Allou K.P., Choudhary V., Christoffels A., Clutterbuck D.R., Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., A Fletcher C.F., Fwundshima T., Furno M., Futaki S., Gariboldi M., Georgii-Hemming P., Gingeras T.R., Golobori T.K., Hirokawa N., Hill D., Huminiacki L., Iacono M., Ikeo K., Iwama A., Ishikawa T., Alli D., Huminiacki L., Iacono M., Ikeo K., Klamura H., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Kanapin A., Katoh M., Kawasawa Y., Klamura H., Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L., Anteradu L.F., Lazarevic D., Lipovich L., Liu J., Liuni S., McWilliam S., Miki H., Mignone F., Miyake S., Morris K., Anteradu Y., Salzberg S.L., Sandelin A., Schneider C., Sersa L., Sheng Y., Schonbach C., Selyuchi K., Semple C.A., Seno S., Sessa L., Sheng Y., Schonbach C., Selyuchi K., Semple C.A., Seno S., Sessa L., Sheng Y., Tammola M., Tan S.L., Tang S., Taylor M.S., Tegenra J., Takenaka Y., Shimada H.R., Van Nimwegen E., Sulutana R., Hide W., Bult C., Tang S., Taylor M.S., Tegenra J., Tang S., Taylor W., Wei C.L., Yagi K., Tannishi H., Zabarovsky E., Zhumer S., Hide W., Hide W., Hide W., Hide W., Tang Y., Shimada Y., Hide W., Hide W., Hide W., Hide W., Hide W.
                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                10 days neonate skin CDNA, RIKEN full-length enriched library, clone:4732491L07 product:hypothetical BTB/POZ domain|Kelch repeat|Type 1 antifreeze|Alanine-rich region containing protein, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CS7BL/6J; TISSUE=Skin;
MEDLINE=99279253; Pubmed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                      ö
                                                                                                        Length 708;
                                                                                         Score 49; DB 2; Lengtn vv., Pred. No. 1.8e+02;
                                                                           708 AA; 80411 MW; A9CE144CE3310CBB CRC64;
                                                                                                                                                                                                                                                                                                      01-MAR-2003, integrated into UniProtKB/TrEMBL, 01-MAR-2003, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; TISSUE=Skin;
PubMed=16141072; DOI=10.1126/science.1112014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                          709 AA.
                                                                                                                                      1; Mismatches
PROSITE; PS00598; CHROMO_1; UNKNOWN_1.
PROSITE; PS50013; CHROMO_2; 2.
PROSITE; PS50016; ZF_PHD_2; 2.
                                                                                                                                                                                                                                                                           PRT;
                                                                                                       92.5%;
                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                218 AAVAAAAAAAAA 230
                                                                                                                                                                    1 AAMAAAAAAAA 13
                                                                                                                                     12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE
                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                Nuclear protein.
                                                                                                                                                                                                                                                                        Qēce33 mouse
Qece33;
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                                                             NON TER
SEQUENCE
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                                                                                                                                     Matches
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Grimmond S.W. Totatick, J.S., Nine D.M., Faller, Stankin Property, Rahlenged C., Nettick, J.S., Nine D.M., Faller, S., Stankin P.M., Paller, S., Kannameri-Katayam M., Studik M., Andra M., Andra M., Stankin M.,

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Pubmed=15496914; DOI=10.1038/nature03025;

Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,

Anduceli E., Bouneau L., Fischer C., Ozouf-Cozlaz C., Bernot A.,

Micaud S., Jaffe D., Fischer C., Lutfalla G., Dossat C., Segurens B.,

Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

Arra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

Kellis M., Volff J.-M., Guigo R., Zody M.C., Mesirov J.,

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Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Scarpelli C.,

Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.,

"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                      Terraodon nigroviridis (Green puffer).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Neopterygii; Neopterygii; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontoidea; Tetraodontidae; Tetraodon.
                                                                        shotgun sequence. (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preliminary data.
-!- FUNCTION: Binds calmodulin in a calcium dependent manner. Ma function as scaffolding or signaling protein (By similarity)
-!- SUBCELLULAR LOCATION: Cytoplasmic and membrane-bound (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FBS-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.5%; Score 49; DB 2; Length 805; 100.0%; Pred. No. 1.9e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            805 AA; 87779 MW; FEC67F3387228E7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; CAAED1014537; CAF97462.1; -; Genomic_DNA.
InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 6.
PRINTS; PR00320; GPROTEINBRPT.
PROMOTO, PD000018; WD40; 3.
SMART; SM00320; WD40; 5.
PROSITE; PS500618; WD REPEATS 1; 1.
PROSITE; PS50082; WD REPEATS 2; 4.
PROSITE; PS50082; WD REPEATS 2; 4.
PROSITE; PS50082; WD REPEATS 2; 4.
PROSITE; PS50294; WD REPEATS REGION; 1.
19-JUL-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          815 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the early vertebrate proto-karyotype.";
                        19-JUL-2005, sequence version 1.
07-MAR-2006, entry version 8.
Chromosome 16 SCR14537, whole genome
ORFNames=GSTENG00014837001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 AMAAAAAAAAA 13
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                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                          NCBI_TaxID=99883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DROME
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Q9V9W8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOULDELUBE SUPERALE.

ADAGENIUS SUPERALE.

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Rukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

Hayashida K., Hayatsu N., Hirancto K., Hiraoka T., Hirozane T.,

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Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

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Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

Tomaru A., Toya T., Yasuusishi A., Muramatsu M., Hayashizaki Y.;

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                                                                                                STRAIN=C57BL/6J; TISSUB=Skin; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazati Y., Muramatsu M., Hayashizaki Y.; Nibata ion and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                   MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Ttoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamara S., Hazama M., Nishine T., Harada A., Yamamotco R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa K., Tanaka T., Ohara E., Watshiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rike integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
     "Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ensembl; ENSMUSG0000048732; Mus musculus. MGI; MGI:2388648; Klhll1.
GO; GO:0005512; F:protein binding; IEA. InterPro; IPR011705; BACK.
InterPro; IPR013069; BTB.
InterPro; IPR013069; BTB.
InterPro; IPR01655; Kelch_rep.
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Pfam; PF00651; BTB; 1.
Pfam; PF01344; Kelch_1; 3.
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PROSITE; PS50097; BTB; 1.
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nes 12; Conservative
                                Nature 409:685-690(2001)
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Gaps

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19-SEP-2002, integrated into UniProtKB/Swiss-Prot.

01-MAY-2000, sequence version 1. 21-FEB-2006, entry version 39.

805 AA.

PRT;

Q4SPHO\_TETNG PRELIMINARY; Q4SPHO;

TETNG

RESULT 25 Q4SPH0 ID Q4 AC Q4

Matches

8 g

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Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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RXAN=Berkeley,
RXAN=Berkeley,
Adams M.D. Celniker S.E., Holt R.A., Evans C.A. Gocayne J.D.,
Adams M.D. Celniker S.E., Holt R.A., Evans C.A. Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A. Gocayne J.D.,
RX Amanatides D.G., Scherer S.E., Holt R.A., Eshburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazel, R.G., Champe M., Pfeiffer B.D.,
Abril J.E., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RX Ballew R.M., Baran M., Barandale M.D., Borkerein P., Borthery E.M.,
Berkova D., Botchen M.R., Bouck J., Brycktaroglu L., Beasley E.M.,
Borkova D., Botchen M.R., Bouck J., Broketein P., Brottier P.,
RX Borkova D., Botchen M.R., Bouck J., Broketein P., Brottier P.,
RX Borkova D., Botcher A., Demg Z., Mays A.D., Dew I., Dietz S.M.,
A Borkova D., Botcher A., Demg Z., Mays A.D., Dew I., Dietz S.M.,
A Bortis K.C. Gabriellan A.E., Gargen N.S., Gelbart W.M., Glasser K.,
RX Bouch K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischman W.,
RX B. Adellos B., Delcher A., Bowles M., Dugarl Rocha S., Fleischman W.,
RX Gabriellan A.E., Gary N.S., Gelbart W.M., Glasser K.,
Alali M., Kalush F., Katpen G.H., Ke Z., Kannison J.A., Ketchum K.A.,
Alali M., Kalush F., Katpen G.H., Ke Z., Kannison J.A., Ketchum K.A.,
Alali M., Kalush F., Katpen G.H., Ke Z., Kannison J.A., Mattei B.E., Kodirez C.D., Kraft C., Mortis J., Mosherson D.,
Alali M., Mayne B., McIntosh T.C., McLeod M.P., Purit V., Resee M.G.,
Reinert K., Moy M., Wurphy B., Murphy L., Murny D.M., Nelson D.L.,
Rushon D.R., Pittuan G.S., Pan S., Pollard J., Weissenbech J.M.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Syriekas R., Medonge T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RY B., Mang Z.-Y., Wassarman D.A., Weissenbech J.,
Ry Gibbs R.A., Wayers E.W., Rubin G.M., Weissenbech J.,
Ry Gibbs R.A., Wayers E.W., Rubin G.M., Ventry S., Shul M.,
Ry Gibbs R.A., Wayers E.W., Rubin G.M., Ventre T., Wasserbech J.,
Ry Gibbs R.A., Wayers E.W., Rubin G.M., Wang S
                                                                                                                                                                               MEDLINE=21952490; PubMed=11955446; DOI=10.1016/S0092-8674(02)00679-7; Kramps T., Peter O., Brunner E., Nellen D., Froesch B., Chatterjee S., Murone M., Zuellig S., Basler K., Murone M., Zuellig S., Basler K., Whit/Wingless signaling requires BCL9/legless-mediated recruitment of pygopus to the nuclear beta-catenin-TCF complex.";
                                                                                                                                                                                                                                                                                                                          MEDLINE=22010046; PubMed=12015286;
Parker D.S., Jemison J., Cadigan K.M.;
"Pygopus, a nuclear PHD-finger protein required for wingless signaling
in Drosophila.";
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Protein pygopus (Gammy legs protein).
Name=pygo; Synonyms=gam, ORFNames=CG11518;
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                        Development 129:2565-2576(2002)
                                                                                                                                                                                                                                                                  Cell 109:47-60(2002).
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GO: GO: 0005641; C: nucleus; NAS.
GO: GO: 0005641; C: nucleus; NAS.
GO: GO: 00055241; P: eye-antennal disc development; IMP.
GO; GO: 00035242; P: eye-antennal disc development; IMP.
GO; GO: 00030177; P: postitive regulation of Wnt receptor signali. . .; IPI.
GO; GO: 00016055; P: Wnt receptor signaling pathway; IMP.
InterPro; IPR001965; Znf_PHD.
InterPro; IPR001965; Znf_PHD.
Fam; PR006281; PHD; 1.
PROSITE; PS01159; ZF_PHD_1; 1.
PROSITE; PS01159; ZF_PHD_1; 1.
Complete proteome; Developmental protein; Metal-binding;
Nuclear protein; Segmentation polarity protein; Wnt signaling pathway;
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MEDLINE-22426066; PubWed=12537569;
MEDLINE-222426066; PubWed=12537569;
MEDLINE-22426066; PubWed=12537569;
MEDLINE-22426066; PubWed=12537569;
Rubin G.M., Carlson J.W., Brokstein P., Yu C., Champe M.,
Rubin G.M., Celniker S.E.;
M. Drosophila H.J. Hength CDNA resource.";
A Drosophila Hull-length CDNA resource.";
Genome Biol. 3:RESEARCH0080.1-RESEARCH
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                                     'Annotation of the Drosophila melanogaster euchromatic genome:
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Pred. No. 2e+02;
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S -> P (in Ref. 1).
                                                                                                                Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BioCyc; DMEL-XXX-02:DMEL-XXX-02-014325-MONOMER; -.
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/FIId=PRO_000097124.
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11-0CT-2005, sequence version 1.
07-FEB-2006, entry version 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF457206; AAL91369.1; -; mRNA.
EMBL; AX075095; AAL79357.1; -; mRNA.
EMBL; AE003778; AAF57161.1; -; Genomic_DNA.
EMBL; AX058500; AAL13729.1; -; mRNA.
Ensembl; CG11518; Drosophila melanogaster.
Flybase; FBgn0043900; pygo.
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03UG42;
Lewis S.E.;
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Query Match
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                            MGI, MGI:1913/66; Shand2.

MGI, MGI:1913/66; Shand2.

GO; GO:000507; C:lamellipodium; IDA.

GO; GO:0005078; F:Practain binding; IDA.

GO; GO:0005518; P:Practain binding; IDA.

GO; GO:0005518; P:regulation of JNK cascade; IDA.

InterPro; IPR00145; SH3.

InterPro; IPR00145; SH3.

InterPro; IPR00184; Znf. RING.

Pfam; PF00018; SH3 1; 3.

Pfam; PF00019; SH3 1; 3.

Pfam; PF00097; Zf-73HC4; I.

PRINTS; PR00452; SH3DOMAIN.

PRINTS; PR00452; SH3DOMAIN.

PRODOM; PR00196; SH3; 3.

SMART; SM00126; SH3; 3.

PROSITE; PS00021; ZF-RING 1; I.

PROSITE; PS00051; ZF-RING 1; I.

PROSITE; PS00051; ZF-RING 1; I.

PROSITE; PS00518; ZF-RING 2; I.
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01-AUG-1998, sequence version 1.
07-FEB-2006, entry version 26.
Plenty of SH3s.
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Mus musculus (Mouse).
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les 12; Conservative
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HSSP; P19878; 1K4U.
MGI; MGI:1913066; Sh3md2.
                         NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE.

NUCLEOTIDE S. C., Scherer S. E., Lip P. W., Hoskins R. A., Galle R. F.,

RA Amanatides P.G., Scherer S. E., Lip P. W., Hoskins R. A., Galle R. F.,

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Ra Nelson D.R., Nelson K.A., Nixon S., Pollard J., Puri V., Rese M. G.,

Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
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Name-CG15803; ORFNames-Dmel_CG15803;
Drosophila melanogaster (Fruir fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 49; DB 2; Length 892;
Pred. No. 2.1e+02;
L; Mismatches 0; Indels
                                                                                                                                                 InterPro; IPRO0106; New Cyt_fact_2.
InterPro; IPRO0106; New Cyt_fact_2.
InterPro; IPRO01041; Znf_RING.
Pfam; PPO0018; SH3_1, 4.
R Ffam; PRO0097; Zf_C3HC4; 1.
R PRINTS; PR00499; P67PHOX.
R PRINTS; PR00499; P67PHOX.
R PRINTS; PR00409; P67PHOX.
R PRODOM; PR000066; SH3; 4.
SWART; SW00184; RING; 1.
SWART; SW00184; RING; 1.
R PROSITE; PS00018; ZF_RING_1; 1.
R PROSITE; PS00018; ZF_RING_1; 1.
R PROSITE; PS00018; ZF_RING_2; 1.
SEQUENCE 892 AA; $3435 MW; 5A1030857777B3B0 CRC64;
GO:0030027; C:lamellipodium; IDA.
GO:0005078; F:MAP-Kinase scaffold activity; IDA.
GO:005512; F:MAP-Kinase scaffold activity; IDA.
GO:0045128; P:regulation of JNK cascade; IDA.
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21-FEB-2006, entry version 28.
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897 AA; 94372 MW; 3A74789E08FD1A2F CRC64;

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                                                                                                                                                                 NUCLECTIDE SEQUENCE.
MEDLINE=22456065; PubMed=12537568;
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MEDLINE=22456065; PubMed=12537568;
MEDLINE=22456065; PubMed=12537568;
MEDLINE=22456065; PubMed=12537568;
Medline M., Champe M., Dugam S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Paclefor B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstick G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUCLEOTIDE SEQUENCE.
MEDLINE=22446069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Misra S., Crosby M.A., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.
Yu C., Rubin G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lewis S.E.;
"Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QUUBP2:CG5053; NDExp=1; IntAct=EBI-172540, EBI-202525; Q9VQM7:ed; NDExp=1; IntAct=EBI-172540, EBI-85823; SIMILARITY: Contains 4 PDZ (DHR) domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FlyBase;
Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                      a genomics perspective.";
Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
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HSSP; Q64512; 10ZI.
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Pred. No. 2.1e+02;
1; Mismatches 0; Indels
               Length 897;
                                                     Indels
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R GO; GO:0002078; C:lamellipodium; IDA.

GO; GO:0005078; F:MAP-kinase scaffold activity; IDA.

GO; GO:0005078; F:Protein binding; IPI.

GO; GO:0005078; F:Protein binding; IPI.

R GO; GO:0006218; F:Protein binding; IPI.

S GO; GO:0006218; F:Protein binding; IPI.

S InterPro; IPR001042; SH3.

InterPro; IPR001041; ZH3.

R PENNTS; PR00491; F:C3HC4; I.

R PRINTS; PR00499; F:C3HC4; I.

R PRINTS; PR00499; F:C3HC4; I.

R PRNST; SN00184; RING; I.

R SMART; SN00184; RING; I.

R RRAST; SN00184; RING; I.

R RRAST; SN00184; RING; I.

R RROSITE; PS50009; ZFRING; I.

R PROSITE; PS50099; ZFRING; I.

R MRCA1-binding; SH3 demain; Zinc; Zinc-finger.
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13-SEP-2004, integrated into UniprotKB/TrEMBL.
13-SEP-2004, sequence version 1.
07-FEB-2006, entry version 12.
MKIAAL194 protein (Fragment).
MMRAAL194 Synonyms-mKIAAL494;
Mus musculus (Mouse).
                                                                                                                                                                                                                               914 AA.
                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AK173185; BAD32463.1; -; mRNA.
                                                                                                                                                                                                                               PRT;
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133 AAVAAAAAAAAA 145
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Matches 12; Conservative
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                                                         12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE
                                   Best Local Similarity
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RY CALLENTILES SEQUENCE.

RY CALLENTILES SEQUENCE.

RY CATALLOCY TISSUES-Medulla oblongata;

RA CATHOLOCY TISSUES-Medulla oblongata;

RA CATHOLOCY TISSUES-Medulla oblongata;

RA CATHOLOCY TASSUKAWA T., Katayama S., Gough J., Frith M.C., Maeda N.,

RA Bajic V. B., Brenner S.E., Baralov S., Forrest A.R., Zavolan M.,

Bayic W. Baxter L., Deisel R., Adinis V., Allen J.E.,

RA Ambesi-Impicombato A., Apweiler R., Aturaliya R.N., Balley T.L.,

RA Ambesi-Impicombato A., Apweiler R., Aturaliya R.N., Balley T.L.,

RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,

RA GONG WILL, Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,

RA GONG T., Down T., Engstrom P., Fagiolini M., Faulkner G.,

RA GONGTI-Hemming P., Gligeras T.R., Gojobori T., Green R.E.,

RA GORGIN-Hemming G., Krishman S.P., Kluger A., Klumara T.,

RA Jakt M., Kanapin A., Katoh M., Hayashi Y., Hensch T.K., Hirokawa N.,

RA Hill D., Huminieck M., Mayashi Y., Hensch T.K., Hirokawa N.,

RA Hill D., Huminieck G., Krishman S.P., Kluger A., Klumara T.,

RA Mctsuda H., Macquawa S., Mikh H., Mignone F., Miyake S., Morris K.,

RA Mctsuda H., Macquawa S., Mikh H., Mignone F., Miyake S., Morris K.,

RA Motsagui-Tabar S., Malder N., Nakano N., Nakauchi H., Ng P.,

RA Misson R. Nishiquchi S., Nishikawa S., Nori B., Ohar D.,

RA Rost B., Ruan Y., Salzberg S.L., Sanddell N., Rano S., Stockied C.,

RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sacusa L., Sheng Y.,

RA Shibata Y., Shibada H., Shinada K., Silva D., Pavesi G.,

Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sacusa L.,

RA Shibata Y., Shibada H., Shinada K., Shilak Y., Hing B.Z., Hang J.,

Ramoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Techman S.A.,

Ramonishi H., Zabarovsky B., Zhu S., Zhumer A., Hide W., Bult C.,

RA Amanishi H., Zabarovsky B., Zhu S., Zhumer A., Hide W., Bult C.,

RA Amanishi H., Zabarovsky B., Zhu S., Kanashi S., Nori S., Sacka J.,

RA Amanishi M., Sasalak R., Shinada K., Shiraki Y.,

RA Asamima K., Yan Nimwegen B., Wan C., Shiraki Y., Kawashima T., Ko
                                                                                                     11-OCT-2005, integrated into UniProtKB/TrEMBL.
11-OCT-2005, sequence version.1.
07-FEB-2006, entry version 3.
Adult male medulla oblongata cDNA, RIKEN full-length enriched library,
                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CS7BL/6J; TISSUE=Medulla oblongata;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                         clone:6330596E03 product:hypothetical Transforming protein Ski/SAND-
like/Putative DNA binding containing protein, full insert sequence.
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PubMed=16141073; DOI=10.1126/science.1112009;
RIKEN Genome Exploration Research Group, and Genome Science Group
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                                   PRT;
                                   PRELIMINARY;
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Q3UYA4;
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MOUSE
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RECEDING SEQUENCE:

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"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20499374; PubMed=11042159; DOĬ=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Functional annotation of a full-length mouse cDNA collection.";
(Genome Network Core Team) and the FANTOM Consortium; "Antisense Transcription in the Mammalian Transcriptome."; Science 309:1564-1566(2005).
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MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                         Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K., Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K., Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S., Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N., Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D., Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A., Muramatsu M., Hayashizaki Y.,
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Mateumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Yuneda Y., Ishikawa T., Ozawa K., Tanaka T., Mateunia S., Kawai J., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Mateuria S., Kawai J., Narski Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated Sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
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21-FEBB-2006, entry version 31.
CG32466-PA, isoform A.
Name=rn, ORFNames=Dmel CG32466;
Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta; Pterygota;
Neoptera; Endopterygota, Diptera; Brachycera; Muscomorpha;
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                  MGI; MGI:2443473; Lbxcorl.
GO; GO:0005634; C:nucleus; RCA.
GO; GO:0005634; C:nucleus; IDA.
GO; GO:00056614; C:rranscription factor complex; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:000714; F:transcription corepressor activity; IDA.
GO; GO:000875; P:negative regular physiological process; RCA.
GO; GO:0016481; P:negative regularion of transcription; IDA.
InterPro; IPR02437; Ski_Sno; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92.5%; Score 49; DB 2; Length 935; 92.3%; Pred. No. 2.2e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                              Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l protein.
935 AA; 96933 MW; A9C2953F4A77E367 CRC64;
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                                                                                                                                                                                                                                                                                                                                                    EMBL; AK134840; BAE22308.1; -; mRNA.
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Q9V193;
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484 AAVAAAAAAAAA 496
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Matches 12, Conservative
                                                                                                                                                                NUCLEOTIDE SEQUENCE
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Borkova D., Botchan M.R., Block J., Galoskein P., Conter M., Chaire A., Chair
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us-10-617-568-3.rup

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Name=1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COLLED
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   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRAIN-C57BL/6J; TISSUB-Cerebellum, and Testis;

TRAIN-C57BL/6J; TISSUB-Cerebellum, and Testis R., Shimokawa K., Bajic V.B., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Bremner S.E., Batalov S., Forrest A.R., Zavolan M., Ambesi-Impiombato A., Agweller R., Aturaliya R.N., Bailey T.L., Ambesi-Impiombato A., Agweller R., Aturaliya R.N., Bansal M., Bansal M., Barter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., Crowe M.L., Dalla E., Dalla B.P., Chigtoffels A., Clutterbock D.R., Crowe M.L., Dalla E., Dallamary V., Christoffels A., Clutterbock D.R., Allandary V., Christoffels A., Clutterbock D.R., Allandary D., Churana T., Furuno M., Futaki S., Gariboldi M., Fletcher C.F., Futushima T., Furuno M., Futaki S., Gariboldi M., Anduriniecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T., All D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T., Altano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S., Kitano H., Kulliam S., Madan Babu M., Madera M., Marchionni L., Liu J., Liu J., Liu J., Liu J., Liu J., Liu J., Liuni S., McWilliam S., Madan Babu M., Madera M., Matchionni L., Liu J.,
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2), FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND INTERACTION WITH LBX1.

TISSUE=Embryonic brain.

TISSUE=Embryonic brain.

Pubmed=15528197; DOI=10.1074/jbc.M411652200;

Mizuhara E., Nakatani T., Minaki Y., Sakamoto Y., Ono Y.;

"Corll, a novel neuronal lineage-specific transcriptional corepressor for the homeodomain transcription factor Lbx1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QBBX46; QSW812; Q8C0T2; 21-UIN-2005, integrated into UniProtKB/Swiss-Prot. 01-MAR-2003, sequence version 1. 07-FBB-2006, entry version 20. Ladybird homeobox corepressor 1 (Transcriptional corepressor Corll).
                                                                                                                ElyBase; FBGIN001263; rn.

GO; GO:0007456; P:eye development (sensu Endopterygota); IMP.

GO; GO:0007480; P:ley morphogenesis (sensu Endopterygota); IMP.

GO; GO:0007480; P:ley morphogenesis (sensu Endopterygota); IMP.

InterPro; IPRO00089; Znf C2H2; G.

PRODOM; PRO0018; Znf C2H2; G.

PROSITE; PSGO183; ZnC FINGER C2H2 1; 6.

PROSITE; PSSO157; ZINC FINGER C2H2 2; 6.

Metal-binding; Nuclear protein; Zinc; Zinc-finger.

SEQUENCE 946 AA; 100948 MW; 05EA01C8F64F61A3 CRC64;
                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                          92.5%; Score 49; DB 2; Length 946; 92.3%; Pred. No. 2.2e+02; ive 1; Mismatches 0; Indels
            Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases.
                            -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                964 AA.
                                                                                                       EMBL; AE003672; AAF54032.3; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                        1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=Lbxcorl; Synonyms=Corll;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                        1 AAMAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                        Best Local Similarity 92.3
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LBXCO_MOUSE
                                                                                                                                                                                                                                                                                                           Query Match
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RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K., Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P., Nishiguchi S., Nishikawa S., Nori F., Ohara O., R. A. Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G., Rad Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M., RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Sheng Y., RA Schbach Y., Shimada H., Semple C.A., Seno S., Sessa L., Sheng Y., RA Schotach K., Silva D., Sinclair B., Shibata Y., Shimada H., Shimada K., Siltana R., Takenaka Y., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Bada H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K., Mannishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C., Artick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., RA Wahllestedt C., Mattlok J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., R. Hida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N., Rawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N., Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki H., Kawai J., Markanizaki Y., Kawalizaki Y., Suzuki H., Kawai J., Kaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isoid=Q8BX46-3; Sequence=VSP_014178, VSP_014180, VSP_014181; Note=No experimental confirmation available; TISSUE SPECIFICITY: Expressed in brain with higher levels in embryo than adult. Also expressed in adult testis. In embryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          brain, expressed in a subset of postmitotic neurons generated posterior to the midbrain-hindbrain border. In the developing spinal cord, selectively expressed in dorsal horn interneurons.-:- SIMILARITY: Belongs to the SKI family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF02437; Ski_Sno; 1.
Alternative splicing; Coiled coil; Nuclear protein; Repressor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ladybird homeobox corepressor 1./FTId=PRO_000129391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O9QVT4:- (xeno); NDExp=1; IntAct=EB1-604451, EB1-604706; O88712:Ctbp1; NDExp=1; IntAct=EB1-604451, EB1-604547; O09106:Hdac1; NDExp=1; IntAct=EB1-604451, EB1-301912; P52955:Lbx1; NDExp=1; IntAct=EB1-604451, EB1-804594; Q62440:Tle1; NDExp=1; IntAct=EB1-604451, EB1-604594; SUBCELLULAR LOCATION: Nucleus.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Intact; QBBX46; ...
Ensembl; ENSWUSG0000022245; Mus musculus.
MGI; MGI:A4473; Lbxcorl.
GO; GO:0005634; C:nucleus; IDA.
GO; GO:0005667; C:transcription factor complex; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:000714; F:transcription corepressor activity; IDA.
GO; GO:000714; P:negative regulation of transcription; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: Acts as a transcriptional corepressor of LBX1.
-!- SUBUNIT: Interacts with LBX1.
-!- INTERACTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The transcriptional landscape of the mammalian genome."; Science 309:1559-1563(2005).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=Q8BX46-1; Sequence=Displayed;
Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q8BX46-2; Sequence=VSP_014179;
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EMBL, AKO29916; BAC26674.1; -; mRNA.
EMBL, AKO49035; BAC35520.1; -; mRNA.
HSSP; P12755; 1MR1.
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CHAIN
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RY CYLLEAD B. SAUCHER CHANGE SCHILL STRANIBED STRANIBE
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                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Eurchoncoglires, Glires, Rodentia, Sciurognathi; Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                           Gaps
/FTId=VSP 014179.
LQGGGGGGA--> PARGRRRR (in isoform 3)
/FTId=VSP 014180.
                                                                                                                                           ..
0
                                                                                                           Score 49; DB 1; Length 964;
Pred. No. 2.2e+02;
1; Mismatches 0; Indels
                                                                  961 961 0.5 (1 Ref. 1).
964 AA, 100276 MW, B1ECDB443D789E2C CRC64;
                                       Missing (In isoform 3) /FIId=VSP_014181.
                                                                                                                                                                                                                                                                                                 21-JUN-2005, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA)
                                                                                                                                                                                                                                                                        964 AA.
                                                                                                                                                                                                                                                                                                                21-JUN-2005, sequence version 1. 07-MAR-2006, entry version 8. Ladybird homeobox corepressor 1.
                                                                                                               92.5%;
                                                                                                                              92.3%;
                                                                                                                                                                                                  512 AAVAAAAAAAA 524
                                                                                                                                                                       1 AAMAAAAAAAA 13
                                                                                                                            Local Similarity 92.3
nes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                        STANDARD;
                                            964
                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
                                            291
                                                                                                                                                                                                                                                                                                                                                             Name=Lbxcorl;
                                                                                                                                                                                                                                                                          LBXCO RAT
                                                                                     SEQUENCE
                                                                                                                  Query Match
                                            VARSPLIC
                VARSPLIC
                                                                     CONFLICT
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                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Kent W.J., Rosenbloom K.R., Trumbower H., Weirauch M., Cooper D.N.,
                           Stenson P.D., Ma B., Brent M., Arumugam M., Shteynberg D., Copley R.R., Taylor M.S., Riethman H., Mudunuri U., Peterson J., Guyer M., Felsenfeld A., Old S., Mockrin S., Collins F., Genome sequence of the Brown Norway rat yields insights into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human chromosome 15 international sequencing consortium;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
-!- FUNCTION: Acts as a transcriptional corepressor of LBX1 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                   Nature 428:493-521(2004).
-!- FUNCTION: Acts as a transcriptional corepressor of LBX1 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ladybird homeobox corepressor 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ladybird homeobox corepressor /FTId=PRO_0000129392.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.5%; Score 49; DB 1; Length 965; 92.3%; Pred. No. 2.2e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 49; DB 1; Length 964;
Pred. No. 2.2e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AC009292; -; NOT ANNOTATED_CDS; Genomic_DNA.
HGNC; HGNC:21326; LBXCOR1.
Coiled coil; Nuclear protein; Repressor; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         857 921 Potential.
964 AA; 100234 MW; 78D1B922CAB29B7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AABR03062264; -; NOT_ANNOTATED_CDS; Genomic_DNA. RGD; 1307687; RGD1307687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99831 MW; 313E95B0430A979B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:- SUBUNIT: Interacts with LBX1 (By similarity).
-:- SUBCELLULAR LOCATION: Nucleus (By similarity).
-:- SIMILARITY: Belongs to the SKI family.
                                                                                                                                                                                                                                   -!- SUBUNIT: Interacts with LBX1 (By similarity).
-!- SUBCELLULAR LOCATION: Nucleus (By similarity).
-!- SIMILARITY: Belongs to the SKI family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUN-2005, integrated into UniProtKB/Swiss-Prot.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  965 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Potential
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUN-2005, sequence version 1. 07-MAR-2006, entry version 6. Ladybird homeobox corepressor 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               512 AAVAAAAAAAA 524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcription regulation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 92.3
les 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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Best Local Similarity
Matches 12; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
                                                                                                                                      mammalian evolution."
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965 AA;
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                                                                                                                                                                                                                     similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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A PubMed-15496914; DOI=10.1038/nature03025;
A Jailon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
A Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
A Nicaud S., Jaffe D., Fischer S., Lutfalla G., Dossat C., Segurens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
Arthouard V., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
Rellis M., Volff J.-N., Güigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.,
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
II. Nature 431:946-957(2004).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                   Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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07-FBB-2006, entry version 19.
CG1770-PB, isoform B.
Name=HDAC4; ORFNames=Dmel CG1770;
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 49; DB 2; Length 1065;
Pred. No. 2.4e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genoscope, Whitehead Institute Centre for Genome Research; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; CAAE01014537; CAF97427.1; -; Genomic DNA.
SEQUENCE 1065 AA; 118021 MW; EDDB6A851F655E0F CRC64;
                                                                                                                                19-JUJ-2005, sequence version 1.
07-FEB-2006, entry version 3.
Chromosome 16 SCAF14537, whole genome shotgun sequence.
ORFNames=GSTENG0014784001;
                                                                                                                       19-JUL-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003, integrated into UniProtKB/TrEMBL
                                                                                                PRT; 1065 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1181 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.5%;
                                                                                              Q4SPK5_TETNG PRELIMINARY;
                                   515 AAVAAAAAAAA 527
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           1 AAMAAAAAAAA 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preliminary data.
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Best Local Similarity
                                                                                                                                                                                                                                              NCBI_TaxID=99883;
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QBIR69;
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TETNG
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ID . Q8
AC . Q8
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DT . 07
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OK Neopecers, Endopenerygota Dipters: Brachycers, Mascomorpha;

OK NGELTAXAD-7227;

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EMBL; AE003492; AAX52490.1; -; Genomic_DNA.
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  MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Li P.W., Hoskins R.A., Galle R.F., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Raxter E.G., Helf G., Nelson C.R., Miklos G.L.G., Wan K.H., Doyle C., Baxter E.G., Helf G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolahakov S., Borkova D., Botchan M.R., Bulck H., Cadleu E., Center P., Chardra I., Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I., A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Diezer S., Dunn P., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Pleischmann W., Bosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                       NUCLEOTIDE SEQUENCE.
Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith
                              Lewis S.E.; "Annotation of the Drosophila melanogaster euchromatic genome: a
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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Drosophila melanogaster (Fruit fly).
Bukaryota; Merazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 49; DB 2; Length 1181;
Pred. No. 2.6e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FlyBase; FBGN0041210; HDAC4.

InterPro; IPR000286; His deacetylse.

InterPro; IPR001220; Lectin legB.

PANTHER; PTHX10625; His deacetylse; 3.

Pfam; PF00850; Hist deacetyls; 1.

PRNTKS; PR01270; HDASUPER.

PRNTKS; PS0037; LECTIN LEGUME BETA; UNKNOWN 1.

SEQUENCE 1181 AA; 126044 WW; AD451B406E8719B1 CRC64;
                                                                                                                                                                                                                                                                                                 "Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases
                                                                                                        Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-APR-2005, integrated into UniProtKB/TrEMBL. 26-APR-2005, sequence version 1. 07-FEB-2006, entry version 5. CG1770-PC, isoform C.
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423 AAVAAAAAAAAA 435
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nes 12; Conservative
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                                                                                     review
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                                                                                                                                                                                                                                                                   Yu C., Rubin G.
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Q59E49;
                                                                               systematic
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RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Ra Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
Ra Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Ra Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Ra Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lus K., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Ra Markulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Molson D.R., Nolson K.A., Ni Morary C., Morris J., Moshrefi A.,
Ra Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Ra Reinert K., Remington K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
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Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weisenbach J.,
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MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.,
The transposable elements of the Drosophila melanogaster euchromatin:
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Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
Yu C., Rubin G.;
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MEDLINE=2245069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Misra S., Crosby M.A., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.
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Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter Starskas R., Tabor E.B., Myers E.W., Gibbs R.A., Rubin G.M., "Finishing a whole-genome shotgun: release 3 of the Drosophila;
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
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Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
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Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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Ephydroidea; Drosophilidae; Drosophila
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01-MAR-2003, sequence version 1.
07-FBB-2006, entry version 1.
Histone deacetylase dHDAC4 isoform a.
Name-HDAC4; Synonyas-HDAC4a; ORFNames-CG1770;
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota; Neoptera; Endopterzyogota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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01-WAY-2000, integrated into UniProtKB/TrEMBL.
01-MAY-2000, sequence version 2.
07-FEB-2006, entry version 26.
CG1770-PA, isoform A.
Name-EhDAC4; ORFNames-Emel CG1770;
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                   Score 49; DB 2; Length 1199;
Pred. No. 2.6e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92.5%; Score 49; DB 2; Length 1203; 92.3%; Pred. No. 2.6e+02; ive 1; Mismatches 0; Indels
                                                                                                         PROSITE; PS00307; LECTIN LEGUME BETA; UNKNOWN 1.
SEQUENCE 1199 AA; 128125 MW; 40C97AD33F86169C CRC64;
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SEQUENCE 1203 AA; 128666 MW; 04B5D0B12088979F CRC64;
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                                                                                                                                                                                                                   1; Mismatches
InterPro; IPR000286; His_deacetylse.
InterPro; IPR001220; Lectin legB.
PANTHER; PTHR10625; His_deacetylse; 3.
Pfam; PF00850; Hist_deacetyl; 1.
PRINTS; PR01270; HDĀSUPER.
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InterPro; IPR001220; Lectin legB.
PANTHER; PTHR10625; His deacetylse; 3.
Pfam; PF00850; Hist deacetyl; 1.
PRINTS; PR01270; HDĀSUPER.
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                                                                                                                                                                                                                                                                                                       445 AAVAAAAAAAAA 457
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les 12, Conservative
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                                                                                                                                                                       Query Match
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Matches 12; Conserva
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Adams M.D., Celniker S.E., 11 P. W., Hoskins R.A., Galle R.F.,

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Rander R., Spradling A.C., Stapleton
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Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., Pacleb J.M., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeifer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstrock G., Scherer S.E., Myers B.W., Gibbs R.A., Rubin G.M.; Filishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence.", Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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MEDIANE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R., Patel S., Perise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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RY Amoreacion of the Drosophila melanogaster euchromatic genome: a systematic review.";
RI Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RI Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RI Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RA HOWCLEOTIDE SEQUENCE.
RA HOSKINE K., Stapleton M., Wan K., Pfeiffer B., Frise E., George R., Calnin G., Sapleton M., Pacleb J., Park S., Svirskas R., Smith E., RA YU C., Rubin G., Sapleton M., Pacleb J., Park S., Svirskas R., Smith E., RA YU C., Rubin G., Sapleton M., Pacleb J., Park S., Svirskas R., Smith E., RA YU C., Rubin G., Submitted (WAR-2000) to the EMBL/GenBank/DDBJ databases.
RI Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RI Submitted (ANA-2000) to the EMBL/GenBank/DDBJ databases.
CC Plantisch Sequence.", Proposition Revention of Common Attribution NoDerive License CC Distributed by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Opyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
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Run ĕ

Sequence:

Minimum DB Maximum DB

Database

Result No.

Searched:

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Abp52286 HLA-DR2 m
Abp52212 HLA-DR2 m
Abp52210 HLA-DR2 m
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Adj57516 Cop-1 rel
Add5960 Copolymer
Add5960 Copolymer
Add5961 Copolymer
Add91224 Copolymer
Add81231 Copolymer
Add81232 Copolymer
Add81232 Copolymer
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Add8538 Copolymer
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Adc1896 M

Adc1990 D

Abc1897 M

Adc1897 M

Adc1991 M
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Aay99163
Aay99245
   ABP52286
ABP52212
ABP52212
ABP52212
ABP52212
ABP52213
ABP52214
ABP52214
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ABD55538
ABD659606
ABD659606
ABD659606
ABD6961233
ABD691224
ABB69127
ABB71277
ABB712773
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       \begin{array}{c} \text{$_{0}$}\\ \text{$_
       Copeptide
Copeptide
Copeptide
MHC class
MHC class
MHC class
Peptide w
Peptide w
Peptide w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human MHC
HLA-DR2 m
HLA bindi
HLA bindi
HLA bindi
HLA bindi
Drosophil
Prostate
Human MHC
Lung spec
Drosophil
Plant full
Novel hum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adi29008 Human M
Adw35215 HLA-DR2
Adw35752 HLA bin
Adw34341 HLA bin
Adw345752 HLA bin
Adw345312 Prostat
Adh75312 Prostat
Adh75312 Prostat
Adf28997 Human N
Adr28997 Lung E
Abb65204 Drosoph
Ady09213 Plant f
AbJ15667 Novel I
Ady82075 MHC cli
Ady82077 MHC cli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      results predicted by chance to have a to the score of the result being printed, of the total score distribution.
                                                                                                                                       7; Search time 97.4177 Seconds (without alignments) 61.014 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                       GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                             2589679
                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                     2589679 segs, 457216429 residues
                                                                                                                                         22:37:17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  summaries
                                                                                                   sw model
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ADW35574
ADW35574
ADW34519
ADB7644
ADB7619
ADB7619
ADF89917
ADF69220
ADX98917
ADX98917
ADX98917
AAX58983
AAX58983
AAX589983
AAX62075
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AAX62071
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Gapop 10.0 , Gapext 0.5
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genescqp1990s:*
genescqp2001s:*
genescqp2001s:*
genescqp2003s:*
genescqp2003as:*
genescqp2004s:*
genescqp2004s:*
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score greater than or equal to
and is derived by analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum Match 0%
Maximum Match 100%
Listing first 100 s
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                                                                                                                                         9, 2006,
                                                                                                   protein search, using
                                                                                                                                                                                                                                                        AAFAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                   seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                  US-10-617-568-4
54
1 AAFAAAAAAAAA
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                                                                                                                                         September
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0 Autoantig 1 Autoantig 4 Autoantig T-lymphoc

Human gen
Novel hum
Novel

Antigenic Human MHC HLA class HLA class HLA class

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The present invention describes an isolated MHC class II compound (I) comprising: (a) an MHC class II component comprising at least a portion of an MHC class II alpha chain and at least a portion of an MHC class II beta beta chain, such that the MHC class II alpha chain and MHC class II beta chain form a peptide binding groove; (b) a spaceholder Molecule; and (c) an effector component, where the effector component is linked to the MHC class II component. Also described: (I) a pharmaceutical composition comprising the MHC class II molecule and a carrier; (2) a method of producing an MHC class II compound; (3) a method of directly identifying an antigen-specific T cell; (4) a method of regulating an immune response in a subject; (5) a method of treating an immune disorder in a subject; (7) a method of treating an immune disorder in a subject; (1) has virucide, antibacterial, antiparasitic, cytostatic and immunosuppressive activities, and can be used in gene therapy. The MHC class II compound (I) can be used for preparing a composition for treating immune cativities, and can be used in gene therapy. The MHC class II compound confections, neoplastic disease, autoimmunity or toxicity. The present sequence represents a spaceholder molecule peptide, which can be used in the present invention.
Adw35620 HLA bindi
Adw34387 HLA bindi
Adn64988 HLA bindi
Adv78640 Cell atta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MHC class II compound; MHC class II component; MHC class II alpha chain; MHC class II beta chain; peptide binding groove; spaceholder molecule; effector component; immune response; immune disorder; virucide; antibacterial; antiparastic; cytostatic; immunosuppressive; gene therapy; viral infections; bacterial infection; parastic infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New MHC class II compound, useful for preparing a composition for treating immune disorders e.g. viral infections, bacterial infections, parasitic infections, neoplastic disease, autoimmunity or toxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human MHC class II compound spaceholder molecule SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neoplastic disease; autoimmunity; toxicity; human.
                                                                                                                                                                                                      ALIGNMENTS
                                  ADW34387
ADN64988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; SEQ ID NO 4; 92pp; English
      ADW35620
                                                                                                      ADV78640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DAND ) DANA FARBER CANCER INST INC.
                                                                                                                                                                                                                                                                                                                                                                      ADI29008 standard; peptide; 13 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JUL-2003; 2003WO-US021767.
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2002US-0397893P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
          133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-122876/12.
   85.2
85.2
85.2
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22-JUL-2002;
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          Homo
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ADII 1008

XXX
XXX ADII 1008

WHO WAS ADII 1008

WHO WAS ADII 1008

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WHO WAS 
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Sequence 13 AA,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral
                                                                                                                                                                                                                                                                                  Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                               Gaps
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100.0%; Score 54; DB 8; Length 13; 100.0%; Pred. No. 0.14;
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                             0; Indels
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0
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                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       anti-tumour necrosis factor agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 30; 54pp; English.
                                                                                                                                                                    ABP52215 standard; peptide; 15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fridkis-Hareli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JAN-2001; 2001US-0263569P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 92.33,
Best Local 12; Conservative
                                                                                                                                                                                                                                16-OCT-2002 (first entry)
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                                                              1 AAFAAAAAAAA 13
                                                                                         AAFAAAAAAA 13
                                13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-608439/65.
                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encephalomyelitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strominger JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200259143-A2
                                                                                                                                                                                                                                                                                                                                                                                                     sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
 Query Match
Best Local S:
Matches 13,
                                                                                                                                                                                                    ABP52215;
                                                                                                                                          RESULT 2
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Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell; MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 52-379; 382pp; English.
                                                                                                                                                                                                                                                                                                             18-OCT-2001; 2001WO-US051650.
                                                                                                                                                                                                                                                                                                                                                   19-OCT-2000; 2000US-0242350P.
20-APR-2001; 2001US-0285624P.
                                                            HLA binding epitope #5091.
                                                                                                                                           viral disease; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                  (EPIM-) EPIMMUNE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sette A, Sidney J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-441519/41
                                                                                                                                                                                                                             WO2003040165-A2.
                                                                                                                                                                                    Unidentified.
                                                                                                                                                                                                                                                                    15-MAY-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  having an isolated, prepared epitope selected from any of the sequences from 30 lists given in the specification. Also disclosed is a method for inducing a cytotoxic T cell response against a pre-selected antigen in a patient expressing a specific MHC class I allele by contacting cytotoxic T cells from the patient with the composition cited above. The composition comprises an epitope that is joined by an amino acid linker. The epitope is admixed or joined to a CTL or HTL epitope. The epitope is bound to an HIA molecule on the antigen-presenting cell, where when an A2 restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL binds to a complex of the HIA molecule and the epitope. Specifically claimed are peptides having allele-specific binding motifs for HIA. The compositions and methods are useful for preventing, treating or diagnostic agents for evaluating immune responses, for making antibodies and for evaluating efficacy of a vaccine. Sequences given in ADW39251-ADW37745 represent epitopes of the invention as given in Tables 2-31.
                                                                                                                                                                                                                                            Virucide, cytostatic, gene therapy, vaccine, epitope, cytotoxic T cell, MHC class I; CTL, HTL, A2-restricted cytotoxic lymphocyte, HLA; viral disease, cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New composition comprising at least one peptide having allele-specific binding motifs for HLA, useful for preventing, treating or diagnosing viral diseases and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a composition comprising at least one peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 49; DB 7; Length 13;
Pred. No. 0.71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 52-379; 382pp; English.
                                                                           ADW35574 standard; peptide; 13 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Southwood
                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-OCT-2001; 2001WO-US051650.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-OCT-2000; 2000US-0242350P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-APR-2001; 2001US-0285624P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 90.7%;
Local Similarity 92.3%;
les 12; Conservative (
                                                                                                                                                            (first entry)
                                                                                                                                                                                                     HLA binding epitope #6324.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sidney J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-441519/41.
                                                                                                                                                                                                                                                                                                                                                                       WO2003040165-A2
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                                                                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                            10-MAR-2005
                                                                                                                                                                                                                                                                                                                                                                                                               15-MAY-2003
                                                                                                                      ADW35574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sette A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                        RESULT 3
                                                            ADW355
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Southwood S;

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The invention relates to a composition comprising at least one peptide having an isolated, prepared epitope selected from any of the sequences from 30 lists given in the specification. Also disclosed is a method for inducting a cytotoxic T cell response against a pre-selected antigen in a patient expressing a specific MHC class I allele by contacting cytotoxic CT cells from the patient with the composition cited above. The composition comprises an epitope that is joined by an amino acid linker. The epitope is admixed or joined to a CTL or HTL epitope. The epitope is composition comprises an epitope that is joined by an amino acid linker. The epitope is admixed or joined to a CTL or HTL epitope. The epitope is composition on the antigen-presenting cell, where when an A2 restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL binds to a complex of the HLA molecule and the epitope. Specifically claimed are peptides having allele-specific binding motifs for HLA. The compositions and methods are useful for preventing, treating or diagnostic agents for evaluating immune responses, for making antibodies and for evaluating efficacy of a vaccine. Sequences given in ADW29251.

ADW37745 represent epitopes of the invention as given in Tables 2-31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 0.71;
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es 12, Conservative
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Gaps ; 0

1; Indels

0; Mismatches

1 AAFAAAAAAAA 13 AAFAAAAAKAAA 13

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Matches

ADW34341 standard; peptide; 13 AA.

RESULT 4 ADW34341

ADW34341;

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pharmaceutical
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                                                                                                                                                       Sette A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a composition comprising at least one peptide having an isolated, prepared epitope selected from any of the sequences from 30 lists given in the specification. Also disclosed is a method for inducing a cytotoxic reall response against a pre-selected antigen in a patient expressing a specific MHC class I allele by contacting cytotoxic reals from the patient with the composition cited above. The composition comprises an epitope that is joined by an amino acid linker. The epitope is admixed or joined to a CTL or HTL epitope. The epitope is composition composition on the antigen-presenting cell, where when an AZ restricted cytotoxic lymphocyte (CTL) is presenting cell, where when an AZ restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL binds to a complex of the HLA molecule and the epitope. Specifically claimed are peptides having allele-pepcific binding motifs for HLA. The compositions and methods are useful for preventing, treating or diagnostic agents for evaluating immune responses, for making antibodies and for evaluating efficacy of a vaccine. Sequences given in ADM29251.
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                                                                                                                                                                                                                                                                                                                                                                             New composition comprising at least one peptide having allele-specific binding motifs for HLA, useful for preventing, treating or diagnosing viral diseases and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 0.77;
0; Mismatches 1; Indels
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20-APR-2001; 2001US-0285624P.
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Matches 12; Conservative
  viral disease; cancer
                                                                                                                                                                                                                                                                 (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                                                                                                         Sette A, Sidney J,
                                                                                                                                                                                                                                                                                                                                              WPI; 2003-441519/41
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                                       Unidentified
                                                                                                                    15-MAY-2003
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15-MAY-2003

ADW34519

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The invention relates to a composition comprising at least one peptide chaving an isolated, prepared epitope selected from any of the sequences from 30 lists given in the specification. Also disclosed is a method for inducing a cytotoxic real response against a pre-selected antigen in a cc material a specific MFC class I allele by contacting cytotoxic relistrom the patient with the composition cited above. The composition comprises an epitope that is joined by an amino acid linker. The epitope is admixed or joined to a CTL or HTL epitope. The epitope is composition composition composition complex of the HLA molecule and the epitope. Specifically claimed are peptides having allele-specific binding motifs for HLA. The compositions and methods are useful for preventing, treating or capangosing viral diseases and cancer. The peptide epitopes are useful as diagnostic agents for evaluating immune responses, for making antibodies and for evaluating immune responses, for making antibodies and for evaluating efficacy of a vaccine. Sequences given in ADW29251-
                                                                                                                                                                                                                                                              New composition comprising at least one peptide having allele-specific binding motifs for HLA, useful for preventing, treating or diagnosing viral diseases and cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 49; DB 7; Length 14; Pred. No. 0.77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 52-379; 382pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB70644 standard; protein; 422 AA.
                                                                                                                                                                      Southwood S;
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11-JUL-2000; 2000US-00614150.
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18-OCT-2001; 2001WO-US051650.
                                             19-OCT-2000; 2000US-0242350P.
20-APR-2001; 2001US-0285624P.
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                                                                                                                      (EPIM-) EPIMMUNE INC
                                                                                                                                                                      Sidney J,
                                                                                                                                                                                                                   WPI; 2003-441519/41.
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Best Local Similarity
Matches 12; Conser
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(first entry)
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                                                                                                                                                                                  12; Conservative
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                                                                                                                                                                         Local Similarity
                                                                                                                                          Sequence 465 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004007528-A2.
                                                                                                                                                                                                                                                                                                                    15-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
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                                                                                                                                                                                  Matches
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ADI29007
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                                                                                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-ABR30021). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wlpo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to newly discovered cancer markers associated with the cancerous state of prostate cells. Also disclosed is a method of
                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid molecule, useful for diagnosing or treating prostate
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Anderson D;
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                                                                                      Disclosure; SEQ ID NO 38724; 21pp + Sequence Listing; English.
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Pred. No. 17;
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Glatt K, Zhao X,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Prostate; cancer; cytostatic; gene therapy; marker.
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Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , Endege WO, Wonsey AM,
                                                                                                                                                                                                                                                                                                                                                           ADB75312 standard; protein; 465 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                         Prostate cancer marker protein.
PWD,
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12-DEC-2001; 2001US-0341746P.
05-MAR-2002; 2002US-0362158P.
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hes 12; Conservative
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Adams M,
                    WPI; 2001-656860/75
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                            N-PSDB; ABL14747
                                                                                                                                                                                                                          Sequence 422 AA;
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                                                                     interactions
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Venter JC,
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assessing whether a patient is afflicted with prostate cancer. The method of the invention involves assessing whether a patient is afflicted with prostate cancer by comparing the level of expression of a marker in a patient sample and the normal level of expression of the marker in a control non-prostate cancer sample, where a significant increase in the level of expression of the marker in the patient sample and the normal level indicates that the patient is afflicted with prostate cancer. Nucleic acids of the invention are useful for diagnosing or treating prostate cancer, and may be useful in gene therapy. Sequences given in ADB7577-ADB75631 represent marker cDNA and proteins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MHC class II compound; MHC class II component; MHC class II alpha chain; MHC class II beta chain; peptide binding groove; spaceholder molecule; effector component; immune response; immune disorder; virucide; antibacterial; antiparastic; cytostatic; immunosuppressive; gene therapy; viral infections; bacterial infection; parasitic infection; neoplastic disease; autoimmunity; toxicity; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes an isolated MHC class II compound (I) comprising: (a) an MHC class II component comprising at least a portion of an MHC class II alpha chain and at least a portion of an WHC class II beta chain, such that the MHC class II alpha chain and MHC class II beta chain form a peptide binding groove; (b) a spaceholder molecule; and (c) an effector component, where the effector component is linked to the MHC class II component. Also described: (1) a pharmaceutical composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New MHC class II compound, useful for preparing a composition for treating immune disorders e.g. viral infections, bacterial infections, parasitic infections, neoplastic disease, autoimmunity or toxicity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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22-JUL-2002; 2002US-0397893P.
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comprising the MHC class II molecule and a carrier; (2) a method of producing an MHC class II compound; (3) a method of directly identifying an antigen-specific T cell; (4) a method of regulating an immune response in a subject; (5) a method of treating an immune disorder in a subject; (6) a method of treating an immune disorder ex vivo in a subject; and (7) a method of treating an immune disorder ex vivo in a subject; and extracting, antiparasitic, cytostatic and immunesuppressive activities, and can be used in gene therapy. The MHC class II compound (1) can be used for preparing a composition for treating immune disorders, e.g., viral infections, bacterial infections, parssitic infections, neoplastic disease, autoimmunity or toxicity. The present sequence represents a spaceholder molecule peptide, which can be used in an MHC class II compound from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated human lung specific nucleic acid molecule, useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous diseases of the lung.
                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytostatic; gene therapy; vaccine; lung; diagnosis; cancer; non-cancerous lung disease; lung tissue; antagonist; gene therapy; transgenic animal; splice variant.
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                                                                                                                                                                                                                                                                                                                 Score 48; DB 8; Length 13;
Pred. No. 1;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specific gene splice variant encoded protein #89.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADR98917 standard; protein; 278 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-DEC-2002; 2002US-0431307P.
06-DEC-2002; 2002US-0431510P.
06-DEC-2002; 2002US-0431516P.
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                                                                                                                                                                                                                                                                                                                     88.9%;
92.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                 1 AAFAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AAMAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DIAD-) DIADEXUS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-635553/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ADR98780
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                                                                                                                                                                                                                                                                                 Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-NOV-2004
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
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polypeptide of the invention, gene therapy, production of transgenic animals and production of engineered lung tissue for treatment and research. Lung specific genes (LSGs) were identified by a systematic analysis of gene expression data in the LIFESEO Gold database using the data mining software package candidate lead automatic search program (CLASP). Genes were grouped into gene bins where each bin is a cluster of sequences grouped together where they share a common contig. Differentially expressed tissue-specific genes were selected based on the percentage level in the targeted tissue versus all the other tissues. The expression levels for each gene in libraries of normal tissues or non-tumour tissues from cancer patients were compared with the expression levels in tissue libraries associated with tumour or disease. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 22404; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                    88.9%; Score 48; DB 8; Length 278; 92.3%; Pred. No. 16; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster polypeptide SEQ ID NO 22404.
                                                                                                                                                                                                                                      sequence represents a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li PWD, Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB65204 standard; protein; 285 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                     1 AAFAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAMAAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                               12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-656860/75.
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Matches 12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ABL09307
                                                                                                                                                                                                                                                                                  Sequence 278 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pharmaceutical
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Gaps

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Score 48; DB 8 Pred. No. 36; 0; Mismatches

88.9%;

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(first entry)

8; Length 646; Indels

or for modifying seed oil or protein yield and/or the amino acid sequence of a plant full length insert can be used in the recombinant DNA construct of the

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us-10-617-568-4.rag

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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human diagnostic protein #15658.
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                                                                                                                                                                                                                                           1 AAFAAAAAAAA 13
                                                                                                                                                                                                                                                                                      4 AAMAAAAAAAA 16
                                                                                                                                                                                                  12; Conservative
                                                                                                                                                     Query Match
Best Local Similarity
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stress condition
content. This is
polypeptide that
                                                                                                              Sequence 646 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-FEB-2002
                                                                   invention.
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                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at available in electronic form from the US patent office at from the US patent office at the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme improving plant tolerance to cold, heat, drought, herbicides, extreme commotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosyntheeis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                           plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
                                                                                        Gaps
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                                        DB 4; Length 285;
                                                                                     1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                  Plant full length insert polypeptide segid 65028.
                                                                                        0; Mismatches
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                                          Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                    ADY09213 standard; protein; 646 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhou Y, Kovalic DK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-MAY-1999; 99US-00304517.
05-NOV-2001; 2001US-00985678.
                                          88.9%;
92.3%;
                                                                                                                                                                         189 AAIAAAAAAAA 201
                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                      Query Match
Best Local Similarity 92.3:
                                                                                                                                1 AAFAAAAAAAA 13
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TABASKA J E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-180133/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2004034888-A1.
Sequence 285 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           improving yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein content
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ZHOU Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                                                                          21-APR-2005
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(SCRE/)
(TABA/)
(CAOY/)
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                                                                                                                                                                                                                                           RESULT 12
                                                                                                                                                                                                                                                             ADY09213

XX A ADY0

ADY
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The invention relates to isolated polymucleotide (I) and polypeptide (II)

sequences. (I) is useful as hybridisation probes, polymerase chain

caction (PCR) primers, aligomers, and for chromosome and gene mapping,

and in recombinant production of (II). The polymucleotides are also used

in diagnostics as expressed sequence tags for identifying expressed

cartivity of (II) or to treat disease states involving (II). (II) is

cusful for generating antibodies against it, detecting or quantitating a

cutivity of (II) and its binding partners are useful in medical imaging

co sites expressing (II). (I) and its binding partners are useful for treating disorders

co polypeptide and polymucleotide sequences have applications in

co sites expressing (II). (I) and (II) are useful in medical imaging

cof sites expressing (II). (I) and its binding partners are useful for treating disorders

convolving aberrant protein expression or biological activity. The

convolving aberrant protein expression or biological activity. The

convolving aberrant protein expression or biological activity. The

convolving aberrant protein expression or biological activity.

convolving aberrant protein expression or biological activity or and activity activity.

convolving aberrant protein expression or biological activity or and activity or acti
                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; SEQ ID NO 46026; 103pp; English.
Tang YT;
        Drmanac RT, Liu C,
                                                                                                                                                                        WPI; 2001-639362/73
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02-OCT-1998;
12-NOV-1998;
09-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY58972;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copeptide; copolymer 1; autoimmune disease; multiple sclerosis; autoimmune haemolytic anaemia; autoimmune oophoritis; autoimmune thyroiditis; autoimmune uveoretinitis; chronic immune thrombocytopenic purpura; colitis; contact sensitivity disease; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; Hashimoto's disease; idiopathic myxedema; myaschenia gravis; psoriasis; pemphigus vulgaris; rheumatcid arthritis; systemic lupus erythematcosus; immunosuppressant; neuroprotective; antiannaemic; antithyroid; antidiabetic; thyromimetic; antipsoriatic; antithematchritic; dermatological; antiinflammatory; therapy; major histocompatibility complex; MHC class II; human lymphocyte antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a copeptide that can be used to treat autoimmune conditions. It is an example of copeptides of the invention that were designed to bind to the groove of human leukocyte antigen HLA-DR1 and HLA-DR4 molecules. The copeptides show a high affinity for major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New terpolymers, copeptides and copolymer 1 which contain three amino acids randomly joined in a linear array where one is aromatic, one is aliphatic and the other is charged, used to treat autoimmune diseases.
                                                                                                                                                 Gaps
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                                                                                                    Length 1444;
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                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copeptide useful for treatment of autoimmune disease.
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                                                                                                      88.9%; Score 48; DB 92.3%; Pred. No. 74;
                                                                                                                                                 Mismatches
  electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 137; Page 69; 147pp; English.
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98US-0101825P.
98US-0102960P.
98US-0108184P.
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                                                                                                                                                                                                                                  782 AAIAAAAAAAA 794
                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                         1 AAFAAAAAAAAA 13
                                                                                                        Query Match
Best Local Similarity 92.3
Matches 12; Conservative
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                                                                Sequence 1444 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                 AAY58983;
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histocompatability complex (MHC) class II proteins associated with an autoimmune disease, especially HLA-DR1, HLA-DR2 or HLA-DR4, bind to antigen presenting cells, and inhibit T cell responses. They are especially used to treat multiple sclerosis, autoimmune haemolytic anaemia, autoimmune coophoritis, autoimmune thyroiditis, autoimmune thyroiditis, autoimmune sensitivity disease, diabetes mellitus, Graves disease, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, dilliain-Barre's syndrome, Hashimoto's disease, idiopathic myxedema, myasthenia gravis, psoriasis, pemphigus vulgaris, rheumatoid arthritis and systemic lupus erythematosus (all claimed)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 47; DB 3; Length 15;
Pred. No. 1.6;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copeptide useful for treatment of autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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98US-0101825P.
98US-0102960P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           87.0%;
91.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 AFAAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 AYAAAAAAAAA 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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(HARD ) HARVARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15 AA;
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(YEDA ) YEDA RES & DEV CO LTD. (HARD ) HARVARD COLLEGE.
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                                                                           Aharoni R,
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                                                                                                                                                                                                                                                                                          uveoretinitis, chronic immune thrombocytopenic purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxedema, myasthenia gravis, psoriasis, pemphigus vulgaris, rheumatoid arthritis and systemic lupus erythematosus (all claimed). The present peptide is a high level inhibitor of both HLA-DR-1 and -DR-4-restricted type II collagen-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chronic immune thrombocytopenic purpura; collitis; contact sensitivity disease; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; Hashimoto's disease; idiopathic myxedema; Guillain-Barre's syndrome; Hashimoto's disease; idiopathic myxedema; myasthenia gravis; psoriasis; pemphigus vulgaris; rheumatoid arthritis; systemic lupus erythematosus; imunosuppressant; neuroprotective; systemic lupus erythematosus; imunosuppressant; neuroprotective; antianthyroid, antidiabetic; thyromimetic, antipsoriatic; antiarthritic; dermatological; antiinflammatory; therapy; major histocompatibility complex; MHC class II; human lymphocyte antigen;
                                                                                    The present sequence represents a copeptide that can be used to treat autoimmune conditions. It is an example of copeptides of the invention that were designed to bind to the groove of human leukcoyte antigen HiA-DR1 and HIA-DR4 molecules. The copeptides show a high affinity for major histocompatability complex (MHC) class II proteins associated with an autoimmune disease, especially HIA-DR1, HIA-DR2 or HIA-DR4, bind to antigen presenting cells, and inhibit T cell responses. They are especially used to treat multiple sclerosis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune
aliphatic and the other is charged, used to treat autoimmune diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 47; DB 3; Length 15;
Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "may be substituted by Val or Phe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune haemolytic anaemia; autoimmune oophoritis; autoimmune thyroiditis; autoimmune uveoretinitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copeptide useful for treatment of autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
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                                            Claim 82; Page 88; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY58985 standard; peptide; 15
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98US-0102960P.
98US-0108184P.
99US-0123675P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 AYAAAAAAAAA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15 AA;
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02-OCT-1998;
12-NOV-1998;
09-MAR-1999;
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The present sequence represents a copeptide that can be used to treat autoimmune conditions. It is an example of copeptides of the invention that were designed to bind to the groove of human leukocyte antigen HLA-DR1 and HLA-DR4 molecules. The copeptides show a high affinity for major histocompatability complex (MHC) class II proteins associated with an autoimmune disease, especially HLA-DR2 or HLA-DR2 or HLA-DR2. They are especially used to treat multiple sclerosis, autoimmune obportits, and inhibit T cell responses. They are especially used to treat multiple sclerosis, autoimmune had autoimmune ophoritis, autoimmune thyroidatis, autoimmune employeritis, autoimmune thyroidatis, autoimmune employeritis, autoimmune weoretinitis, chronic immune thrombocytopenic purpura, colitis, contect sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxedema, myasthenia gravis, psomphigus vulgaris, rheumatosid arthritis and systemic lupus erythematosus (all claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MHC class II; major histocompatibility complex; autoimmune disease; inflammatory disease; binding; rheumatoid arthritis; antiinflammatory; antiarthritic; multiple sclerosis.
                                                                                                                                                                       New terpolymers, copeptides and copolymer 1 which contain three amino acids randomly joined in a linear array where one is aromatic, one is aliphatic and the other is charged, used to treat autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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   Fridkis-Hareli M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 47; DB 3;
Pred. No. 1.6;
   Sela M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
Teitelbaum D, Arnon R,
                                                                                                                                                                                                                                                                                                                  Claim 137; Page 69; 147pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY82075 standard; peptide; 15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87.0%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US016617
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99US-0123675P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 AYAAAAAAAAA 14
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                                                                                                      WPI; 2000-182641/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-205374/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                Strominger JL;
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The present invention describes synthetic peptides having an amino acid sequence comprising at least 3 residues selected from the group of amino acids consisting of aromatic acids, negatively charged amino acids, positively charged amino acids, and aliphatic amino acids, the synthetic peptides being at least 7 amino acid residues in length and capable of binding to a major histocompatibility complex (MHC) class II protein associated with an autoimmune disease. The synthetic peptides have anticinflammatory and anti-arthritic activities. They are used to treat inflammatory and demyelinating autoimmune diseases, especially rheumatoid arthritis and multiple sclerosis. The peptides are specific for particular MHC class II alleles. Purified, short and synthetic peptides should have fewer side effects than mixtures of random peptides; may include many repeats of the active sequence and/or contain amino acid analogues that improve stability (or other desired features). AAV8201 to AAV82044 represent specifically claimed peptide sequences which can be used as part of the synthetic peptides of the present invention; AAV82045 to AAV82063 represent specifically claimed examples of the synthetic peptides of the present invention; AAV82045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   beptides from the present invention; and AAY82064 to AAY82080 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    other peptides used in the exemplification of the present invention
                             Example 8; Page 32; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15 AA;
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Score 47; DB 3; Length 15 Pred. No. 1.6; ; Mismatches 87.0**%**; 91.7**%**; 11; Conservative 2 AFAAAAAAAAA 13 3 AYAAAAAAAAA 14 Similarity Query Match Best Local S Matches 셤 ð

WHC class II protein binding peptide SEQ ID NO:33. AAY82061 standard; peptide; 15 AA. (first entry) 01-JUN-2000 AAY82061; RESULT 18 

MHC class II; major histocompatibility complex; autoimmune disease; inflammatory disease; binding; rheumatoid arthritis; antiinflammatory; antiarthritic; multiple sclerosis.

Synthetic

WO200005249-A2

03-FEB-2000.

99WO-US016617 98US-0093859P 22-JUL-1999; 09-MAR-1999; 23-JUL-1998;

(HARD ) HARVARD COLLEGE

99US-0123675P.

Ξ Fridkis-Hareli WPI; 2000-205374/18. Strominger JL,

Claim 24; Page 41; 57pp; English.

New synthetic peptide, useful for treating autoimmune disease, rheumatoid arthritis.

The present invention describes synthetic peptides having an amino acid sequence comprising at least 3 residues selected from the group of amino acids consisting of aromatic acids, negatively charged amino acids,

positively charged amino acids, and aliphatic amino acids, the synthetic peptides being at least 7 amino acid residues in length and capable of binding to a major histocompatibility complex (MHC) class II protein associated with an autoimmune disease. The synthetic peptides have anticifiammatory and anti-archritic activities. They are used to treat inflammatory and demyelinating autoimmune diseases, especially rheumatoid archritis and multiple sclerosis. The peptides are specific for archritis and multiple sclerosis. The peptides are specific for particular MHC class II alleles. Purified, short and synthetic peptides should have fewer side effects than mixtures of random peptides; may include many repeate of the active sequence and/or contain amino acid analogues that improve stability (or other desired features). AAY8204 represent specifically claimed peptide sequences which can be used as part of the synthetic peptides of the present invantion; AAY82045 to AAY82063 represent specifically claimed examples of the synthetic peptides from the present invention and AAY82080 represent contain and AAY82080 represent present invention

Sequence 15 AA; 

ö Gaps .. 0 Length 15; 0; Indels Score 47; DB 3; Pred. No. 1.6; 1; Mismatches ( 87.0%; 11; Conservative Local Similarity Query Match datches

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Gaps

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0; Indels

AAY82077 standard; peptide; 15 AA. (first entry) 01-JUN-2000 AAY82077; RESULT 19 AAY82077 

MHC class II protein binding peptide SEQ ID NO:27.

MHC class II; major histocompatibility complex; autoimmune disease; inflammatory disease; binding; rheumatoid arthritis; antiinflammatory; antiarthritic; multiple sclerosis.

Synthetic

WO200005249-A2.

22-JUL-1999; 03-FEB-2000

98US-0093859P 99US-0123675P 23-JUL-1998; 09-MAR-1999;

(HARD ) HARVARD COLLEGE

Strominger JL,

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Fridkis-Hareli

WPI; 2000-205374/18.

New synthetic peptide, useful for treating autoimmune disease, e.g. rheumatoid arthritis.

Example 8; Page 32; 57pp; English.

The present invention describes synthetic peptides having an amino acid sequence comprising at least 3 residues selected from the group of amino acids consisting of aromatic acids, negatively charged amino acids, positively charged amino acids, and aliphatic amino acids, the synthetic positively charged amino acids, and aliphatic amino acids, the synthetic binding to a major histocompatibility complex (MrG) class II protein associated with an autoimmune disease. The synthetic peptides have anti-inflammatory and anti-arthritic activities. They are used to treat inflammatory and demyelinating autoimmune diseases, especially rheumatoid

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particular MHC Class II alleles. Purified, short and synthetic peptides should have fewer side effects than mixtures of random peptides; may include many repeats of the active sequence and/or contain amino acid analogues that improve stability (or other desired features). AAY82021 to AAY82044 represent specifically claimed peptide sequences which can be used as part of the synthetic peptides of the present invention, AAY82045 to AAY82063 represent specifically claimed examples of the synthetic peptides from the present invention; and AAY82064 to AAY82080 represent other peptides used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         copolymer 1; Cop 1; spin cord injury; injury; insease; i Cell; haemorrhagic stroke; spin cord injury; blunt trauma; trauma; haemorrhagic stroke; schaemic stroke; diabetic neuropathy; Bell's palsy; senile dementia; Alzheimer's disease; Parkinson's disease; glaucoma; facial nerve palsy; Huntington's chorea; amyotrophic lateral sclerosis; status epilepticus; non-arteritic optical neuropathy; vitamin deficiency; HIA-DR molecule.
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Pred. No. 1.6;
1; Mismatches 0; Indels
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07-JUN-2000; 2000US-0209799P.
20-JUL-2000; 2000US-00620216.
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91.7%;
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(MCIN/) MCINNIS
                                                                                                                                                                               Sequence 15 AA;
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The specification describes a method for preventing or inhibiting neuronal degeneration, or for promoting nerve regeneration, or treating neuronal degeneration caused by injury or disease. The method comprises administering activated T cells which have been activated by copolymer 1 (Cop 1) or a Cop 1-related peptide or polypeptide; or Cop 1 or a Cop related peptide. The method is used for preventing or inhibiting neuronal degeneration, or for promoting nerve regeneration, or

Disclosure; Page 32; 105pp; English.

polypeptide.

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treating neuronal degeneration caused by injury or disease comprising spinal cord injury, blunt trauma, penetrating trauma, haemorrhagic stroke, ischaemic stroke, idabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea, amyotrophic lateral sclerosis, status epilepticus, non-arteritic optical neuropathy, or vitamin deficiency. Cop lor the Cop 1-related peptide or polypeptide is useful in the preparation of a medicament for preventing or inhibiting neuronal degeneration, or for promoting nerve regeneration. AAG631206 represent peptides which bind to the peptide binding groove of HLA-DR molecules. The peptides are homologous to the binding motifs of Cop 1, and have similar activities to Cop 1. As such, they may be used in the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neuronal degeneration; nerve regeneration; injury; disease; T cell;
copolymer 1; Cop 1; spinal cord injury; blunt trauma; trauma;
haemorrhagic stroke; ischaemic stroke; diabetic neuropathy; Bell's palsy
senile dementia; Alzheimer's disease; Parkinson's disease; glaucoma;
facial nerve palsy; Huntington's chorea; amyotrophic lateral sclerosis;
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Pred. No. 1.6;
1; Mismatches 0
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07-JUN-2000; 2000US-0209799P.
20-JUL-2000; 2000US-00620216.
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                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HLA-DR molecule.
                                                                                                                                                                                                                                                                    Sequence 15 AA;
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cc neuronal degeneration, or for promoting nerve regeneration, or treating neuronal degeneration caused by injury or disease. The method comprises administering activated T cells which have been activated by copolymer 1 (Cop 1) or a Cop 1-related peptide or polypeptide; or Cop 1 or a Cop 1-crelated peptide or polypeptide; or Cop 1 or a Cop 1-crelated peptide. The method is used for preventing or inhibiting neuronal degeneration, or for promoting nerve regeneration, or treating neuronal degeneration, or for promoting rauma, haemorrhagic spinal cord injury, blunt trauma, penetrating trauma, haemorrhagic stroke, ischaemic stroke, diabetic neuropathy, senile dementia, caroke, ischaemic stroke, diabetic neuropathy, senile dementia, caroke, ischaemic stroke, diabetic neuropathy, senile dementia, captured platicus, non-arteritic optical neuropathy, or vitamin deficiency. Cop copilepticus, non-arteritic optical neuropathy, or vitamin deficiency. Cop reparation of a medicament for preventing or inhibiting neuronal degeneration, or for promoting nerve regeneration. AAG63175-AAG63206 copperation, or for promoting nerve regeneration. AAG63175-AAG63206 copperation of a medicament for preventing or inhibiting neuronal degeneration, or for promoting nerve regeneration. AAG63175-AAG63206 copperation and have similar activities to Cop 1. As such, they may be used in the method of the invention

Sequence 15 AA;

clop 1) or a Cop 1-related peptide or polypeptide; or Cop 1 or a Cop 1celated peptide or polypeptide. The method is used for preventing or
inhibiting neuronal degeneration, or for promoting nerve regeneration, or
treating neuronal degeneration, or for promoting nerve regeneration, or
treating neuronal degeneration caused by injury or disease comprising
spinal cord injury, blunt trauma, penetrating trauma, haemorrhagic
stroke, ischaemic stroke, diabetic neuropathy, senile dementia,
Alzheimer's disease, Parkinson's disease, facial nerve (Bell's) palsy,
glaucoma, Huntington's chorea, amyotrophic lateral sclerosis, status
c pilepticus, non-arteritic optical neuropathy, or vitamin deficiency. Cop
1 or the Cop 1-related peptide or polypeptide is useful in the
preparation of a medicament for preventing or inhibiting neuronal
c degeneration, or for promoting nerve regeneration. Add61175-Ad663206
represent peptides which bind to the beptide binding groove of HLA-DR
molecules. The peptides are homologous to the binding motifs of Cop 1,
and have similar activities to Cop 1. As such, they may be used in the ö Neuronal degeneration; nerve regeneration; injury; disease; T cell; copolymer 1; Cop 1; spinal cord injury; blunt trauma; trauma; haemorrhagic stroke; ischaemic stroke; diabetic neuropathy; Bell's palsy; senile dementia; Alzheimer's disease; Parkinson's disease; glaucoma; facial nerve palsy; Huntington's chorea; amyotrophic lateral sclerosis; status epilepticus; non-arteritic optical neuropathy; vitamin deficiency; HLA-DR molecule. Gaps Peptide which binds to peptide binding groove of HLA-DR molecules. ö Score 47; DB 4; Length 15; Pred. No. 1.6; 1; Mismatches 0; Indels AAG63194 standard; peptide; 15 AA 20-JAN-2000; 2000US-00487793. 07-JUN-2000; 2000US-0209799P. 20-JUL-2000; 2000US-00620216. 22-JAN-2001; 2001WO-US002117. 87.0%; 91.7%; (first entry) Local Similarity 91.7 Les 11, Conservative |:||||||||||||| AYAAAAAAAAAA 15 2 AFAAAAAAAAA 13 method of the invention Sequence 15 AA; WO200152878-A2 01-OCT-2001 26-JUL-2001 Synthetic. AAG63194; Query Match Matches AAG63194 ઠે 셤

ô New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis. Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; Gaps .. Length 15; 0; Indels Score 47; DB 4; Pred. No. 1.6; HLA-DR2 molecule binding peptide SEQ ID NO:10. 1; Mismatches Example 1; Page 30; 54pp; English. anti-tumour necrosis factor agent. ABP52216 standard; peptide; 15 AA. Fridkis-Hareli M; 24-JAN-2002; 2002WO-US002071. 87.0%; 24-JAN-2001; 2001US-0263569P 16-OCT-2002 (first entry) Best Local Similarity 91.7 Matches 11; Conservative 2 AFAAAAAAAA 13 AYAAAAAAAAA 14 (HARD ) HARVARD COLLEGE WPI; 2002-608439/65. Strominger JL, WO200259143-A2. sapiens. 01-AUG-2002 Synthetic ABP52216; Query Match Ношо RESULT 23 ABP5221( 8 셤

The present invention describes compositions (I) comprising a peptide

Promoting nerve regeneration or preventing, inhibiting or treating neuronal degeneration caused by injury or disease comprises administering T cells activated by copolymer 1 (Cop 1) or a Cop 1-related peptide or

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Cohen IR,

Eisenbach-Schwartz M, MCINNIS P A.

WPI; 2001-476094/51

RES & DEV CO LTD.

(YEDA ) YEDA (MCIN)

The specification describes a method for preventing or inhibiting

Disclosure; Page 32; 105pp; English

polypeptide.

demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

ABP52305 represent peptides used in the exemplification of the present

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Gaps

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Length 15; 0; Indels

Score 47; DB 5; Pred. No. 1.6; L; Mismatches

87.0%; 91.7%;

11; Conservative 2 AFAAAAAAAA 13 4 AYAAAAAAAAA 15

Best Local Similarity

Query Match Matches

Sequence 15 AA;

invention

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ABP52212 standard; peptide; 15

RESULT 25 ABP52212

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with an amino acid sequence with tyxosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility immune response. The complex of the peptide with a major histocompatibility immune response. (1) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, poet-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autocantigen-specific HLA-DRZ-resericted T cell clones. ABP52207 to ABP52205 represent peptides used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.
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New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral
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                                                                                                                     Human leukocyte antigen, HLA; major histocompatibility complex, MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response, antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.
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                                                                                       HLA-DR2 molecule binding peptide SEQ ID NO:6.
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                                                  (first entry)
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                                                                                                                                                                                                                                                                                 Synthetic.
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               ABP52212;
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with an amino acid sequence with tyrosine (Y), Iysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine

present invention describes compositions (I) comprising a

Example 1; Page 34; 54pp; English.

encephalomyelitis.

4 AYAAAAAAAAA 15

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with an amino acid sequence with tyrosine (Y), lysine (K), and/or value residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
                                                                                                                                                                                                                                                                                                                          Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition;
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                                 Gaps
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Pred. No. 1.6;
1; Mismatches 0; Indels
Length 15;
                                 0; Indels
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                                                                                                                                                                                                                                                                                            HLA-DR2 molecule binding peptide SEQ ID NO:8.
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                                   1; Mismatches
 Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 30; 54pp; English.
                                                                                                                                                                                          ABP52214 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                   anti-tumour necrosis factor agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fridkis-Hareli M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JAN-2002; 2002WO-US002071.
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 87.0%;
91.7%;
                                                                                                                                                                                                                                                             (first entry)
                                   11; Conservative
                                                                     AFAAAAAAAAA 13
                                                                                                     AYAAAAAAAA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-608439/65.
 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens.
                                                                                                                                                                                                                                                             16-0CT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention
                                                                                                                                                                                                                            ABP52214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
                                     Matches
                                                                                                                                                        RESULT 26
                                                                                                                                                                        ABP52214
ID ABP
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with an amino acid sequence with tyrosine (Y), lysine (K), and/or value residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral
                                                                                                                                                 Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention describes compositions (I) comprising a peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                   HLA-DR2 molecule binding peptide SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADJ57538 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 30; 54pp; English.
              ABPS2210 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fridkis-Hareli M;
                                                                                                                                                                                                                                                                                                                                                                                                                 24-JAN-2002; 2002WO-US002071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-JAN-2001; 2001US-0263569P
                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-608439/65.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encephalomyelitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strominger JL,
                                                                                                                                                                                                                                                                                                                                          WO200259143-A2
                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                     16-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                01-AUG-2002.
                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention
                                                  ABP52210;
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ADJ57538
ID ADJ57
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ABP5221
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Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative

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WPI; 2003-569005/53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADJ57541;
                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 30
ADJ57541
ID ADJ57
                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                         The invention relates to a vaccine that comprises an active agent from Copolymer 1 (Cop-1), Cop-1 related peptide, Cop-1 related polypeptide or poly-Glu,Tyr. The vaccine comprises the active agent without adjuvant or is emulsified in an adjuvant. The vaccine is useful for reducing disease protection from protection of motor nerve degeneration and/or protection from glutamate toxicity in motor neuron disease e.g. protection from glutamate toxicity in motor neuron disease e.g. mulscular atrophy, progressive pulbar palsy (PBP or bulbar onset). It may be used in combination with another drug e.g. Riluzole for treating motor neuron disease. The non-pathogenic synthetic copolymers protects autoimmunity and thus reduces further injury-induced damage and protects central nervous system cells from glutamate toxicity; protects retinal ganglion cells from glutamate toxicity; protects retinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                             Vaccine useful in the treatment of motor neuron disease e.g. amyotrophic lateral sclerosis and progressive muscular atrophy, comprises copolymer-1 or related peptide or polypeptide, or poly-Glu, Tyr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                            Cop-1; copolymer 1; vaccine; neuroprotective; glutamate toxicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cop-1; copolymer 1; vaccine; neuroprotective; glutamate toxicity;
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1; Mismatches
                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 20; 49pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADJ57547 standard; peptide; 15 AA
                                        Cop-1 related-peptide, SEQ ID 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cop-1 related-peptide, SEQ ID 29
                                                                                                                                                       05-DEC-2002; 2002WO-IL000979.
                                                                                                                                                                            06-DEC-2001; 2001US-0336139P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.08;
                   06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 AFAAAAAAAA 13
                                                                                                                                                                                                 (YEDA ) YEDA RES & DEV
                                                                                                                                                                                                                      Eisenbach-Schwartz M,
                                                                       motor neuron disease.
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                                                                                                                                                                                                                                           WPI; 2003-569005/53.
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Best Local Similarity
                                                                                                              WO2003047500-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15 AA;
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                                                                                                                                    12-JUN-2003
                                                                                            Synthetic
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ADJ57538;
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The invention relates to a vaccine that comprises an active agent from Copolymer I (Cop-1), Cop-1 related peptide, Cop-1 related polypeptide or poly-Glu, Tyr. The vaccine comprises the active agent without adjuvant or is emulsified in an adjuvant. The vaccine is useful for reducing disease progression and/or protection of meter nerve degeneration and/or protection of meter nerve degeneration and/or protection of motor neuron disease e.g. muscular atrophic lateral sclerosis, primary lateral sclerosis, progressive muscular atrophy, progressive bulbar palsy (PBP or bulbar onset). It may be used in combination with another drug e.g. Riluzole for treating motor neuron disease. The non-pathogenic synthetic copolymers protects autoimmunity and thus reduces further injury-induced damage and protects central nervous system cells from glutamate toxicity; protects retinal ganglion cells from glutamate toxicity. The present sequence represents a Cop-1 related-peptide.
                                                                                                                                                                                                                                                                                                                                                                          Vaccine useful in the treatment of motor neuron disease e.g. amyotrophic lateral sclerosis and progressive muscular atrophy, comprises copolymer-1 or related peptide or polypeptide, or poly-Glu, Tyr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 29; 49pp; English.
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05-DEC-2002; 2002WO-IL000979.
                                                                      06-DEC-2001; 2001US-0336139P.
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                                                                                                                                                (YEDA ) YEDA RES & DEV
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                                                                                                                                                                                                                                                                                                WPI; 2003-569005/53.
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peripheral nervous system (e.g. Alzheimer's disease), comprises Copolymer

The invention relates to a vaccine that comprises an active agent from Copolymer I (Cop-1), Cop-1 related peptide, Cop-1 related polypeptide or poly-Glu,Tyr. The vaccine comprises the active agent without adjuvant or is emulaified in an adjuvant. The vaccine is useful for reducing disease progression and/or protection of metor nerve degeneration and/or protection of metor nerve degeneration and/or protection from glutamate toxicity in metor neuron disease e.g. muscular atrophic lateral sclerosis, primary lateral sclerosis, progressive muscular atrophy, progressive bulbar palsy (PBP or bulbar onset). It may be used in combination with another drug e.g. Riluzole for treating motor neuron disease. The non-pathoganic synthetic copolymers protects autoimmunity and thus reduces further injury-induced damage and protects central nervous system cells from glutamate toxicity; protects retinal cop-1 related-peptide. Vaccine useful in the treatment of motor neuron disease e.g. amyotrophic lateral sclerosis and progressive muscular atrophy, comprises copolymer-1 or related peptide or polypeptide, or poly-Glu, Tyr. Disclosure; SEQ ID NO 23; 49pp; English. 

Query Match Best Local Similarity Sequence 15 AA; Matches

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Gaps ö

0; Indels

Score 47; DB 7; Length 15; Pred. No. 1.6; 1; Mismatches 87.0%; 11; Conservative 2 AFAAAAAAAAA 13 3 AYAAAAAAAAA 14 8 셤

ADQ59600 standard; peptide; 15 AA. (first entry) 07-0CT-2004 AD059600; RESULT 31 ADQ59600 

Copolymer 1-related peptide SEQ ID NO:23.

eye-drop vaccine; eye drop; vaccine; immunisation; Copolymer 1; Copolymer 1-related peptide; ophthalmological; neuroprotective; nootropic; antiparkinsonian; anticonvulsant; analgesic; antidabetic; hepatotropic; respiratory; osteopathic; neuronal degeneration; central nervous system; CNS; peripheral nervous system; PNS; glutamate toxicity; spinal cord injury; blunt trauma; haemorrhagic stroke; ischaemic stroke; senile dementia; allatelmer's disease; action disease; motor neuron disease; amyotrophic lateral sclerosis; prion disease; Creutzfeldt-Jakob disease; vitamin deficiency; epilepsy; amnesia; anxiety; autoimmune disease; multiple sclerosis; peripheral neuropathy; retinal disorder; glaucoma.

Synthetic.

WO2004060265-A2.

22-JUL-2004.

07-JAN-2003; 2003US-0438310P.

06-JAN-2004; 2004WO-IL000006.

(YEDA ) YEDA RES & DEV CO LTD

Eisenbach-Schwartz M,

Fulga V;

Bakalash S,

WPI; 2004-543774/52

Eye-drop vaccine for the therapeutic immunization of a mammal against glaucoma and neuronal degeneration caused by a disease in the central or

The present invention describes an eye-drop vaccine (I) for the therapeutic immunisation of a mammal. (I) comprises an active agent selected from Copolymer I, a Copolymer I. related peptide, and a Copolymer cleared from Copolymer II, a Copolymer I. analgeaic, antidiabetic, on cotropic, antiparkinsonian, anticonvulsant, analgeaic, antidiabetic, hepatchtopic, respiratory and costeopathic activities. The eye-drop caused by an injury anticonvulsant, analgeaic, antidiabetic, hepatchtopy and costeopathic activities. The eye-drop caused by an injury of sease, disorder or condition in the Central nervous system (CNS) or peripheral nervous system (CNS) or peripheral nervous system (CNS) for promoting nervo regeneration in the CNS or in the PNS after an injury, disease, disorder or condition or for pretecting CNS and PNS cells from glutamate toxicity, where the injury is contrecoup, haemorrhagic stroke or ischemic stroke, and where the contrecoup, haemorrhagic stroke or ischemic stroke, and where the contrecoup, haemorrhagic stroke or ischemic stroke, and where the clisease is a semile dementia including Alzheimer's disease, and short contractory is palsy, huntington's chorca, a motor neuron disease, and control is disease, huntington's chorca a motor neuron disease including any control is disease, bather disease, including Creutzfeldtakody disease, status epilepsicus, carpal tunnel syndrome, intervertebral disc hermiation, vitamin deficiency such as vitamin deficiency such as vitamin deficiency such as vitamin disease, status epilepsicus, carpal tunnel syndrome, intervertebral curp polypric polymeuropathy, hyperal neuropathy, uremic neuropathy, ordenic ataxic neuropathy, uremic neuropathy, diabetic neuropathy, uremic playman and indisease, acromegaly, mansia, obstructive lung disease, acromegaly, mansia, optively lung disease, acromegaly, mansia, optively lung disease, acromegaly, and lung such as nitrofurantoin, metronidazole, isonizaid and toxing such as alcohol or organophosphates, cherval as associated with a disea abnormally elevated intraocular pressure such as glaucoma. The present sequence represents a copolymer 1 related peptide, which is given in the such as retinal degeneration, or a disease associated with exemplification of the present invention. Disclosure; SEQ ID NO 23; 49pp; English Sequence 15 AA; disorder 

Gaps ö Score 47; DB 8; Length 15; Pred. No. 1.6; 0; Indels Mismatches 87.0%; Local Similarity 91.7 nes 11; Conservative Query Match datches

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2 AFAAAAAAAAA 13

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ADQ59606 standard; peptide; 15 AA. 07-OCT-2004 (first entry) 3 AYAAAAAAAAA 14 ADQ59606; RESULT 32 ADQ59606 셤

eye-drop vaccine; eye drop; vaccine; immunisation; Copolymer 1; Copolymer 1-related peptide; ophthalmological; neuroprotective; nootropic; antiparkinsonian; anticonvulsant; analgesic; antidiabetic; hepatotropic; respiratory; osteopathic; neuronal degeneration; central nervous system; CNS; peripheral nervous system; PNS; dlutamate toxicity; spinal cord injury; blunt trauma; haemorrhagic stroke; ischaemic stroke; senile dementia; Copolymer 1-related peptide SEQ ID NO:29. 

Alzheimer's disease, Parkinson's disease, motor neuron disease, amyotrophic lateral sclerosis, prion disease, Creutzfeldt-Jakob disease, vitamin deficiency; epilepsy; amnesia, anxiety; autoimmune disease, multiple sclerosis, peripheral neuropathy; retinal disorder; glaucoma. S, Fulga V; Bakalash (YEDA ) YEDA RES & DEV CO LTD 06-JAN-2004; 2004WO-IL000006. 07-JAN-2003; 2003US-0438310P. Eisenbach-Schwartz M, WPI; 2004-543774/52. WO2004060265-A2. 22-JUL-2004. Synthetic. 

Eye-drop vaccine for the therapeutic immunization of a mammal against glaucoma and neuronal degeneration caused by a disease in the central or peripheral nervous system (e.g. Alzheimer's disease), comprises Copolymer

Disclosure, SEQ ID NO 29; 49pp; English.

Caused by an injury, disease, disorder or condition in the central nervous system (CNS) or peripheral nervous system (PNS), for preventing nervous system (CNS) or peripheral nervous system (PNS), for preventing or inhibiting neuronal secondary degeneration which may otherwise follow a primary injury in the CNS, for promoting nerve regeneration in the CNS or in the PNS after an injury, disease, disorder or condition or for protecting CNS and PNS cells from glutamate toxicity, where the injury is spinal cord injury, blunt trauma, penetrating trauma, brain coup or contraccoup, hemorrhagic stroke or lachaemic stroke, and where the disease is a senile dementia including Alzheimer's disease, a coup or contraccoup, hemorrhagic stroke or lachaemic stroke, and where the disease is a senile dementia including Alzheimer's disease, a more nerve disease, a more repeated in the contraction in contraction, schorea, a more neuron disease including amyotrophic lateral sclerosis, a prion disease including creutzfeldtusk disease, Alber's disease, Batten disease, Cockaptne syndrome, Lewy body disease, status epilepticus, carpal tunnel syndrome, intervertebral disc herniation, vitamin deficiency such as vitamin B deficiency, cordative stress, opiate tolerance and dependence, an autoimmune disease (e.g. multiple sclerosis), or a peripheral neuropathy, uremic neuropathy, popplycaemia, Sjognen-Larsson syndrome, acute such as amyloid polyneuropathy, diabetic neuropathy, malabsorption syndromes, polycythemia vera, igh and igg gammapathies, complications of such as alcohol or organophosphates, derromedally, independence, and autoimmapathies, porphyrications of various drugs such as nitrofurantoin, metromapathy, age-related macular degeneration, a retinal degeneration, or a disease, ataxia cells of soniared by an retinal degeneration, or a disease, importation, a retinal disease, shark a retinal degeneration, or a disease, importation, a retinal disease, in the contraction of the contraction or contractions or contractions or contractions The present invention describes an eye-drop vaccine (I) for the therapeutic immunisation of a mammal. (I) comprises an active agent selected from Copolymer 1, a Copolymer 1-related peptide, and a Copolymer 1-related polypeptide. (I) has ophthalmological, neuroprotective, nootropic, antiparkinsonian, anticonvulsant, analgesic, antidiabetic, hepatotropic, respiratory and osteopathic activities. The eye-drop vaccine (I) can be used for treating or preventing neuronal degeneration abnormally elevated intraocular pressure such as glaucoma. The present sequence represents a copolymer 1 related peptide, which is given in the exemplification of the present invention.

Sequence 15 AA;

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                    Gaps
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Score 47; DB 8; Length 15;
Pred. No. 1.6;
                   Indels
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0
                   1; Mismatches
87.0%;
                   11; Conservative
         Best Local Similarity
Query Match
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nootropic, antiparkinsonian, anticonvulsant, neuroprocective, nootropic, antiparkinsonian, anticonvulsant, analgesic, antidiabetic, hopatotropic, respiratory and osteopathic activities. The eye-drop vaccine (1) can be used for treating or preventing neuronal degeneration caused by an injury, disease, disorder or condition in the central nervous system (CMS) or peripheral nervous system (CMS) or promoting nerve regeneration in the CMS or inhibiting neuronal secondary degeneration which may otherwise follow or in the PMS after an injury, disease, disorder or condition or for protecting CMS and PMS cells from glutamate toxicity, where the injury is spinal cord injury, blunt trauma, penetrating trauma, brain coup or contrecoup, haemorrhagic stroke or ischaemic stroke, and where the disease is a senile dementia including Alzheimer's disease, a contrecoup, parkinsona including Parkinson's disease, and where the care amyotrophic lateral sclerosis, a prion disease, facial nerve amyotrophic lateral sclerosis, a prion disease, cockayne syndrome, Lewy body disease, status epilepticus, carpal tunñel syndrome, intervertebral disc herniation, vitamin deficiency such as vitamin B deficiency,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eye-drop vaccine for the therapeutic immunization of a mammal against glaucoma and neuronal degeneration caused by a disease in the central or peripheral nervous system (e.g. Alzheimer's disease), comprises Copolymer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copolymer
                                                                                                                                                                                                                                                                                                                                                                               Copolymer 1-related peptide, ophthalmological; neuroprotective; nootropic; antiparkinsonian; anticonvulsant; analgesic; antidabetic; hepatrotropic; respiratory; osteopathic; neuronal degeneration; central nervous system; CNS; peripheral nervous system; PNS; glutamate toxicity; spinal cord injury; blunt trauma; haemorrhagic stroke; ischaemic stroke; senile dementia; Alzhaimer's disease; Parkinson's disease; motor neuron disease; amyotrophic lateral sclerosis; prion disease; Creutzfeldt-Jakob disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vitamin deficiency; epilepsy; amnesia; anxiety; autoimmune disease; multiple sclerosis; peripheral neuropathy; retinal disorder; glaucoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapeutic immunisation of a mammal. (I) comprises an active agent selected from Copolymer 1, a Copolymer 1-related peptide, and a Copol 1-related polypeptide. (I) has ophthalmological, neuroprotective,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention describes an eye-drop vaccine (I) for the
                                                                                                                                                                                                                                                                                                                                                              eye-drop vaccine; eye drop; vaccine; immunisation; Copolymer 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fulga V;
                                                                                                                                                                                                                                                                                                            Copolymer 1-related peptide SEQ ID NO:20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 20; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bakalash S,
                                                                                                                                                                  ADQ59597 standard; peptide; 15 AA.
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                                                                                                                                                                                                                                                                (first entry)
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| AYAAAAAAAAA 15
2 AFAAAAAAAA 13
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                                                                                                                                                                                                                                                              07-OCT-2004
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                                                                                                                                                                                                                 ADQ59597;
                                                                                                                                            ADQ59597
                                                                                                                   RESULT
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stress, opiate tolerance and dependence, an autoimmune disease teress, opiate tolerance and dependence, an autoimmune disease (e.g. multiple sclerosis), or a peripheral neuropathy associated with a disease such as amyloid polymeuropathy, diabetic neuropathy, uremic neuropathy, popplycaemia, Sjogren-Larsson syndrome, acute sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary amyloidosis, obstructive lung diseases, acromegaly, malabsorption syndromes, polycythemia vera, IgA and IgG ammapathies, complications of various drugs such as nitrofurantoin, metronidazole, isoniazid and toxins such as alcohol or organophosphates, Charcot-Marie-Tooth disease, ataxia telangiectasia, Friedreich's ataxia, adernomy-loneuropathy, giant axonal neuropathy, Refsum's disease, Patry's disease, lipoproteinemia, non-arteritic optic neuropathy, age-related macular degeneration, a retinal disonerally elevated intraocular pressure such as glaucoma. The present sequence represents a copolymer 1 related peptide, which is given in the amnesia, anxiety, hyperalgesia, psychosis, seizures, oxidative exemplification of the present invention. %

Sequence 15 AA;

Gaps ö Score 47; DB 8; Length 15; Pred. No. 1.6; 1; Mismatches 0; Indels 87.0%; 91.7%; 11; Conservative Local Similarity Query Match Matches

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2 AFAAAAAAAA 13 AYAAAAAAAA 14

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RESULT 34 ADQ8122

ADQ81224 standard; peptide; 15 AA. ADQ81224; 

(first entry) 21-OCT-2004

Copolymer 1-related peptide SEQ ID NO:20.

pharmaceutical composition; copolymer 1; copolymer 1-related polypeptide; copolymer 1-related peptide; inflammatory bowel disease; antiinflammatory; antiulcer; gastrointestinal; regulatory T cell inducer; Crohn's disease; ulcerative colitis.

Synthetic.

WO2004064717-A2.

05-AUG-2004

20-JAN-2004; 2004WO-IL000054.

2003US-0441136P. 21-JAN-2003; (YEDA ) YEDA RES & DEV CO LTD

WPI; 2004-571593/55.

Aharoni R, Arnon R,

Kayhan B;

Composition useful for the treatment of a patient suffering from an infilammetory bowel disease comprises an active agent selected from copolymer 1, a copolymer 1-related polypeptide, and a copolymer 1-related peptide and a carrier.

Example 2; SEQ ID NO 20; 55pp; English.

an active agent selected from copolymer 1, a copolymer 1-related polypeptide, and a copolymer 1-related peptide and a carrier. Also described is an article of manufacture comprising packaging material and the pharmaceutical composition (preferably containing copolymer 1) contained within the packaging material. The packaging material includes present invention describes a pharmaceutical composition comprising The

ö pharmaceutical composition; copolymer 1; copolymer 1-related polypeptide; copolymer 1-related peptide; inflammatory bowel disease; antiinflammatory; antiulcer; gastrointestinal; regulatory T cell inducer; Crohn's disease; ulcerative colitis. a label that indicates that the agent is used for treating an inflammatory bowel disease. The pharmaceutical composition has antiinflammatory, antiulder and gastrointestinal activities, and can be used as an inducer of regulatory T cells of the Th2 type. It can be used for the treatment of a patient suffering from an inflammatory bowel disease e.g. Crohn's disease and ulcerative colitis. The copolymer 1 binds promiscuously and with high affinity to various classes II MHC molecules of mouse and human origin, and can even displace antigens from the MHC antigen binding groove. In this way, the presentation of other antigens and, consequently, the persistence of inflammatory process, are down regulated. In addition, Copolymer 1 is a potent inducer of regulatory T cells of the Th2 type. The present sequence represents a copolymer 1-related peptide which is used in the exemplification of the Gaps ö Score 47; DB 8; Length 15; Pred. No. 1.6; 0; Indels 1; Mismatches Copolymer 1-related peptide SEQ ID NO:29. ADQ81233 standard; peptide; 15 AA. 21-OCT-2004 (first entry) 14 11; Conservative 2 AFAAAAAAAA 13 3 AYAAAAAAAAA Local Similarity present invention. Sequence 15 AA; ADQ81233; Query Match Matches RESULT 3 ò g

Composition useful for the treatment of a patient suffering from an inflammatory bowel disease comprises an active agent selected from copolymer 1, a copolymer 1-related polypeptide, and a copolymer 1-related Kayhan B; (YEDA ) YEDA RES & DEV CO LTD. 20-JAN-2004; 2004WO-IL000054. 21-JAN-2003; 2003US-0441136P. Aharoni R, Arnon R, WPI; 2004-571593/55. WO2004064717-A2. 05-AUG-2004. Synthetic.

Example 2; SEQ ID NO 29; 55pp; English. peptide and a carrier

The present invention describes a pharmaceutical composition comprising an active agent selected from copolymer 1, a copolymer 1-related peptide, and a copolymer 1-related peptide and a carrier. Also described is an article of manufacture comprising packaging material and the pharmaceutical composition (preferably containing copolymer 1) contained within the packaging material. The packaging material includes a label that indicates that the agent is used for treating an includes inflammatory bowel disease. The pharmaceutical composition has antiinflammatory, antiulcer and gastrointestinal activities, and can be

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pharmaceutical composition; copolymer 1; copolymer 1-related polypeptide; copolymer 1-related peptide; inflammatory bowel disease; antiinflammatory; antiulcer; gastrointestinal; regulatory T cell inducer; Crohn's disease; ulcerative colitis.
used as an inducer of regulatory T cells of the Th2 type. It can be used discase e.g. cron's disease and ulcerative colitis. The copolymer 1 binds promiseuously and with high affinity to various classes II MHC molecules of mouse and with high affinity to various classes II MHC molecules of mouse and human origin, and can even displace antigens from the MHC antigen-binding groove. In this way, the presentation of other antigen-binding groove. In this way, the presentation of other down regulated. In addition, Copolymer 1 is a potent inducer of regulatory T cells of the Th2 type. The present sequence represents a copolymer 1-related peptide which is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an active agent selected from copolymer 1, a copolymer 1-related polypeptide, and a copolymer 1-related peptide and a carrier. Also described is an article of manufacture comprising packaging material and the pharmaceutical composition (preferably containing copolymer 1) contained within the packaging material. The packaging material includes a label that indicates that the agent is used for treating an inflammatory bowel disease. The pharmaceutical composition has antilnflammatory antilocar and gastrointestinal activities, and can be used as an inducer of regularory T calls of the Thi type. It can be used for the treatment of a patient suffering from an inflammatory bowel disease and ulcerative colitis. The copolymer 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a pharmaceutical composition comprising
                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                              Score 47; DB 8; Length 15;
Pred. No. 1.6;
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0
                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copolymer 1-related peptide SEQ ID NO:23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; SEQ ID NO 23; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADQ81227 standard; peptide; 15 AA.
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                                                                                                                                                                                                                                                                              87.0%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                   11; Conservative
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                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                   present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2004064717-A2.
                                                                                                                                                                                                                                         Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-OCT-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADQ81227;
                                                                                                                                                                                                                                                                                                                   Matches
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This invention relates to a novel method for treating or preventing graft rejection. Specifically, it refers to administering at least one copolymer 1 or its related heteropolymer with at least one immunosuppressive drug. The present invention describes the copolymer as containing at least three of the following proups: lysine and arginine; glutamic acid and appartic acid; alanine, glycine and alanine; and tyrosine, tryptophan and phenylalanine. In addition, the immunosuppressive drug is an antiproliferative drug, inhibitor of lymphocyte acitivation, steroid, purine antimetabolite, antibody or immunoaculator. Accordingly, these immunosuppressive compositions can be used for treating or preventing or graft rejection associated with transplantation of cells, tissue or or organs (HiA-matched or mismatched) selected from hematopoietic cells, cremit cells, heart, lung, kidney, liver or skin. The copolymer 1 or its related heteropolymer in combination with other immunosuppressive drugs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treating or preventing graft rejection associated with transplantation of cells, tissue or organs comprises administering combination comprising copolymer 1 or its related heteropolymer with immunosuppressive drug for.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   increases the effectiveness of the drugs at lower dosages, reducing toxic side effects such that they are useful for host-versus-graft (HVG)
                  molecules of mouse and human origin, and can even displace antigens from the MHC antigen-binding groove. In this way, the presentation of other antigens and, consequently, the persistence of inflammatory process, are down regulated. In addition, Copolymer 1 is a potent inducer of regulatory T cells of the Th2 type. The present sequence represents a copolymer 1-related peptide which is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ordered copolymer peptide used to treat graft versus host disease Seq 29
                                                                                                                                                                                                                                                                Gaps
binds promiscuously and with high affinity to various classes II MHC
                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                        Length 15;
                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            graft rejection; immunosuppressive; immunomodulator; graft versus host disease.
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                                                                                                                                                                                                                      Score 47; DB 8
Pred. No. 1.6;
                                                                                                                                                                                                                                                            1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ADW86548 standard; peptide; 15 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sela M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                           present invention.
                                                                                                                                                                               Sequence 15 AA;
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Gaps

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Indels

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Query Match

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Matches

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This invention relates to a novel method for treating or preventing graft rejection. Specifically, it refers to administering at least one copolymer 1 or its related heteropolymer with at least one compositions to resent invention describes the copolymer as containing at least three different amino acids each selected from at containing at least three different amino acids each selected from at cast three of the following groups: lysine and arginine; glutamic acid and aspartic acid; alanine, glycine and alanine; and tyrosine, tryptophan can phroliferative drug, inhibitor of lymphocyte activation, steroid, antiproliferative drug, inhibitor of lymphocyte activation, steroid, curine antimetabolite, antibody or immunomodulator. Accordingly, these immunosuppressive compositions can be used for treating or preventing graft rejection associated with transplantation of cells, tissue or cyans (HiA-matched or mismatched) selected from hematopoietic cells, stem cells, heart, lung, kidney, liver or skin. The copolymer 1 or its increases the effortiveness of the immunosuppressive drugs increases the effortiveness of the immunosuppressive drugs increases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating or preventing graft rejection associated with transplantation of cells, tissue or organs comprises administering combination comprising copolymer 1 or its related heteropolymer with immunosuppressive drug for.
                                                                                                                                                                                                                                                                                                                                                                                           Ordered copolymer peptide used to treat graft versus host disease Seg 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               increases the effectiveness of the drugs at lower dosages, reducing side effects such that they are useful for host-versus-graft (HVG) response, as well as graft-versus-host disease (GVHD). This peptide sequence is an ordered copolymer of the invention.
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Pred. No. 1.6;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      graft rejection; immunosuppressive; immunomodulator;
Pred. No. 1.6;
; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; SEQ ID NO 23; 63pp; English.
                                                                                                                                                                                                                                                     ADW86542 standard; peptide; 15 AA.
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                                                                                                                                                                                                                                                                                                                                                         21-APR-2005 (first entry)
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Best Local Similarity 91.7
Matches 11; Conservative
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                                                                          2 AFAAAAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2005-152159/16.
     Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to a novel method for treating or preventing graft rejection. Specifically, it refers to administering at least one copolymer 1 or its related heteropolymer with at least one immunosuppressive drug. The present invention describes the copolymer as containing at least three different amino acids each selected from at least three of the following groups: lysine and arginine; glutamic acid and abspartic acid; alanine, glycine and alanine; and tyrosine, tryptophan and phenylalanine. In addition, the immunosuppressive drug is an antiproliferative drug, inhibitor of lymphocyte activation, steroid, purine antimerabolite, antibody or immunomodulator. Accordingly, these immunosuppressive compositions can be used for treating or preventing graft rejection associated with transplantation of cells, tissue or crans (HiA-matched or mismatched) selected from hematopoietic cells, stem cells, heart, lung, kidney, liver or skin. The copolymer 1 or its related heteropolymer in combination with other immunosuppressive drugs increases the effectiveness of the drugs at lower dosages, reducing toxic side effects such that they are useful for host-versus-graft (HVG) response, as well as graft-versus-host disease (GVHD). This peptide sequence is an ordered copolymer of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating or preventing graft rejection associated with transplantation of cells, tissue or organs comprises administering combination comprising copolymer 1 or its related heteropolymer with immunosuppressive drug for.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ordered copolymer peptide used to treat graft versus host disease Seg 20.
                                                                                                                                                                                    Gaps
  response, as well as graft-versus-host disease (GVHD). This peptide sequence is an ordered copolymer of the invention.
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                                                                                                                                Length 15;
                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              graft rejection; immunosuppressive; immunomodulator;
                                                                                                                              Score 47; DB 9;
Pred. No. 1.6;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yussim A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.0%; Score 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; SEQ ID NO 20; 63pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                  ADW86539 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sela M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JUL-2003; 2003US-0491236P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JUL-2004; 2004WO-IL000695
                                                                                                                                   87.0%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           graft versus host disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (YEDA ) YEDA RES & DEV CC
(MORR-) MOR RES APPL LTD.
                                                                                                                                                        Local Similarity 91.7 tes 11; Conservative
                                                                                                                                                                                                                                     2 AFAAAAAAAAA 13
                                                                                                                                                                                                                                                               Aharoni R, Arnon R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2005-152159/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2005009333-A2.
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                                                                                  Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-APR-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADW86539;
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RESULT 38
ADM86539
ID ADM86539
XX ADW86
XX DT 21-AP
XX SYNTh
XX SYNTh
XX WO200
XX WO

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Gaps

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lower dosages, reducing toxic

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This peptide represents a peptide derived from Cop 1 (Copolymer 1). This peptide was tested for binding to the peptide binding groove of HLA-DR. The method of the invention for treating a neurodegenerative disorder or disease in which there is accumulation of misfolded and/or aggregated proteins, excluding prion-related diseases, comprises administering to an individual an agent selected from Copolymer 1, a Copolymer 1 related polypeptide, and T cells activated with then. The invention also includes methods for: reducing disease copy protection from glutamate toxicity in a patient suffering from a neurodegenerative disease or disorder selected from Huntington's disease, Alzheimer's disease or disorder selected from Huntington's disease.

Alzheimer's disease and Parkinson's disease, and treating or preventing neurodegenerative and cognitive decline and offsenting from a neurodegenerative disease, Alzheimer's disease or Parkinson's disease.

Specifically, treating a patient suffering from a neurodegenerative comprises immunizing the patient with a vaccine comprising Copolymer 1 for reducing disease progression or for protection from neurodegeneration in the patient. A pharmaceutical composition as administered in the method above, is useful for reducing disease.

Cromprising Copolymer 1 for reducing disease progression or for protection from neurodegeneration in the patient. A pharmaceutical composition as administered in the method above, is useful for reducing disease.

Cromprising corder or protection from neurodegenerative disorder or disease, such as Huntington's disease, Alzheimer's disease or Parkinson's disease. The active agent is useful for reducing a medicament for treatment of neurodegenerative disorder or disease, such as Huntington's disease.

Alzheimer's disease on Parkinson's disease. The active agent is useful for aggregated proteins, excluding prion-related diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treating a neurodegenerative disorder or disease where there is accumulation of misfolded and/or aggregated proteins e.g. Parkinson's disease comprises using an agent e.g. Copolymer 1 or a Copolymer 1-related peptide.
                                                                                                                                                                                                                                    Anticonvulsant; Nootropic; Neuroprotective; Antiparkinsonian; Cop 1; Copolymer 1; HLA-DR; neurodegenerative disease; glutamate toxicity; Huntingtons disease; Alzheimers disease; Parkinsons disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 87.0%; Score 47; DB 9; Length 15; Best Local Similarity 91.7%; Pred. No. 1.6; Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yoles E, Butovsky O, Kipnis J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 20; 63pp; English.
                                          AEA35261 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-NOV-2004; 2004WO-IL001037.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-NOV-2003; 2003US-0518627P. 20-SEP-2004; 2004US-0610966P.
                                                                                                                                         28-JUL-2005 (first entry)
                                                                                                                                                                                      Cop 1 binding motif #20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eisenbach-Schwartz M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2005-372283/38.
                                                                                                                                                                                                                                                                                                                                                                                  WO2005046719-A1.
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                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                          AEA35261;
RESULT 40
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0; Gaps

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AFAAAAAAAAA 13
               3 AYAAAAAAAAA 14
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Search completed: September 9, 2006, 22:48:09 Job time : 99.4177 secs

ribosomal protein achaete-scute locu probable MASH-2 pr

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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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9, 2006, 22:48:41; Search time 13.6709 Seconds (without alignments) 84.457 Million cell updates/sec

1 AAMAAAAAAMA 12 US-10-617-568-2 50 Perfect score: Sequence:

homeoric protein H hypothetical protein for-finger protein E protein kinase C-b gene NKx6.1 protein probable homeobox homeotic protein H bZIP DNA-binding p paired box protein H bZIP DNA-binding p paired box protein homeotic protein homeotic protein homeotic protein homeotic protein homeotic protein e

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 10% Maximum Match 100% Listing first 100 summaries PIR 80: \* 1: pir1: \* 2: pir2: \* 3: pir3: \* 1: pir4: \* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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DB	0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2
Length	85 94 94 94 94 94 94 94 94 95 96 96 96 96 96 96 96 96 96 96	172
% Query Match	82.0 88.0 88.0 88.0 88.0 88.0 88.0 88.0	76.0
Score	女母母母母母母母母母母母母母母母母母母母母母母母	38
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zinc-finger protei basic helix-loop-h phosphatidylinosit transcription fact

polyomavirus enhan

transcription fact
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nitrate reductase
ecdysone-induced p
puff 74E protein DNA-binding protein
dachshund isoform

ovo protein - frui spalt protein - fr hypothetical prote hypothetical prote related to PAN2 pr hypothetical prote

hypothetical prote gene hindsight pro homeotic protein c

eyelid - fruit fly hypothetical prote microtubule-associ

dachshund protein dachshund protein dachshund protein hypothetical prote

stripe a/b protein bumetanide-sensiti bumetanide-sensiti

ALIGNMENTS

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Cyccossion: T03285

RiLee, J.Y.K.; Hodges, T.K.

submitted to the EMBL Data Library, July 1994

A.Description: Genomic DNA sequence of a rice anther-specific gene.

A;Reference number: Z14882

A;Reference number: Z14882

A;Accession: T03285

A;Accession: T03285

A;Accession: T03285

A;Residues: 1-94 cLEBA

A;Residues: 1-94 cLEBA

A;Residues: 1-94 cLEBA

A;Residues: 1-95 cLEBA

A;Residues
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A;Cross.references: UNIPROT:P06602; UNIPARC:UPI000016BBE4; GB:M14767; NID:g157386; PIDN:
A;Accession: B26066
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A;Residues: 1-299,'L',301-376 <FRA>
A;Cross-references: UNIPARC:UPI0000124746; GB:X05138; NID:97957; PIDN:CAA28784.1; PID:97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04213
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cispecies: Drosophila melanogaster
Cipate: 25-Oct-1987 #sequence revision 25-Oct-1987 #text_change 31-Dec-2004
Cipate: 25-Oct-1987 #sequence revision 25-Oct-1987 #text_change 31-Dec-2004
Cipate: 25-Oct-1987 #sequence revision 25-Oct-1987 #text_change 31-Dec-2004
Rimacdonald, P.M.; Ingham, P.; Struhl, G.
Cell 47, 721-734, 1986
A; Title: 1solation, structure, and expression of even-skipped: a second pair-rule gene of the constant of the constan
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A,Residues: 32-268;279-376 <MA2>
A,Cross-references: UNIPARC:UP1000017A27C; UNIPARC:UP1000017A27D; GB:M14767
A;Cross-references: UNIPARC:UP1000017A27C; UNIPARC:UP1000017A27D; GB:M14767
B;Frasch, M.; Hoey, T.; Rushlow, C.; Doyle, H.; Levine, M.
BMBO J. 6, 749-759, 1987
A;Title: Characterization and localization of the even-skipped protein of Drosophila.
A;Reference number: A26636; MUID:87218536; PMID:2884106
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C;Species: Oryza sativa (rice)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
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C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;71-127/Domain: homeobox homology <HOX>
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Pred. No. 79;
1; Mismatches
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Pred. No. 27;
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Matches 10; Conservative
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Best Local Similarity
Matches 10; Conserv
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A,Gene: RTS2
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                                                                                                                                                                                                        hypothetical protein Vng1530h [imported] - Halobacterium sp. NRC-1
C; Species: Halobacterium sp. NRC-1
C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C; Accession: F84106
R; Ng. W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablc Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A; Title: Genome sequence of Halobacterium species NRC-1.
A; Reference number: A04160; MUID:20504483; PMID:11016950
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A;Residues: 1-443 <STE1>
A;Cross-references: UNIPROT:P41225; UNIPARC:UPI000003F546; EMBL:X71135; NID:9468790; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-85 <STO>
A;Cross-references: UNIPROT:Q9HPP9; UNIPARC:UPI0000638F2; GB:AE004437; NID:g10581018;
C;Genetics:
A;Gene: VNG1530H
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A;Molecule type: mRNA
A;Residues: 143-158, P',160-218 <STE2>
A;Cross-references: UNIPARC:UPI0000071C8Ç; EMBL:X71137; NID:g468793; PIDN:CAAS0467.1;
C;Genetics:
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C)Species: Homo sapiens (man)
C)Species: Homo sapiens (man)
C)Accession: 138239; 138242; $67816
R)Stevanovic, M.; Lovell-Badge, R.; Collignon, J.; Goodfellow, P.N.
Hum. Mol. Genet. 2, 2013-2018, 1993
A)ritle: SOX3 is an X-linked gene related to SRY.
A;Reference number: 138239; MUID:94154672; PMID:8111369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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A,Cross-references: GDB:250376; OMIM:313430
A,Amap position: XG2-Kq27
C;Superfamily: human SOX3 protein; HWG box homology
F;136-211/Domain: HMG box homology <HMG>
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Pred. No. 18;
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A,Status: preliminary; translated from GB/EMBL/DDBJ
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anther-specific protein - rice

RESULT 3

352 AAAAAAAAAMS 363

1 AAMAAAAAAMA 12

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Best Local Similarity 83.3 Matches 10; Conservative

Query Match

1100.0%; Pred. ... 0; Mismatches

82.08;

Query Match Best Local Similarity 100. Matches 10; Conservative

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engrailed homeodomain-containing protein En-1 - mouse
N;Alternate names: homeotic protein En-1
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: A48423; 813009; A24778
R;Logan, C.; Hanks, M.C.; Noble-Topham, S.; Nallainathan, D.; Provart, N.J.; Joyner, A.J.A;Title: Cloning and sequence comparison of the mouse, human, and chicken engrailed gen A;Reference number: A48423; MUD:93185339; PMID:1363401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P09065; UNIPARC:UPI00000299A1
A;Experimental source: CD-1, embryo
A;Note: sequence extracted from NCBI backbone (NCBIP:126620)
R;Holland, P.W.H.; Williams, N.A.
FEBS Lett. 277, 250-252, 1990
A;Title: Conservation of engrailed-like homeobox sequences during vertebrate evolution.
A;Reference number: S13009; MUID:91099509; PMID:1980115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Geneë Dev. 1, 29-38, 1987
Aftile: En.1 and En.2, two mouse genes with sequence homology to the Drosophila engrai.
A/Reference number: A91620; MUID:88112776; PMID:2892757
A/Accession: A26629
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A; Residues: 278-401 < JOY>
A; Residues: 278-401 < JOY>
A; COSS-references: UNIPARC:UPI00016CA7C; GB:Y00201; GB:M11987; NID:g49587; PIDN:CAA68: R; JOyner, A.L.; Kornberg, T.; Coleman, K.G.; Cox, D.R.; Martin, G.R.
Cell 43, 29-37, 1985
A; Title: Expression during embryogenesis of a mouse gene with sequence homology to the IA; Reference number: A24778; MUID:86079501; PMID:2416459
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Mol. Cell. Biol. 12, 3967-3977, 1992
A;Title: Sequence analysis reveals homology between two proteins of the flagellar radia
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C;Species: Chlamydomonas reinhardtii
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Oct-2004
C;Accession: B44498
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A;Map position: 1
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
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Pred. No. 83;
1; Mismatches
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A;Molecule type: mucleic acid
A;Molecule type: mucleic acid
A;Residues: 321-380 <HOL>
A;Cross-references: UNIPARC: UPI000017A2AF
B;JOyner, A.L.; Martin, G.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 311-401 <JO2>
A;Cross-references: UNIPARC:UP1000017A2B0
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| Similarity 83.3%;
10; Conservative 1
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A; Residues: 1-401 <LOG>
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C;Species: Homo sapiens (man)
C;Species: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Oct-2004
C;Accession: B48423
R;Logan, C.; Hanks, M.C.; Noble-Topham, S.; Nallainathan, D.; Provart, N.J.; Joyner, A.I.
Dev. Genet. 13, 345-358, 1992
A;Title: Cloning and sequence comparison of the mouse, human, and chicken engrailed gene A;Reference number: A48423; MUID:93185339; PMID:1363401
A;Accession: B48423
A;Status: preliminary; not compared with conceptual translation
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C;Date: 10-Un-1993 #sequence_revision 18-Nov-1994 #text_change 02-Jul-1998
C;Accession: A4443
R;Wainwright, S.M.; Ish-Horowicz, D.
Mol. Cell. Biol. 12, 2475-2483, 1992
A;Title: Point mutations in the Drosophila hairy gene demonstrate in vivo requirements A;Reference number: A44443; MUID:92269819; PMID:1588951
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basic helix-loop-helix transcription repressor H - fruit fly (Drosophila virilis)
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                                                                                        A,Molecule type: DNA
A,Residues: 1-377 <BEV>
A,ECTOGE-references: UNIPROT:Q9TOD3; UNIPARC:UPI000000117B; EMBL:AL049500
A,Experimental source: cultivar Columbia; BAC clone T5C23
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C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;304-360/Domain: homeobox homology <HOX>
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submitted to the Protein Sequence Database, March 1999
A,Reference number: Z15261
                                                                                                                                                                                                                                                                                                         A;Note: T5C23.90
F;60-155/Domain: HSF DNA-binding domain homology <HSF>
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83.3%; Pred. No. 79;
iive 1; Mismatches
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Matches 10; Conservative
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Best Local Similarity
Matches 10; Conserva
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A; Residues: 1-392 <LOG>
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Biochem. Biophys. Res. Commun. 226, 801-809, 1996
A;Title: Members of the MAZ family: A novel CDNA clone for MAZ from human pancreatic isl
A;Reference number: JC5076; MUID:96428591; PMID:8831693
                                                                                                                                                                                            A; Experimental source: pancreatic islet
C; Comment: This protein plays a role in the control of transcriptional initiation of gen
and between the introns of the mouse gene for immunoglobulin M-D.
C; Keywords: phosphoprotein; zinc finger
F;146,204,480/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status pre
F;349/Binding site: phosphate (Tyr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Kania, M.A.; Bonner, A.S.; Duffy, J.B.; Gergen, J.P.
Genes Dev. 4, 1701-1713, 1990
A;Title: The Drosophila segmentation gene runt encodes a novel nuclear regulatory protei
A;Reference number: A36392; MUID:91065517; PMID:2249771
A;Accession: A36392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: UNIPROT: P22814; UNIPARC: UP10000135332; GB: X56432; NID: 98521; PIDN: CA
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C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 05-Nov-1999
C;Accession: 138558
R;Ge, Q.; Nilasena, D.S.; O'Brien, C.A.; Frank, M.B.; Targoff, I.N.
J. Clin. Invest. 96, 1730-1737, 1995
A;Title: Molecular analysis of a major antigenic region of the 240-kD protein of Mi-2. A;Reference number: 138558
A;Accession: 138558
                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-497 <TSU>
A;Cross-references: UNIPARC:UPI0000163B39; DDBJ:D85131; NID:g1752741; PIDN:BAA12728.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C,§pecies: Drosophila melanogaster
C,Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 497;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80.0%; Score 40; DB 2; ilarity 83.3%; Pred. No. 1e+02; Conservative 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                5;
226, 801-809, 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: FlyBase:FBgn0003300
C;Superfamily: transcription factor CBF alpha 2
C;Keywords: transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
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Pred. No.
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Best Local Similarity 83.3
Matches 10; Conservative
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Matches 10; Conserv
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A;Molecule type: DNA
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                                                                                           A; Accession: JC5076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          zincfinger protein MAZ - human (fragment)
NiAlternate names: MYC-associated zinc finger protein MAZ; zinc finger protein ZF87
NiAlternate names: MYC-associated zinc finger protein MAZ; zinc finger protein ZF87
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004
C;Accession: A41170; A46153
R;Pyrc, J.J.; Moberg, K.H.; Hall, D.J.
Biochemistry 31, 4102-4110, 1992
Biochemistry 31, 4102-4110, 1992
A;Title: Isolation of a novel cDNA encoding a zinc-finger protein that binds to two site A;Reference number: A42170; MUID:92232709; PMID:1567856
A;Reference number: A42170
A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Residues: 1-494 < PVR.
A, Residues: 1-494 < PVR.
A, Cross-references: UNIPROT. P56270; UNIPARC: UPI000017C427; GB:J05371
A, Note: it is uncertain whether Met-18 is the initiator or whether translation is initia
B, Bossone, S.A.; Asselin, C.; Patel, A.J.; Marcu, K.B.
R, Bossone, S.A.; Asselin, C.; Patel, A.J.; Marcu, K.B.
Proc. Natl. Acad. Sci. U.S.A. 89, 7452-7456, 1992
P, Title: MAZ, a zinc finger protein, binds to c-MYC and C2 gene sequences regulating tra
A, Reference number: A46153; MUID:92366479; PMID:1502157
                                                                                                                                                 A;Cross-references: UNIPROT:Q01657; UNIPARC:UPI000013521B; GB:M87526; NID:g167435; PIDN:
A;Note: sequence extracted from NCBI backbone (NCBIN:111696, NCBIP:111698)
C;Superfamily: flagellar radial spoke protein
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C;Species: Homo sapiens (man)
C;Dacies: AJan-1997 #sequence_revision 31-Jan-1997 #text_change 05-Nov-1999
C;Accession: JC5076
R;Tsutsui, H.; Sakatsume, O.; Itakura, K.; Yokoyama, K.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Molecule type: mRNA
A,Residues: 18-417,'L',419-494 <BOS>
A,Cross-references: UNIPARC:UPI000012ECF8; GB:M94046
A,Experimental source: HeLa cells
A,ByNote: sequence extracted from NCBI backbone (NCBIN:110666, NCBIP:110667)
C,Keywords: DNA binding; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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            A;Reference number: A44498; MUID:92375065; PMID:1508197
                                                                                                                                                                                                                                                                       Score 40; DB 2; Pred. No. 92; 1; Mismatches
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Pred. No.
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83.3%;
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F;296-318/Region: zinc finger
F;324-346/Region: zinc finger
F;373-405/Region: zinc finger
F;373-405/Region: zinc finger
F;409-430/Region: zinc finger
F;452-468/Region: alanine-rich
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116 AAAAAAAAA 127
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F,174-183/Region: alanine-rich
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Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                                                         A; Residues: 1-459 < CUR>
                                          A,Accession: B44498
A,Status: preliminary
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
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A;Title: The Drosophila gene Hairless encodes a novel basic protein that controls alter:
A;Reference number: A44067; MUID:92387549; PMID:1516831
A;Accession: A44067
                                                                                                A;Molecule type: DNA
A;Residues: 19-1077 cBAN>
A;Cross-references: UNIPROT:Q02308; UNIPARC:UPI000002AB24; GB:M95192; NID:g157621; PID:
A;Note: sequence extracted from NCBI backbone (NCBIN:112622, NCBIP:112623)
                                                                                                                                                                                                                       R;Preiss, A.
submitted to the EMBL Data Library, May 1994
A;Description: Hairless, a Drosophila gene involved in neural development, encodes a no
A;Reference number: A58929
                                                                                                                                                                                                                                                                                                                                                                        A;Rolecule type: mRNA
A;Residues: 1-1077 <PRE>
A;Coss-references: UNIPARC:UPI000012C93C; EMBL:X67239; GB:S49642; NID:g578331; PID:g578
A;Cross-references: UNIPARC:UPI000012C93C; EMBL:X67239; GB:S49642; NID:g578331; PID:g578
B;Maier, D.; Stumm, G.; Vunn, K.; Preiss, A.
Mech. Dev. 38, 143-156, 1992
A;Title: Hairless, a Drosophila gene involved in neural development, encodes a novel, saperence number: S33412; MUID:93041287; PMID:1419850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       displaying segment formation protein pumilio - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Ja-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: A46221; S22026
C;Accession: A46221; S22026
B;Barker, D.D.; Wang, C.; Moore, J.; Dickinson, L.K.; Lehmann, R.
Genes Dev. 6, 2312-2336, 1992
A;Title: Pumilio is essential for function but not for distribution of the Drosophila all A;Reference number: A46221; MUID:93093466; PMID:1459455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Accession: MA6221
A Status: preliminary
A Status: preliminary
A Status: preliminary
A Status: preliminary
A Molecule Lype: mRNA
A Residues: 1-1533 *BAR>
A Cross-references: UNIPROT: P25822; UNIPARC: UPI000016BD14; GB:L07943; NID: G158190; PID: A Cross-reference extracted from NCBI backbone (NCBIN:120203, NCBIP:120204)
A;Note: sequence extracted from NCBI backbone (NCBIN:120203, NCBIP:120204)
B;Nacdonald, P.M.
A;Reference number: S22026
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-361, A, 363-1102, R', 1104-1405, KN', 1408-1495, VV', 1497-1518, S', 1520-1533
A;Cross-references: UNIPARC: UPI00001329FD; EMBL: X62589; NID: G8393; PID: G8394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Reaidues: 1-150,'A',152-701,'LL',704-890,'R',892-963,'RLLP',968-973,975-1077 <MAI>
A;Cross-references: UNIPARC:UP1000017BED1; EMBL:X67239
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Pred. No. 1.8e+02;
1; Mismatches 1; Indels
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Pred. No. 2.4e+02;
1; Mismatches 1; Indels
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A,Cross-references: FlyBase:FBgn0003165
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1050 AAVAAAAAAAA 1061
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Best Local Similarity 83.3
Matches 10; Conservative
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                              A; Accession: A58929
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                                                                                                                                                                                                          finger protein sob - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Spacession: S72227
R;Hart, M.C.; Wang, L.; Coulter, D.E.
Genetics 144, 171-182, 1996
A;Title: Comparison of the structure and expression of odd-skipped and two related genes
A;Reference number: S72227; MUID:97032935; PMID:8878683
A;Reference number: S72227; MUID:97032935; PMID:8878683
A;Reference number: S72277, MUID:97032935; PMID:8878683
A;Residues: 1-577 < HARS
A;Residues: 1-577 < HARS
A;Residues: 1-577 < HARS
A;Cross-references: UNIPROT:Q24571; UNIPARC:UPI000007A28D; EMBL:U62004; NID:g1480193; PI
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A;Residues: 1-892 <TAP>
A;Cross-references: UNIPROT:070254; UNIPARC:UPI0000027BF6; EMBL:AF030131; NID:g3002587;
A;Experimental source: cell line Ras-transformed NIH 3T3 cells
A;Note: activates JNK/SAPK cascade; Rac-binding protein
C;Genetics:
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Serine-rich protein hairless - fruit fly (Drosophila melanogaster)

serine-rich protein hairless - fruit fly (Drosophila melanogaster)

Sylternate names: 109K basic protein H

C;Species: Drosophila melanogaster

C;Date: 10-Jun-1993 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004

C;Accession: A44067; A5980459; $33412; $24639

Genes Dev. 6, 1752-1769, 1992
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09071
ER;Tapon, N.; Nagata, K.; Lamarche, N.; Hall, A.
EMBO J. 17, 1395-1404, 1998
A;Reference number: Z16552; MUID:98151363; PMID:9482736
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83.3%; Pred. No. 1.6e+02;
iive 1; Mismatches 1; Indels
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83.3%; Pred. No. 1.1e+02;
ive 1; Mismatches 1; Indels
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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SH3 domains-containing protein POSH - mouse
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C;Keywords: signal transduction
F;8-58/Domain: RING finger homology <RRN>
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A.Gene: sob
A.Cross-references: FlyBase:FBgn0004892
C.Keywords: zinc finger
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Best Local Similarity 83.3
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419 AAVAAAAAAAA 430
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Best Local Similarity 83.3
Matches 10; Conservative
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273 AAVAAAAAAAA 284
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87 AAVAAAAAAAA 98
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Rianonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A.Fitle: Genome sequence of the nematode C. elegans: a platform for investigating biolog A.Fitle: Genome sequence of the nematode C. elegans: a platform for investigating biolog A.Reference number: A75000; MUID:99069613; PMID:9851916
A.Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_ganger.ac.uk/Projects/C_ele A.Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A.Accession: D88395
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 200

A;Authors: Hunder, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C., Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Rer, M.; Wu, D.; Yu, G.; Praser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A;Reference number: A66141; MUID:21016719; PMID:11130712
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A;Cross-references: UNIPROT:Q05196; UNIPARC:UPI00001311AE; GB:AE005173; NID:97239504; PI
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C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: A36391; A33106; S13514
R;Smoller, D.; Friedel, C.; Schmid, A.; Bettler, D.; Lam, L.; Yedvobnick, B.
Genes Dev. 4, 1688-1700, 1990
A;Title: The Drosophila neurogenic locus mastermind encodes a nuclear protein unusually
A;Reference number: A36391; MUID:91065516; PMID:1701150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:017222; UNIPARC:UPI000017A5BC; GB:chr_III; PIDN:AAB70991.1;
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C;Superfamily: polyadenylate-binding protein; ribonucleoprotein repeat homology
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
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Pred. No. 1.7e+02;
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| AAVAAAAAAEA 38
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Best Local Similarity
Matches 10; Conserv
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A; Residues: 1-451 <STO>
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                                                                                                                                                                            N.Alternate names: membrane protein fsh, 205K
N;Contains: female sterile homeotic protein, 110K
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 03-Mar-1993 #text_change 31-Dec-2004
C;Accession: A43742; B43742
R;Haynes, S.R.; Mozer, B.A.; Bhatia-Dey, N.; Dawid, I.B.
Dev. Biol. 134, 246-257, 1989
A;Title: The Drosophila fsh locus, a maternal effect homeotic gene, encodes apparent mem A;Reference number: A43742; MUID:89276730; PMID:2567251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Molecule type: mRNA
*Residues: 1-2038 - HAY>
A;Cross-references: UNIPROT:P13709; UNIPARC:UPI000012AC6C; EMBL:M23221; NID:g157452; PIC
A;Accession: B43742
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A;Experimental source: strain A3(2)
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                                                                                                                                              female sterile homeotic protein, 205K - fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Keywords: alternative splicing; transmembrane protein
C;Keywords: alternative splicing; transmembrane protein
F;1-2038/Product: female sterile homeotic protein, 205K #status predicted
F;59-116/Product: female sterile homeotic protein, 110K #status predicted
F;59-116/Domain: bromodomain homology <BRO1>
F;503-560/Domain: bromodomain homology <BRO2>
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Pred. No. 3e+02;
1; Mismatches 1; Indels
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A;Molecule type: mRNA
A;Residues: 1-1106 «HA2>
A;Cross-references: UNIPARC:UPI000017A10F; EMBL:M23222
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Pred. No. 90;
1; Mismatches
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A;Gene: SCOEDB:SC4H2.30
C;Superfamily: ADP-ribosylglycohydrolase
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A,Gene: fsh
A,Cross-references: FlyBase:FBgn0004656
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Best Local Similarity 83.3%;
Matches 10; Conservative
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330 AAVAAAAAAAA 341
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Matches 9, Conservative
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165 AMAVAAAAALA 175
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A;Status: preliminary
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A;Molecule type: mRNA
A;Residues: 1-91 - GGUJ-
A;Cross-references: UNIPROT:P07835; UNIPARC:UPI0000125B4B; GB:M10148; NID:g213579; PIDN
R;Gauthier, S.; Wu, Y.; Davies, P.L.
                                                                                                                          homeotic protein ultrabithorax homolog - Junonia coenia (fragment)
N;Alternate names: ultrabithorax homeodomain protein
N;Species: Junonia coenia
C;Decession: S58853
S;Marren, R.W.; Nagy, L.; Selegue, J.; Gates, J.; Carroll, S.
Nature 372, 458-461, 1994
A;Title: Evolution of homeotic gene regulation and function in flies and butterflies.
A;Reference number: S58850; MUID:95075456; PMID:7840822
A;Accession: S58853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antifreeze protein 4 precursor - winter flounder ("Species: Pseudopleuronectes americanus (winter flounder)
C;Species: Pseudopleuronectes americanus (winter flounder)
C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
C;Accession: A03193
R;Lin, Y.; Gross, J.K.
Proc. Natl. Acad. Sci. U.S.A. 78, 2825-2829, 1981
Proc. Natl. Acad. Sci. U.S.A. 78, 2825-2829, 1981
A;Title: Molecular cloning and characterization of winter flounder antifreeze cDNA.
A;Reference number: A03193; MUID:81247379; PMID:6265915
                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-40 - WARS.
A;Cross-references: UNIPROT:Q25210; UNIPARC:UPI000017A2FE; EMBL:L42137
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1995
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
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C; Species: Pseudopleuronectes americanus (winter flounder)
C; Species: Pseudopleuronectes americanus (winter flounder)
C; Date: 05-00cr-1988 #text_change 09-Jul-2004
C; Date: 05-00cr-1988 #text_change 09-Jul-2004
C; Accession: A22592; S12604
R; Gourlie, B.; Lin, Y.; Price, J.; De Vries, A.L.; Powers, D.; Huang, R.C.C.
J. Biol. Chem. 259, 14960-14965, 1984
A; Title: Winter flounder antifreeze proteins: a multigene family.
A; Reference number: A22592; MUID:85084993; PMID:6548752
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C;Superfamily: antifreeze protein
C;Keywords: antifreeze
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-85/Product: antifreeze protein 4 #status predicted <MAT>
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Pred. No. 45;
0; Mismatches
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Best Local Similarity 83.3
Matches 10; Conservative
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Matches 10; Conservative
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C; Species: Drosophila melanogaster
C; Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C; Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C; Accession: T13-Aug
R; Sinclair, D.A.R.; Milne, T.A.; Hodgson, J.W.; Shellard, J.; Salinas, C.A.; Kyba, M.; R
Development 125, 1207-1216, 1998
A; Title: The Additional sex combs gene of Drosophila encodes a chromatin protein that bi
A; Reference number: 217750; MUID: 98146384; PMID: 9477319
A; Accession: T13748
A;Ačcession: A36391
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1596 <SMO>
A;Cross-references: UNIPROT:P21519; UNIPARC:UP1000012EB74; GB:X54251; NID:g8203; PIDN:CA
A;Note: strain Canton S
C;Genetics:
A;Genetics: RiyBase:mam
A;Cross-references: FlyBase:FBgn0002643
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C;Species: Drosophila virilis
C;Species: Drosophila virilis
C;Species: Drosophila virilis
C;Accession: T13998
R;Newfeld, S.J.; Tachida, H.; Yedvobnick, B.
J, Mol. Evol. 38, 637-641, 1994
A;Title: Drive-selection equilibrium: homopolymer evolution in the Drosophila gene maste
A;Reference number: Z17850; MUID:94365848; PMID:8083889
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A;Cross-references: UNIPARC:UPI00000760FA; EMBL:AJ001164; NID:g3292938; PIDN:CAA04568.1;
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Pred. No. 3.3e+02;
0; Mismatches 2
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A;Residues: 1-1655 <NEW>
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Best Local Similarity 83.3%;
Matches 10; Conservative
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Best Local Similarity
Matches 10; Conserv
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R; Tanaka, M.; Tanaka, T.; Harata, M.; Suzuki, T.; Mitsui, Y.
Biochem. Biophys. Res. Commun. 243, 531-537, 1998
A; Title: Triplet repeat-containing ribosomal protein L14 gene in immortalized human endo
A; Reference number: JC5954; MUID:98153799; PMID:9480843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: S28186
R;del Amo, F.F.; Gendron-Maguire, M.; Swiatek, P.J.; Gridley, T.
Biochim. Biophys. Acta 1171, 323-327, 1993
A;Title: Cloning, sequencing and expression of the mouse mammalian achaete-scute homolog
A;Reference number: S28186; MUID:93144349; PMID:8424959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-231 <AMO>
A;Cross-references: UNIPROT:Q02067; UNIPARC:UPI000000BE1; GB:M95603; NID:g193875; PIDN:
C;Keywords: DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable MASH-2 protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: 811563
R;Johnson, J.E.; Birren, S.J.; Anderson, D.J.
Nature 346, 858 861, 1990
A;Title: Two rat homologues of Drosophila achaete-scute specifically expressed in neuror A;Reference number: 811562; MUD1:90363294; PMID:2392153
A;Accession: 811563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPARC:UPI000004E622; DDBJ:D87735; NID:g1620021; PIDN:BAA13443.1; C;Superfamily: rat ribosomal protein L14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 achaete-scute locus protein homolog MASH-1 - mouse
NiAlternate names mammalian achaete-scute homolog 1
C:Species: Mus musculus (house mouse)
C:Species: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                      C.Species: Homo sapiens (man)
C.Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Sep-2000
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Pred. No. 99;
0; Mismatches
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                                                             146 AAAAAAAAAA 157
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Best Local Similarity 83.3
Matches 10; Conservative
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                         1 AAMAAAAAAMA 12
                                                                                                                                                                                                                  ribosomal protein L14 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-220 < TAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: S28186
A;Status: preliminary
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A;Residues: 1-63,'V',65-91 <GAU>
A;Cross-references: UNIPARC:UP10000001382; EMBL:X53718; NID:g64213; PIDN:CAA37754.1; PID
C;Genetics:
A;Introns: 19/2
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A;Residues: 1-172 <TUC>
A;Cross-references: UNIPROT;Q60586; UNIPARC:UPI00000E671C; GB:L29542; NID:g496161; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sex-determining protein Sry - multimammate rat (Mastomys hildebrantii)
C;Species: Mastomys hildebrantii
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Oct-2004
C;Accession: S35568
R;Tucker, P.K.; Lundrigan, B.L.
Nature 364, 715-717, 1993
A;Title: Rapid evolution of the sex determining locus in Old World mice and rats.
A;Reference number: S35565; MUID:93361118; PMID:8355784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C;Accession: T12547
R;Ottenwaelder, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. Biottenwaelder, B.; Obermaier, B.; Mewes, June 1999
A;Reference number: Z17528
A;Reference number: Z17528
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-150 <OTT>
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A;Experimental source: adult uterus; clone DKFZp586E1621
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Nucleic Acids Res. 18, 5303, 1990
A,Title: Nucleotide sequence of a variant antifreeze protein gene.
A,Reference number: S12604; MUID:90384854; PMID:2402466
                                                                                                                                                                                                                                                                  C;Keywords: antifreeze; tandem repeat
C;Keywords: antifreeze; tandem repeat
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-91/Product: antifreeze protein IIA7 #status predicted <MAT>
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Pred. No. 79;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                   Score 38; DB 2; Length 91;
Pred. No. 48;
0; Mismatches 2; Indels
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Pred. No. 70;
0; Mismatches
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C,Keywords: DNA binding
F,2-77/Domain: HMG box homology <HMG1>
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83.3%;
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ilarity 83.3%;
Conservative (
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Best Local Similarity 83.3%;
Matches 10; Conservative
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Best Local Similarity
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Best Local Similarity
Matches 10; Conserva
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A,Note: DKFZp586E1621.1
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Mech. Dev. 50, 177-186, 1995

A; Title: Gsh-2, a murine homeobox gene expressed in the developing brain.
A; Reference number: IS7039; MUID: 95344993; PMID: 7619729
A; Reference number: IS7039
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-305 < RES>
A; Cross-references: UNIPARC: UPI0000024E69; GB: S79041; NID: 91042008; PIDN: AAB34947.1; PII
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Yokoyama, M.; Nishi, Y.; Yoshii, J.; Okubo, K.; Matsubara, K.
MAR Res. 3, 311-320, 1996
A;Title: Identification and cloning of neuroblastoma-specific and nerve tissue-specific A;Reference number: JC5272; MUID:97191543; PMID:9039501
A;Contents: neuroblastma cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q99453; UNIPARC:UP10000131D16; DDBJ:D82344; NID:g1841337; P:
CCOmment: This protein is a transcriptional repressor involved in regulating gene expri
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;99-155/Domain: homeobox homology «HOX»
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C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 05-Oct-2004
C;Accession: S16318; 840403; $57443
R;Izpisua-Belmonte, J.C.; Falkenstein, H.; Dolle, P.; Renucci, A.; Duboule, D.
R;Izpisua-Belmonte, J. 2239-2289; J991
A;Title: Murine genes related to the Drosophila AbdB homeotic gene are sequentially exp. A;Reference number: S16317; MUID:91293104; PMID:1676674
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A;Cross-treferences: UNIPROT:P23813; UNIPARC:UPI0000029F10; EMBL:X60761; NID:g51420; PIDI
R;Gerard, M.; Duboule, D.; Zakany, J.
EMBO J. 12, 3539-3550, 1993
A;Title: Structure and activity of regulatory elements involved in the activation of the A;Reference number: $40403; MUID:94074553; PMID:7902810
A;Accession: $40403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 paired type homeobox protein, NBP - human
C;Species: Homo sapiens (man)
C;Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 05-Oct-2004
C;Accession: JC5273
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C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;204-260/Domain: homeobox homology <HOX>
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                                                                                                                                                                                                                                                                                                                                                                                                                             Score 38; DB 2; Length 305;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
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N,Alternate names: homeotic protein Hoxd-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Accession: JC5273
A,Status: nucleic acid sequence not shown
A,Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 AAAAAAAAAA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 83.3
Matches 10; Conservative
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Best Local Similarity 83.3
Matches 10; Conservative
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C;Species: How sapiens (man)
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
C;Accession: A48279
R;Ball, D;W; Azzoli, C.G.; Baylin, S.B.; Chi, D.; Dou, S.; Donis-Keller, H.; Cumaraswam
Proc. Natl. Acad. Sci. U.S.A. 90, 5648-5652, 1993
A;Title: Identification of a human achaete-scute homolog highly expressed in neuroendocr
A;Reference number: A48279; MUID:93296195; PMID:8390674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Mis muscules (house mouse)
C;Species: Mis muscules (house mouse)
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
C;Accession: A4552
R;Izpisus Belmonte, J.C.; Dolle, P.; Renucci, A.; Zappavigna, V.; Falkenstein, H.; Dubou Development 110, 733-745, 1990
A;Title: Primary structure and embryonic expression pattern of the mouse Hox-4.3 homeobc A;Reference number: A4562; MUID:91209232; PMID:1982431
A;Accession: A43562
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
   A;Cross-references: UNIPROT:P19359; UNIPARC:UP10000047567; EMBL:X53725; NID:g56630; PIDN
C;Keywords: DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Cross-references: UNIPROT:P50553; UNIPARC:UP10000047566; GB:L08424; NID:g306459; PID:g
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C;Species: Mus sp. (mouse)
C;Species: O.2 Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Oct-2004
C;Accession: I57039
R;Hsieh-Li, H.M.; Witte, D.P.; Szucsik, J.C.; Weinstein, M.; Li, H.; Potter, S.S.
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A,Residues: 1-289 - KIZP-
A,Cross-references: UNIPROT:P23463; UNIPARC:UPI0000177DA6
C;Superfamily: homeotic protein Hox A7; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;196-252/Domain: homeobox homology <HOX>
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                                                                                                   Length 233
                                                                                                                                                                  2; Indels
                                                                                               Score 38; DB 2;
Pred. No. 1e+02;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                            Query Match 76.0%;
Best Local Similarity 83.3%;
Matches 10; Conservative
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homeotic protein Hox D8 - mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-238 <RES>
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Gaps

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Length 331;

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C;Accession: A39065
R;D'Esposito, M; Morelli, F.; Acampora, D.; Migliaccio, E.; Simeone, A.; Boncinelli, E. Bononics 10, 43-50, 1991
A;Title: EVX2, a human homeobox gene homologous to the even-skipped segmentation gene, i A;Reference number: A39065; MUID:91257849; PMID:1675198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 31-Dec-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: 2q24.3-2q31
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;46-102/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; not compared with conceptual translation
A;Note: sequence extracted from NCBI backbone (NCBIP:119832)
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Pred. No. 1.3e+02;
                                                                        Score 38; DB 2; I Pred. No. 1.3e+02;
                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: GDB:EVX2
A;Cross-references: GDB:127528; OMIM:142991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: UNIPARC: UPI000017A29D
                                                                                                                                                                                                                                                                                                                                                                                                                                                  homeotic protein EVX2 - human (fragment)
                                                                           76.0%;
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                                                                               Query Match 76.0
Best Local Similarity 83.3
Matches 10; Conservative
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Matches 10; Conservative
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A;Residues: 1-333 <DAE>
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AB1781

hypothetical protein lin2792 [imported] - Listeria innocua (strain Clip11262)

C; Species: Listeria innocua

C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C; Accession: AB1781

C; Accession: AB1781

C; Janser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.

D; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlucter, T.; Simose, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Title: Comparative genomics of Listeria species.

A; Accession: AB1781

A; Accession: AB1781

A; Accession: AB1781

A; Accession: AB1781

A; Residues: preliminary

A; Molecule type: DNA

A; Residues: 1-228 AG18-1;

A; Residues: 1-
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B47236
Zinc-finger protein Pur-1 - golden hamster
Zinc-finger protein Pur-1 - golden hamster)
C;Species: Mesocricetus auratus (golden hamster)
C;Species: Mesocricetus auratus (golden hamster)
C;Species: 1-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 05-Apr-1995
C;Accession: B47236
R;Kennedy, G.C.; Rutter, W.J.
A;Reference auraber: A7236; MUID: 93087555; PMID: 1454839
A;Reference number: A7236; MUID: 93087555; PMID: 1454839
A;Accession: B7236
A;Accession: B7236
A;Accession: B7236
A;Residues: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-331 < KEN>
A;Residues: UNIPARC: UPI000017C615
A;Experimental source: insulinoma cell line T
                               A;Cross-references: UNIPROT:Q927J6; UNIPARC:UPI0000CC998; GB:AL592022; PIDN:CAC98018.1; A;Experimental source: strain Clip11262 C;Genetics:
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C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;252-308/Domain: homeobox homology <HOX>
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Pred. No. 1.3e+02;
2; Mismatches 1; Indels
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Pred. No. 1.3e+02;
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Best Local Similarity 75.0
Matches 9; Conservative
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Best Local Similarity
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091j04
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0382w8
07ggr6
076550
09tvt5
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09FR09 MAIZE
09FR09 MAIZE
07VU06_BORPE
07W473_BORPA
06N082_HUWAN
04 PEI8_USTMA
07SBF2_IT_TETUG
07SBF2_NET_ITETUG
07SBF2_NET_ITETUG
09826_CERAE
HSF7_ARATH
09826_CERAE
HSF7_ARATH
09826_CERAE
HWAIR DROVI
09826_CHAGNAN
04264_HUWAN
04264_HUWAN
04867_HUWAN
09VE69_DROME
09VE69_DROME
PHLPP_HUMAN
040629_ORYSA
09D513_SCHJA
091102_ORYSA
091102_ORYSA
062RT9_ORYSA
02XYH3_DROYA
02XYH3_DROYA
02XYH3_DROYA
02XYH3_DROYA
033A26_ORYSA
065279_ORYSA
065279_ORYSA
065279_ORYSA
095279_CRYSA
095279_CRYSA
096UP9_HUMAN
06CFV6_YARLI
08RYYI_ORYSA
07X6T2_ORYSA
07X6T2_ORYSA
06B6NB_DIDMA
06CRV6_YARLI
08RXYI_ORYSA
07X6T2_ORYSA
06CRV6_YARLI
08RXYI_ORYSA
07X6T2_ORYSA
06CRV6_HUMAN
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060067_9PBRC
07XVH0_0RYSA
06P6C2_HUMAN
RSP6_CHLRE
MAZ_HUMAN
097600_RABIT
091.004_0RYSA
08NFN7_HUMAN
0332248_ACHDO
070386_ANOGA
076550_DROSI
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          GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                          2849598
                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                     2849598 seqs, 925015592 residues
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07XTVE_ORYSA
031UK64 MOUSE
031UG18 MOUSE
031UG18 MOUSE
061UG6_DROME
061UG6_DROME
061UG6_DROME
061UM17_DROME
0703Z9_THETE
0703Z9_THETE
0703Z9_THETE
0703Z9_THETE
0703Z9_THETE
0703Z9_THETE
0703Z9_THETE
070Z0K76_WHEAT
020K76_WHEAT
020K76_WHEAT
020K76_WHEAT
020K76_WHEAT
020K76_WHEAT
020K71_MOUSE
060KF1_MOUSE
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050M4_ORYSA
055KF1_ORYSA
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Q7FV80 ANOGA
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Maximum Match 100%
Listing first 100 summaries
                                               protein search, using sw model
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STRAIN=Taiwan;
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MEDLINE=2239451; PubMed=12504569; DOI=10.1006/viro.2002.1696;
Lin S.T., Chang Y.S., Wang H.C., Tzeng H.F., Chang Z.F., Lin J.Y.,
Wang C.H., Lo C.F., Kou G.H.;
"Ribonucleotide reductase of shrimp white spot syndrome virus (WSSV):
expression and enzymatic activity in a baculovirus/insect cell system
and WSSV-infected shrimp.";
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDILINE=21844071; PubMed=11853398; DOI=10.1006/viro.2001.1273; Chen L.L., Leu J.H., Huang C.J., Chou C.M., Chen S.M., Wang C.H., Lo C.F., Kou G.H.; Identification of a nucleocapsid protein (VP35) gene of shrimp white spot syndrome virus and characterization of the motif important for targeting VP35 to the nuclei of transfected insect cells.";
                                                                                                                                                                                                                                                                                         STRAIN=Talwan;
MEDLINE=20517548; PubMed=11062040; DOI=10.1006/viro.2000.0597;
Tsai M.F., Yu H.T., Tzeng H.F., Leu J.H., Chou C.M., Huang C.J.,
Wang C.H., Lin J.Y., Kou G.H., Lo. C.F.;
Indentification and characterization of a shrimp white spot syndrome virus (WSSV) gene that encodes a novel chimeric polypeptide of cellular-type thymidine kinase and thymidylate kinase.";
Virology 277:100-110(2000).
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Tzeng H.F., Chang Z.F., Peng S.E., Wang C.H., Lin J.Y., Kou G.H.,
                                                                                                                 White spot syndrome virus (WSSV).
Viruses; dsDNA viruses, no RNA stage; Nimaviridae; Whispovirus.
NCBI_TaxID=92652;
                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
MEDLINE=21548311; PubMed=11689662;
DOI=10.1128/4V1.75.23.11811-11820.2001;
Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
"Complete genome sequence of the shrimp white spot bacilliform
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PubMed=15452257; DOI=10.1128/JVI.78.20.11360-11370.2004;
                                                                 UniProtKB/TrEMBL.
                                        82 AA.
                                        PRT;
                                                                01-MAR-2002, integrated into Uni
01-MAR-2002, sequence version 1.
                                                                                                                                                                                                                                                     Virol. 75:11811-11820(2001).
                                                                                       entry version 12.
                                        PRELIMINARY;
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                                                                                          07-FEB-2006,
                                       QBVAT5_WSSV
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STRAINECSTBL/60; TISSUE=Thymus;
PubMed=16141072; DOI=10.1126/science.1112014;
PubMed=16141072; DOI=10.1126/science.1112014;
PubMed=16141072; DOI=10.1126/science.1112014;
PubMed=16141072; DOI=10.1126/science.112014;
PubMed=16141072; DOI=10.1126/science.112014;
Paris Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Bajic V.B., Allen J.E., Allen J.E., Allen J.E., Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L., Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., Chiw K.P., Choudhary V., Christoffels A., Clutterbuck D.R., Chalk B., Dallymple B.P., de Bono B., Della Gatta G., di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Euarchontoglires, Glires, Rodentia, Sciurognathi;
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6J; IISSUE=Thymus;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
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                                                       "Genomic and proteomic analysis of thirty-nine structural proteins shrimp white spot syndrome virus."; J. Virol. 78:11360-11370(2004).
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                                                                                                                                                                                                                                                                                                                                                                                              "The unique stacked rings in the nucleocapsid of the white spot
syndrome virus virion are formed by the major structural protein
VP664, the largest viral structural protein ever found.";
J.M., Wang H.C., Leu J.H., Hsiao H.H., Wang A.H., Kou G.H.,
                                                                                                                                                                                                                                                                    STRAIN=Taiwan;
PubMed=15596810; DOI=10.1128/JVI.79.1.140-149.2005;
Leu J.H., Tsai J.M., Wang H.C., Wang A.H., Wang C.H., Kou G.H.,
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Pred. No. 35;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LO C.-F., Kou G.-H., Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF7E4C81AAF27D44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-OCT-2005, integrated into UniProtKB/TrEMBL
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"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
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EMBL; AF440570; AAL89228.1; -; Genomic_DNA.
SEQUENCE 82 AA; 8635 MW; AF7E4C81AAF27D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Virol. 79:140-149(2005).
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A FIGECRET C.F., FWINGSTHME T., FURTHON M., FULTALA S., GARIDDIGIA M., A GEOTGHI C.F., FWINGSTHME T., Groon M., FULTAL S., Green R. B., Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N., Alli D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T., Alli D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T., Alli M., Kanapin A., Katehnan S.P., Kruger A., Kummerfeld S.K., Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Liuni S., McHiliam S., Madan Babu M., Madera M., Marchionni L., Alliano H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K., Mortagui-Tabar S., Miki H., Mignone F., Miyake S., Morris K., Mottagui-Tabar S., Miki H., Mishikawa S., Nori F., Onlara O., Akazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G., Petrovsky N., Piazza S., Reed J. Reid J.F., Ring B.Z., Ringwald M., Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Shonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Shong Y., Sibata Y., Stukaa B., Stutana R., Takanaka Y., Taki K., Tamanoja K., Tan S.L., Tanglor M.S., Tegner J., Teichmann S.A., Udda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K., Tan S.L., Tang S., Tamper C., Yagi K., Tansanishi H., Zabarovsky E., Zhu S., Zimmer A., Hade W., Bult C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., Kukida S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., Alda J., Imamura K., Itoh M., Kondo S., Konno H., Nakano K., Ninomiya N., Arami M., Waki K., Mathiki A., Okada M., Plessky C., Shiraki T., Suzuki T., Suzuki T., Suzuki H., Aramani M., Maki K., Mathiki A., Okada M., Plessky C., Shiraki T., Suzuki H., Kawashima T., Kojima M., Plessky C., Shiraki T., Suzuki H., Kawashima M., Maki K., Mathiki A., Chammura M., Plessky C., Shiraki T., Suzuki H., Kawashima M., Waki K., Mathiki A., Okada M., Suzuki M., Suzuki M., Suzuki M., Suzuki M., Suzuki M., Suzu
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AN CAZAKI Y. FURUND.

AN OKAZAKI Y. FURUND.

AN OKAZAKI Y. FURUND M., KASUKAWA T., Adachi J., BONO H., KONDO S.,

ANIKAIGO I., OSATO N., SAITO R., SUZUKI H., YAMMARA I., KIYOSAWA H.,

ANIKAIGO I., OSATO N., SAITO R., SUZUKI H., YAMMARA I., KIYOSAWA H.,

ANIKAIGO I., OSATO N., SAITO R., SUZUKI H., YAMMARA I., KIYOSAWA H.,

AN ADALIA E., TOMARU Y., HASGEGAWA H., BATALOV S., BEISEL K. W.,

AN BLAKE J.A., Bradt D., BRUBIC C., HUME D.A., QUACKENDUSH J.,

AN BLAKE J.A., Bradt D., BRUBIC C., HUME D.A., QUACKENDUSH J.,

AN BLAKE J.A., Bradt D., BRUBIC C., HUME D.A., COUGHN J.,

AN BLAKE J.A., Bradt D., BRUBIC C., GOGZIK A., GOUGH J.,

AN ADALA E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

A GAIMMOND T., GAZIBOLDI M., GISSI C., GOGZIK A., GOUGH J.,

AN ANAI A., KAWASAWA Y., KEGAZIECEKI R.M., KING B.L.,

KONAGAYA A., KURCCHKIN I.V., Lee Y., Lenhard B., Lyons P.A.,

AN MAGASIA T., MARCHIONI L., MARCHIONI L., MKCRAIZLE L., MIKI H.,

AN ANGASHAMA T., NAMARA K., OKIGO T., PRVAN W.J., Pertea G., PESCIE G.,

BRA SANDELIN A., Schneider C., Semple C.A., Setou M., Shimada K.,

AN AND C., REACH D., S., Teasdale R.D., Tomita M.,

AN AND C., RABOR D.J., Reid J., Setou M., Shimada K.,

AN HIMING L.G., WYNDSHAW-BOYIS A., YANGISHAWA M., YANG I.,

AND C., ZAVOLAN M., ZAVOLO H., NAKAMURA M., YANG I.,

AND CARRA A., HASHIXUMW W. IMPORTING M., KARAWA I.,

AND CARRA A., HASHIXUMW W., IMPORTING M., KARAWA I.,

AN HATA A., HASHIXUMW W., IMPORTING W., ISHING W.,

AN HATA A., HASHIXUMW W., IMPORTING W., ISHING W.,

AN HATA A., HASHIXUMW W., IMPORTING W., ISHING W.,

AN HATA A., HASHIRUM W., IMPORTING W., ISHING W.,

AN HATA A., HASHIRUM W., IMPORTING W., ISHING W.,

AN HATA A., HASHIRUM W., IMPORTING W., ISHING W.,

AN HATA A., HASHIRUM W., IMPORTING W., ISHING W.,

AN HATA A., HASHIRUM W., IMPORTING W., ISHING W.,

AN HATA A., HASHIRUM W., IMPORTING W., ISHING W.,

AN HATA A., HASHIRUM W., IMPORTING W.,

AN HATA A., HASHIRUM W.,

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Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
Hayashizaki Y.,
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PubMed=16141073; DOI=10.1126/science.1112009;
RIKEN Genome Exploration Research Group, and Genome Science Group
(Genome Network Core Team) and the FANTOM Consortium;
"Antisense Transcription in the Mammalian Transcriptome.";
Science 309:1564-1566(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The transcriptional landscape of the mammalian genome.";
Fletcher C.F., Fukushima T., Furuno M.,
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STRAIN=C57BL/6J; TISSUB=Thymus;

Kayal J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,

Kawal J., Shinagawa A., Shibata K.,

A Arakawa T., Hara A., Fukunishi Y., Komno H., Adachi J., Fukuda S.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Rieischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

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Sakai K., Okido T., Puruno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Ry Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Wumshaw-Booris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nacharia V., Sakani V., Wang K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Thymus; MEDLINE=2049974; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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MGI; MGI:2682305; Hbxap.
SEQUENCE 112 AA; 11657 MW; 3F364EA14DDFD076 CRC64;
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Pred. No. 83;
0; Mismatches
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91.7%;
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Matches 11; Conservative
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Nature 420:563-573(2002).

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us-10-617-568-2.rup

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RK STRAIN=BALBAC;

RK Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Pubbede16141072; DoI=10.1126/science.1112014;

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Distributed under the Creative Commons Attribution-NoDerivs License
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11-OCT-2005, sequence version 1.
07-FEB-2006, entry version 5.
1TB-55 BB88 cDNA, RIKEN full-length enriched library, clone:1730024D14 product:HBV px associated protein 8 large isoform homolog (Fragment).
Name=Hbxap;
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Eukaryota; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang W.,
                                                                                                                                                                                                                                            Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae; BEP clade,
Bhrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                              MUCLEOTIDE SEQUENCE.
MEDLINE=2233737; Pubmed=12447439; DOI=10.1038/nature01183;
Eleng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan D.,
Wh M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin J., Wang Y.,
Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
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GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001471; TF_ERF.
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SEQUENCE 233 AA; 25434 MW; 90B3BF38A3A4A419 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sequence and analysis of rice chromosome 4."; Nature 420:316-320(2002).
                                                                                               01-0CT-2003, integrated into UniProtKB/TrEMBL. 01-MAR-2004, sequence version 2. 07-FBB-2006, entry version 14. 05-3NBa0010D21.10 protein. Name=OSJNBa0010D21.10;
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                                                 233 AA.
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HSSP; 080337; 1GCC.
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QJUK64;
                                                 PRELIMINARY; PRT;
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ProDom; PD001423; TF_ERF; 1.
SMART; SM00380; AP2; 1.
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Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandalin A., Schneider C., Semple C.A., Setcu M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Walls C., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang I., Yang I., Yang I., A Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang I., Raylaka T., Konno H., Nakamura M., Yang I., Hayatsu N., A Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Tishii Y., Itoh M., Kagawa I., Yasunishi A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.; "Analysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                       Kawai J. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arawai J., Shinagawa A., Fukudishi Y., Yoshino M., Itoh M., Ishii Y., Arawai J., Shinagawa A., Fukudishi Y., Kono M., Adchi J., Yakuda S., Alzawa M., Nishi K., Kono H., Adachi J., Yakuda S., Alzawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Asato T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Relacomann W., Gasaterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brackincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Rarchionni L., Mashima J., Mazzarelli J., Monbaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wannian H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wannian H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wannian H., Toyo-Oka K., Wang K.H., Weitz C., Wawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Muramatsu M., Hayashizaki Y.; Pubraction of cap-trapper-selected cDNAs to prepare full-length cDNA lbraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-2050013; Pubmed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa M., Nashi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Tawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rike integrated sequence analysis (RISA) system-384-format genome Res. 10:1757-1771(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=BALB/C;
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Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                    Gaps
                                                                                                    ö
                                                                                Length 309;
                                                                                                    1; Indels
                                                            309 AA; 34639 MW; 8099A6CAA99549E4 CRC64;
                                                                                                                                                                                                                 26-APR-2004, integrated into UniProtKB/Swiss-Prot.
                                                                               88.0%; Score 44; DB 2; I
91.7%; Pred. No. 1.9e+02;
                                                                                                                                                                                                                                          Zinc finger and BTB domain-containing protein Name=Zbtb8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, BC023839; AAH23839.1; -; mRNA.
Ensembl; ENSWUSG0000048485; Mus musculus.
MGI; MGI:2387181; Zbtb8.
InterPro; IPR00210; BTB.
InterPro; IPR010310; BTB.
InterPro; IPR013069; BTB.
InterPro; IPR07087; Znf_C2H2.
Pfam; PF00651; BTB; 1.
ProDom; PD000003; Znf_C2H2; 1.
SMART; SM00225; BTB; 1.
                                                                                                                                                                                              484 AA.
                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                         [1]
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                            EMBL; AK146154; BAE26938.1; -; mRNA.
                                                                                                                                                                                                                           01-MAR-2003, sequence version 1. 07-MAR-2006, entry version 22.
                                                                                                    11; Conservative
                                                                                                                      1 AAMAAAAAAMA 12
                                        MGI; MGI:2682305; Hbxap.
                                                                                                                                          7 AAAAAAAAAAA 18
                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                         STRAIN=FVB/N;
                                                                                                                                                                                              MOUSE
                                                          SEQUENCE
                                                                              Query Match
Best Local S
                                                                                                                                                                                             ZBTB8 MC
Q8CIIO;
                                                                                                                                                                                    MOUSE
                                                                                                    Matches
                                                                                                                                                                          RESULT 5
                                                                                                                                                                                    ZBTB8
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Carrainci P. N. Katayama S., Gough J., Frith M.C., Maeda N., Carrainci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Cyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Adanis V., Aldnis V., Allan J.E., Shimokawa K., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Anweis M.J., Wilming J.G., Addinis V., Allan J.E., Bono H., Chalk A.M., Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., Anweis M.J., Choudhary V., Christoffels A., Clutterbuck D.R., Crowe M.L., Dalla E., Dalrymple B.P., Ge Bono B., Della Gatta G., Aldinis V. Fagiolini M., Faulkner G., Aletcher C.F., Fukushima T., Furuno M., Futeki S., Gariboldi M., Raperi H., Hayashi Y., Hensch T.K., Hirokawa N., All ID., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T., Alat M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Attano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J., Allu J., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K., Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K., Mortagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P., Matsuzawa S., Miki H., Matsuzawa S., Mulder N., Nakauchi H., Ng P., Matsuzawa S., Miki H., Matsuzawa S., Mulder N., Nakauchi H., Ng P., Matsuzawa S., Miki H., Matsuzaw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-OCT-2005, integrated into UniProtKB/TrEMBL.
11-OCT-2005, sequence version 1.
21-FEB-2006, entry version 7.
21-FEB-2006, entry version 7.
11 days embryo head cDNA, RIKEN full-length enriched library, clone:cli30068L6 product:zinc finger and BTB domain containing 8, full insert sequence (0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:c230068H07 product:zinc finger and BTB domain containing 8, full insert sequence) (14, 17 days embryo head cDNA, RIKEN full-length enriched library, clone:3222401B20 product:zinc finger and BTB domain containing 8, full insert sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CS7BL/61; TISSUE=Cerebellum, and Head;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                             Score 44; DB 1; Length 484; Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                            B4FF082555B0CA1A CRC64;
                                                                                                                                                                               protein 8.
/FTId=PRO_0000047722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        484 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                           C2H2-type 1.
C2H2-type 2.
Ala-rich.
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                                                                                                                                                                                                                                                                                                                                            53387 MW;
                                                                                                                                                                                                                                                                                                                                                                                               88.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 AAMAAAAAAAA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Conservative
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382
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                                                                                                                                                                                                                                                                                                                                            484 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q3US18_MOUSE
Q3US18;
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ZN_FING
COMPBIAS
SEQUENCE
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Best Local
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RR NUCLECTIDE STOUENCE.

RX STRAIN=C57BL/63; TISSUE=Cerebellum, and Head;

RX STRAIN=C57BL/63; TISSUE=Cerebellum, and Head;

RX OKAZAKI Y., Furuno M., Kasukawa T., Adachi J., Bono H., Knodo S.,

RA Nikaido I., Osato N., Saitor R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush U.,

Radiarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush U.,

Radiarelli R., Bradt D., Brusic V., Chotchia C., Corbani L.E., Cousins S.,

RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Ganai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Ganai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Konagaya A., Kurchkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Kanajaya A., Wurchkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Malott D.R., Maltais L., Marchiomi L., McKenzie L., Miki H.,

RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RA Ravasi T., Reed J.C., Reed D.J., Rai D., Ramachandran S.,

RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomite M.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Yang I., Yang I.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sakazume N., Sakai K., Kawai J., Alazwa K., Arakwa T., Fukuda S.,

RA Miyazaki A., Sakai K., Kawai J., Alazwa K., Arakwa T., Fukuda S.,

RA Miyazaki A., Sakai K., Kawai J., Shibata K., Shinagawa I.,

Rayasulishi A., Sokaino M., Waterston R., Lander E.S., Rogers J.,

Rayasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

Rayasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

Rayasunishi S., Takanaki Y.,

Rayasunishi S., Takanaki Y.,

Rayasunishi S., Yoshino M., Waterston R., Lander E.S., Rogers J.,

Rayasunishi S., Takanaki Y.,
Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O., Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G., Petrovsky N., Plazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M., Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Sekfguchi K., Semple C.A., Seno S., Schneider C., Sekfguchi K., Semple C.A., Seno S., Schneider C., Shinada H., Shimada K., Sultana R., Takenaka Y., Shinada H., Shimada K., Sultana R., Takenaka Y., Taki K., Tamaoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K., Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C., Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J., Amanishi H., Zabarovsky E., Zhu S., Xananishi D., Tomaru Y., Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J., Nahlestedt C., Mattick J.S., Hume D.A., Kal C., Sasaki D., Tomaru Y., Ruwda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., Inda J., Imamura K., Itch M., Kando T., Kawajashira N., Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S., Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CSTBL/6J; TISSUB=Cerebellum, and Head;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Itoh M., Itoh M., Itoh M., Itah I.,
Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H.,
Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium; "Antisense Transcription in the Mammalian Transcriptome."; Science 309:1564-1566(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The transcriptional landscape of the mammalian genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J, TISSUB=Cerebellum, and Head,
PubMed=16141073; DOI=10.1126/science.1112009;
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Hayashizaki Y.;
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Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownerein M.J., Bult C., Fletcher C., Fujite M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaeres P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Suzaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y., "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/63; TISSUE=Cerebellum, and Head; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA lbraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CS7BL/6J; TISSUB=Cerebellum;
Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.
Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
Shibata K., Shizaki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
Muramatsu M., Hayashizaki Y.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa M., Ohara E., Watshiwayi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Wixen Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., RIKE integrated sequence analysis (RISA) system-384-format Sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CS7BL/6J; TISSUB=Head;
Arakwa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
Muramatsu M., Hayashizaki Y.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
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EMBL; AK163910; BAE37541.1; -; mRNA.
EMBL; AK132152; BAE20999.1, -; mRNA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005637; F:metal ion binding; IEA.
GO; GO:0005515; F:protein binding; IEA.
GO; GO:0005515; F:protein binding; IEA.
GO; GO:0008270; F:zinc_ion binding; IEA.
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InterPro; IPR013069; BTB POZ.
InterPro; IPR007087; Znf_C2H2.
Pfam; PF00651; BTB; 1.
Pfam; PF00096; zf-C2H2; 2.
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ProDom; PD000003; Znf\_C2H2; 1.

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REAL STEALMEST SEQUENCE:

REAL GATEAL SECONDEST STEAMEN S., GORDH J., Frith M.C., Maeda N., RA GATEAL S., GORDH J. F., Kashawa K., RA GATEAL S., GORDH J. E., Shimokawa K., RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., RA Mabesi-Impiombato A., Aphweller R. Aturaliya R.N., Bailey T.L., Adhins V.C., Aldinis V., Altanis R.N., Bailey T.L., Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., RA Mabesi-Impiombato A., Aphweller B.P., de Bono B., Della Gatta G., RA Growe M.L., Dalla E., Dalrymple B.P., Gelbono B., Della Gatta G., RA Georgii-Hemming P., Gingeras T.R., Golobori T., Green R.E., Austinoich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa T., RA Georgii-Hemming P., Gingeras T.R., Golobori T., Krapin M., Ranapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Katano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Autonion L., Liu J., Lareau L.F., Lazarevic D., Lipovich L., Liu J., RA Jakk M., Madan Babu M., Madera M., Marchionni L., RA Matsudawa S., Maki H., Mignone F., Miyake S., Morris K., Mortagui-Tabar S., Midel H., Matanone F., Miyake S., Morris K., Randori A., Schobari Y., Orlando V., Pang K.C., Pand M.J., Sensa L., Sheng Y., Rochobach C., Sekfguch K., Sandelin A., Schobach C., Sekfguch K., Sendelin A., Schobach C., Sekfguch K., Sender B., Rabranda H., Shimada K., Silva D., Sinclair B., Schobach C., Tang S., Taylor M.S., Tegener J., Taig K., Tamoja K., Tan S.L., Tang S., Taylor M.S., Tegener J., Taig K., Tamoja K., Hamoja K., Tan S.L., Tang S., Zimmer A., Hide W., Bult C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CS7BL/63; TISSUE=Stomach;
MEDLINE=99279255; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency Hayashiz-langh Cloning.";
Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-OCT-2005, sequence version 1.
07-FEB-2006, entry version 5.
17 days embryo stomach cDNA, RIKEN full-length enriched library, clone:1920040M16 product.hepatitis B virus x associated protein,
                                                                                                                                                                                                                 ;
0
                                PROSITE; PS50097, BTB; 1.
PROSITE; PS50097, BTB; 1.
PROSITE; PS00193; ZINC FINGER C2H2 1; 1.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.
Metal-binding; Nuclear protein; Repeat; Zinc; Zinc-finger.
SEQUENCE 484 AA; 53414 MW; ACA81D5402A2E7F4 CRC64;
                                                                                                                                                                       Length 484;
                                                                                                                                                                                                               1; Indels
                                                                                                                                                                     Score 44; DB 2; I
Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                               11-OCT-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                          998 AA.
                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                     88.0%;
91.7%;
SMART; SM00225; BTB; 1.
SMART; SM00355; ZnF_C2H2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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Name=Hbxap;
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                                                                                                                                                                                                               11; Conservative
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Best Local Similarity
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Q3UJ04;
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Principle of C. Warrick C. S. D. Mariok C. Sanaki D. Tomanu Y. Philade G. C. Warrick C. S. D. W. Philade G. C. Warrick C. S. D. Warrick C. S. D. Warrick C. S. D. Warrick C. S. Warrick C. Warrick C.

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                                                                                                                                                                                                              Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Wonno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Muramatsu M., Hayashizaki Y.; Muramatsu M., Hayashizaki Y.; Pubbraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Itoh M., Aizawa N., Bishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Ritki integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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MOI; MOI:2663305; Hbxap.

GO; GO:0005515; F:protein binding; IEA.

GO; GO:00063519; P:rainc ion binding; IEA.

GO; GO:0006359; P:rainc ion binding; IEA.

GO; GO:0006359; P:rainc ion binding; IEA.

InterPro; IPR001965; Znf_PHD.

SNART; SM00249; PHD; 1.

PROSITE; PS01359; ZF_PHD 1; 1.

PROSITE; PS01359; ZF_PHD 1; 1.
"Functional annotation of a full-length mouse cDNA collection.", Nature 409:685-690(2001).
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Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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                                                                                                                                                      STRAIN=C57BL/6J; TISSUE=Stomach;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
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QBIGN6_DROME PRELIMINARY; PRT;
QBIGN6;
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Best Local Similarity 91...
Best Local 11; Conservative
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                                                                                                                     SEQUENCE
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Q8IGN6_DR
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Name-CG18599; ORFNames=Dmel_CG18599;
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                            01-MAY-2000, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                              01-OCT-2002, sequence version 2.
21-FEB-2006, entry version 32.
CG18599-PA.
                                                                                                                                 PRELIMINARY;
                                                                                                                                 OFVEA3_DROME
                                                                                                                                                        O9VEA3
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                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae; Mamiellales; Mamiellaceae; Ostreococcus.
                                                                                                      Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., Goorge R., Gonzallez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Khadaroo B., Robbens S., Ferraz C., Derelle E., Eychenie S., Coo
Peaucellier G., Delseny M., Demaille J., Van De Peer Y., Picard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The First Green Lineage cdc25 Dual-Specificity Phosphatase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AY330645; AAQ16122.1; -; Genomic_DNA.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:00004725; F:protein tyrosine phosphatase activity; IEA.
GO; GO:000087; P:m phase of mitotic cell cycle; IEA.
GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.0%; Score 43; DB 2; Length 395; 90.9%; Pred. No. 3.2e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          86.0%; Score 43; DB 2; Length 235; 83.3%; Pred. No. 2.1e+02; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                       Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                               EMBL; BT001688; AAN71443.1; -; mRNA.
FlyBase; FBgn0038592; CG18599.
SEQUENCE 235 AA; 24886 MW; A88629B97C919948 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS50206; RHODANESE 3; 1.
395 AA; 43146 MW; 8AEA2E381C122C9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         395 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000751; MPI Phosphatase.
InterPro; IPR001763; Rhodanese-like.
PANTHER; PTHR10828; MPI_Phosphatase; 1.
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QEVRGS OSTTA PRELIMINARY; PRT; QEVRGS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004, sequence version 1.
07-FEB-2006, entry version 9.
Dual specificity phosphatase Cdc25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00716; MPIPHPHTASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00581; Rhodanese; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 83.3
nes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 90.9
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                                                             NUCLEOTIDE SEQUENCE.
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                      NCBI_TaxID=7227;
                                                                                      STRAIN=Berkeley;
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                                                                                                                                                                                 Patel S., Prov
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RAY MEDLINE-20196006; PubMed=10731132; DOI=10.1126/ecience.287.5461.2185; RAY MEDLINE-20196006; PubMed=10731132; DOI=10.1126/ecience.287.5461.2185; RAY Amanatides P.G., Scherer S.E., Lip Pw., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Burdton G.G., Wortman J.R., Yango Q., Chen L.X., Ray Brandon R.C., Rogers Y.-H.C., Blazel R.G., Nelson C.R., Miklos G.L.G., RA Abril J.F., Agbayani A., An H.-J., Andrews-Fennkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Bennes R.V., Bernan B.P., Bandari D., Bolahakov S., Borkova D., Botcham M.R., Bouck J., Brokstein P., Brothier P., Brother I., Ray Borson K.Y., Bennes P.V., Bernan B.P., Bandari D., Bolahakov S., Borkova D., Botcham M.R., Bouck J., Brokstein P., Brothier E., Bowes M., Dugan-Rochas S., Dunkov B.C., Dunn P., RA Gherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P., Davies P., Davies P., Durbin K.J., Evangalista C.C., Ferraz C., Ferriera S., Plaischman W., RA Hostin D., Houston K.J., Walush F., Rapen G.H., M., Gabriellan A.E., Gary N.S., Gelbart W.M., Glasser K., RA, Gong F., Gorrell J.H., Gul Z., Guan P., Harris M., Alansh F., Ratpen G.H., Ke Z., Kulp D., Lal Z., Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Lasko P., Lei Y., Levitsky A.A., Li J.H., Morntoh T.C., Morleco M.P., Morther S.M., Moy M., Murphy B., Murphy L., Murny D.M., Nalson D.L., Ralazzolo M., Pittman G.S., Pan S., Pollard J., Worther E., Spradling A.C., Stapleton M., Strong R., Sun B., Sanith T., Spradling A.C., Stapleton M., Strong R., Sun B., Sanith H.O., Aliang S., Was B., Shreke B.C., Stapleton K., Stapleton M., Strong R., Sun B., Sanith H.O., Ritskas R., Merchelle R., Wassarman D.A., Walissenbach J., Walls S., Pan S., Pollard J., Pan S., Pollard J., Stan S., Pol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Sacieb J.M., Park S., Pfeifer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstrock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence."; Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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MEDLINE=22426065; PubMed=12537568;
                                                        [1]
NUCLEOTIDE SEQUENCE
NCBI TaxID=7227;
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NUCLEOTIDE SEQUENCE

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R WIGGOTIDE SEQUENCE.

RAMAGES SECURING.

RAMAGES N. Celniker S.E., Holt R.A., Evans C.A., Gocaptu J.D.,

RAMAGES N.D. Celniker S.E., Holt R.A., Evans C.A., Gocaptu J.D.,

RAMAGES N.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Roctean J.R., Yandell M.D., Zhang O., Chen L.X.,

RAMAGES R.A., Lewis S.E., Richards S.A., Ashburner M., Pfelifer B.D.,

RAME R.M., Barden Y., Holt R.A., An H.J., Andraws Pfannkoch C., Baldwin D.,

RAME R.M., Banco P.V., Bernan B.P., Bandari D., Bolankavy S.,

RAME R.M., Banco P.V., Bernan B.P., Bandari D., Bolankavy S.,

RAME R.M., Banco P.V., Bernan B.P., Bandari D., Bolankavy S.,

RAME R.M., Banco P.V., Bernan B.P., Bandari D., Bolankavy S.,

RAME R.M., Banco P.V., Bernan B.P., Brottler P.,

RAME R.M., Banco P.V., Bernan B.P., Brottler P., Brottler P.,

RAME R.M., Banco P.V., Bernan B.P., Brottler P.,

RAME R.M., Banco P.V., Bernan B.P., Brottler P., Brottler P.,

RAME R.M., Banco P.V., Bernan B.P., Brottler P., Brottler P.,

RAME R.M., Banco P., Buller H., Cadieu E., Center A., Chandra I.,

RAME R.M., Banco P., Buller A., Davenport L.B., Davies P.,

RAME R.M., Banco P., Buller R., Davenport L.B., Davies P.,

RAME R.M., Banco P., Helman T.J., Herrian M., Glasser K.,

RAME R.M., Gabrielian A.E., Garzel J. H., G. Z., Guban P., Harris M.,

RAME R.M., Ralush F., Karpen G. H., Ke Z., Kannison J.A., Kecchun K.A.,

RAME R.M., Markel B., McIntosh T.C., McLeod M.P., McGord R.,

RAME R.M., Moy M., Murphy B., Murphy L., Murany D.M., Nelson D.L.,

RAME R.M., Moy M., Murphy B., Murphy L., Murany D.M., Nelson D.L.,

RAME R.M., Palazzolo M., Pittuma G.S., Pan S., Pollard J., Weissenbach J.,

Rame B.C., Siden Kamos I., Simpson M., Stupski M.P., Smith H.O.,

RAME R.M., Ramen D.R., Weinster E., Wang A.H., Wang S., Yao Q.A.,

RAME R.M., Ramen D.R., Weinster E., Wang A.H., Wang S., Yao Q.A.,

RAME R.M., Ramen D.R., Wolley K.C., Wu D., Yang S., Yao Q.A.,

RAME R.M., Ramen D.R., Rubin G.M., Weissenbach J.,

RAME R.M., Ramen D.M., Worley K.C., Wu D., Yang S., Yang S., Yang S., Yan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Centiker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeifer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Mar K., Stapleton M., Sutton G.G., Venter S. Frishing a whole-genome shotgun releases 3 of the Drosophila melanogaster euchromatic genome sequence.", Genome Biol. 3:RESEARCH0079-(2002).
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MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.,
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                       Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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MEDLINE=22426065; PubMed=12537568;
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NUCLEOTIDE SEQUENCE.
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                                    Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R., Patel S., Frise B., Mheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.; "The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                             Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield B.J., Bayraktaroglu L., Berman B.P. Bettenocurt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO:0005634; C:nucleus; IEA.
GO:0003700; F:transcription factor activity; IEA.
GO:0007275; P:development; IEA.
GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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PROSITE; PS50071; HOMECBOX 2; 1.
DNA-binding; Developmental protein; Homeobox; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.0%; Score 43; DB 2; Length 475;
83.3%; Pred. No. 3.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases -! - SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Iranscription; Transcription regulation.
SEQUENCE 475 AA; 50950 MW; 7DAC89752B1FA99D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
                                                                                                                                                 a genomics perspective.";
Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE003721; AAF55524.2; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR001356; Homeobox.
Interpro; IPR012287; Homeodomain-rel.
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                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
MEDLINE=22426069; PubMed=12537572;
              MEDLINE=22426070; PubMed=12537573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2003, sequence version 1.
07-FBB-2006, entry version 14.
CG34422-PA.
ORFNames=CG31422, Dmel_CG31422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P06601; 1FJL.
FlyBase; FBgn0038592; CG18599.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00024; HOMEOBOX.
SMART; SM00389; HOX; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lewis S.E.;
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Best Local

Matches

DROME QBIMU7;

RESULT 11
Q81MU7 DRC
ID Q81MU
DAC Q81MU
DT 01-MU
DT 01-MU
DT 01-MC
DT 07-FI
GN ORFN
GN ORFN

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Pred. No. 6.4e+02;

83.3%;

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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004, integrated into UniProtKB/TrEMBL.
05-JUL-2004, sequence version 1.
07-FEB-2006, entry version 9.
Pyruvate-ferredoxin oxidoreductase and related 2-oxoacid-ferredoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=15028704; DOI=10.1128/JB.186.7.2179-2194.2004; Siebers B., Tjaden B., Michalke K., Doerr C., Ahmed H., Zaparty M., Gordon P., Sensen C.W., Zibat A., Klenk H.-P., Schuster S.C.,
                                                                                                                                                                                                                                                                                         Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.
Yu C., Rubin G.;
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                            "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                "Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FlyBase; FBgn0051422; CG31422.
SEQUENCE 305 AA; 32565 MW; 472F8AA40CFF9953 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
Thermoproteaceae; Thermoproteus.
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                                                                                                                                                                 systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oxidoreductases gamma-alpha subunit (EC 1.-.-.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AJ621314; CAF18495.1; -; Genomic DNA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE003750; AAN14029.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002880; POR N. InterPro; IPR009014; Transketo_C_like. Pfam; PF01855; POR N, 1. Oxidoreductase; Pyruvate.
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Q70329;
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Matches 10; Conservative
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DT 05-JU
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DB 2; Length 637;

84.0%; Score 42;

Query Match

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RY CLEACHIES SEQUENCE (LANGES STAME GENOMIC DNA).

RY CLEACHIES SEQUENCE (LANGES STAME GENOMIC DNA).

RY MADIANE-20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;

RA Adama M.D. (Celniker S.E. I. in Pw. Hoskins R.A., Galle R.F.,

RA Adama M.D. (Celniker S.E. I. in Pw. Hoskins R.A., Galle R.F.,

RA Banaratides P.G., Scherer S.E. I. in Pw. Hoskins R.A., Galle R.F.,

RA Bandon G.G., Wortena J. R., Yandell M.D., Zhang G., Chen L.X.,

RA Bandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pefelfers B.D.,

RA Bandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pefelfers B.D.,

RA BALIL W.R., Basu A., Barachala G., Baldwin D.,

RA Ballew R.M., Gang P.V., Berman B.P., Bhandari D., Beasley E.M.,

Ballew R.M., Cawley S., Dallke C., Davrengort L.B., Davies P.,

Buttis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Buttis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Buttis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Buttis K.J., Evangelista C.C., Perrac C., Ferrica S., Pubkov B.C., Dunn P.,

Buttis K.J., Dendcher A., Howland T.J., Hernandez J.R., Houck J.,

RA Goder K., Doup L.E., Downess M., Dugan-Rochs S., Duhkov B.C., Dunn P.,

Buttis N., Barvey D.A., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D.A., Heiman T.J., Wei M.-H., Ibegama C.,

Jalali M., Kalush F., Kapen G.H., Ke Z., Kannison J.A.,

RA Liu X., Mattei B. Wolloch T.C., Morris J., Morphy M., Natherei A.,

RA Berialto G., Milalhina N.V., Mobarry C., Morris J., Morphy M., Natherei A.,

RA Berialto G., Milalhina N.V., Mobarry C., Morris J., Morphy M., Warphy B., Murphy L., Murphy D., Pull Y., Wanger M.D.,

RA Berialton G., Milalhina N.V., Mobarry C., Morris J., Morphy R., Wang C., Siden F., Spradling A.C., Stapheron M., Stupe R., Spradling A.C., Staphero M., Stupe R., Spradling A.C., Sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Canton-S;
MEDLINE=20296162; PubMed=10839352; DOI=10.1016/S0896-6273(00)81166-6;
Wan H.I., DiAntonio A., Fetter R.D., Bergstrom K., Strauss R.,
Goodman C.S.;
  Gaps
  ö
                                                                                                                                                                                                                                                                                                                                        Name-hiw; ORFNammes-C032592;
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, AND TISSUE SPECIFICITY
1; Indels
                                                                                                                                                                                                                                                                                                      Ubiquitin ligase protein highwire (EC 6.3.2.-) (Protein pam/highwire/rpm-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Highwire regulates synaptic growth in Drosophila.";
                                                                                                                                                                                                                Q9NB71; Q8MZ36; Q9VXZ5; 21-JUN-2005, integrated into UniProtKB/Swiss-Prot. 21-JUN-2005, sequence version 2. 07-WAR-2006, entry version 26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [2]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                  PRT; 5233 AA.
1; Mismatches
                                                                      308 AAIAAAAGAAMA 319
10; Conservative
                                           1 AAMAAAAAAMA 12
                                                                                                                                                                                                  STANDARD;
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Roj GO: GO: 0016023; C:cytoplasmic membrane-bound vesicle; IDA.

Roj GO: 00016023; C:cytoplasmic membrane; IDA.

Roj GO: 0000515; F:protein binding; IPI.

Roj GO: 00006842; F:ubiquitin-protein ligase activity; ISS.

Roj GO: 00006842; F:ubiquitin-protein ligase activity; ISS.

Roj GO: 00006842; F:ubiquitin-protein ligase activity; ISS.

Roj GO: 00011; P:locomotion; NAS.

Roj GO: 00011; P:locomotion; NAS.

Roj GO: 00045886; P:megative regulation of Synaptic growth at n. .; IMP.

Roj GO: 00045886; P:megative regulation of Synaptic growth at n. .; IMP.

Roj GO: 00045886; P:megative regulation of Synaptic growth at n. .; IMP.

Roj GO: 0015567; P:protein ubiquitination; ISS.

RITERPRO; IPR01298; Filamin.

RITERPRO; IPR001298; Filamin.

RITERPRO; IPR001498; Reg_chr_condens.

RITERPRO; IPR001494; RING.

Refam; PR00643; Zf-B box; I.

REM; PR00643; Zf-B box; I.

RRINTS; PR00643; RCLD; FALSENEG.

RROSITE; PS00625; RCLD; FALSENEG.

RROSITE; PS00625; RCLD; FALSENEG.
                                                                                                                                                                                                                                RCIEDCIDE SEQUENCE [LARGE SCALE MRNA] OF 4083-5233.

RC STRAIN=Berkeley; TISSUE=Larva, and Pupae;

RX MEDLINE=2242666; PubMed=12537569;

RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,

RA George R.A., Guarin H., Krommiller B., Pacleb J.M., Park S., Wan K.H.,

RA Rubin G.M., Calliker S.E.;

R A Drosophila full-length cDNA resource.";

R A Drosophila full-length cDNA resource.";

R Bubsequent protessomal degradation of target proteins. Has a role during synaptogenesis; negative regulator of synaptic growth.

-:- FUNCTION: B3 ubiquitin ligase proteins mediate ubiquitination and subsequent protessomal degradation of target proteins. Has a role during synaptogenesis; negative regulator of synaptic growth.

-:- PUNCTION: B3 ubiquitin conjugation; third step.

-:- PUNCTION: B3 ubiquitin ligase proteins mediate ubiquitination and around which the synaptic neuropil forms Expression. Stage 13

-:- SUBCELLULALAR LOCATION: Nucleus (By similarity).

-:- PATHWAY: Ubiquitin conjugation; third step.

-:- TISSUE SPECIFICITY: Nervous system specific expression outside the CNS starts at stage lin presynaptic terminals at the periactive cone which surround the active zone. NMJ and CNS expression is also seen in third instear larvae (at protein level).

-:- MISCELLANBOUS: Flies lacking hiw display NMJ synapses that grow exuberantly and are expanded in both the number of boutons and in the STMTIADITY. Contains at film in the synaptic contains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Contains 1 filamin repeat.
SIMILARITY: Contains 6 RCC1 repeats.
SIMILARITY: Contains I RING-type zinc finger.
CAUTION: Ref.2 sequence differs from that shown due to erroneous
GENOME REANNOTATION.

GENOME REANNOTATION.

MISTA S., CTOSDY M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,

Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.

Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,

Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

Staplecon M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                           "Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                              systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AF262977; AAF76150.1; -; mRNA.
EMBL, AE003497; AAF48411.2; ALT SEQ; Genomic_DNA.
EMBL, AY113376; AAM29381.1; ALT_INIT; mRNA.
Engembl; CG325292; Drosophila melanogaster.
FlyBase; FBgn0030600; hiw.
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN-RNC-1 / ATCC 700922 / JCM 11081;

MEDLINE=20504483; PubMed=11016950; DOI=10.1073/pnas.190337797;

MEDLINE=20504483; PubMed=11016950; DOI=10.1073/pnas.190337797;

MG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,

Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,

Leithanser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,

Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;

"Genome sequence of Halobacterium species NRC-1.",

"Genome sequence Sci. U.S.A. 97:12176-12181(2000).
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RCC1 2.
RCC1 3.
RCC1 4.
RCC1 6.
Filamin.
Filamin.
C -> R (in Ref. 1).
C -> R (in Ref. 1).
G -> E (in Ref. 1).
G -> E (in Ref. 1).
G -> E (in Ref. 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 42; DB 1; Dens...
Pred. No. 3.6e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Halobacterium salinarium (Halobacterium halobium).
Archaea, Buryarchaeota, Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85 AA; 8924 MW; 0CE3258BABC3F334 CRC64;
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100.0%; Pred. No. 1.7e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE005066; AAG19818.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
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BioCyc; HSP64091:VNG1530H-MONOMER; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        565631 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84.0%;
90.9%;
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Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAMAAAAAAV 55
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'The transcriptional landscape of the mammalian genome.";
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=16120803; DOI=10.1093/molbev/msi246;
Comeron J.M., Guthrie T.B.;
"Intragenic Hill-Robertson Interference Influences Selection Intensity
on Synonymous Mutations in Drosophila.";
Mol. Biol. Evol. 22:2519-2530(2005).
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP clade,
Pooideae, Triticeae, Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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0
                                                                                                                                                                                                                                                                                                                CG13448 (Fragment).
Drosophila erecta (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.0%; Score 41; DB 2; Length 174; 100.0%; Pred. No. 3e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.0%; Score 41; DB 2; Length 243; 83.3%; Pred. No. 4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; DQ026517; AAY98505.1; -; mRNA.
SEQUENCE 243 AA; 25932 MW; C2F8705208B73E9B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174 AA; 17861 MW; 76E5A0CDB39E7C7E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-JAN-2006, sequence version 1.
07-FEB-2006, entry version 2.
Dehydration responsive element binding protein.
                                                                                                                                                                                                                               20-DEC-2005, integrated into UniProtKB/TrEMBL.
20-DEC-2005, sequence version 1.
07-FEB-2006, entry version 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-JAN-2006, integrated into UniProtKB/TrEMBL
                                                                                                                                                                          174 AA.
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                                                                                                                                                                          PRT;
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                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  riticum aestivum (Wheat).
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Best Local Similarity 83.3
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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                        AAMAAAAAA 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=7220;
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Q2QK76;
                                                                                                                                                                       QZXY87_DROER
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NON TER
SEQUENCE
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                                                                                                                                           DROER
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                                                                                                            RESULT 15
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RC STRAIN-CSTBL/GJ; TISSUB=Thymus;

RX Dubled=1611072; DCI=10.1126/science.1112014;

RA TAIN-CSTBL/GJ; TISSUB=Thymus;

RA Bajic V. B. Berners E. Batelbuv S., Forrest A.R., Zavolan M.,

RA Bajic V. B. Berners E. Batelbuv S., Forrest A.R., Zavolan M.,

RA Bajic V. B. Berners E. Batelbuv S., Forrest A.R., Sahimokawa K.,

RA Davis M.J., Wilming L.G., Adweiler R., Atteraliya R.M., Balley T.L.,

RA Davis M.J., Wilming L.G., Adweiler R., Atteraliya R.M., Balley T.L.,

RA GLIU K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,

CHU K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,

CHOW M.L., Dalla B. Dalsrymble B.P., de Bono B., Della Gatta G.,

RA Georgi-Hemming P., Glingeras T.R., Grobon H., Chalk A.M.,

RA Hill D., Hundindexl L., Iacono M., Tkeo C.Y., Hirokawa N.,

RA Georgi-Hemming P., Glingeras T.R., Gojobori T.K., Hirokawa T.,

RA Jak M., Kanapin A., Katon M., Kawasawa Y., Kelbo J., Kitamura H.,

RA Liuni S., Marapin A., Katon M., Rawasawa Y., Kelbo J., Kitamura H.,

RA Liuni S., Mowillian S., Midan Babu M., Madera M., Marchionni L.,

Mateuda H., Mateuda Babu M., Nakacho N., Nakachi H., Ng P.,

RA Nateuda H., Mateudawa S., Miki H., Mighone F., Miyake S., Morris K.,

RA RA BERCOWSKY N., Planza S., Reed J., Fasid S., Roiri R., Rakachi H., Ng P.,

ROSARSH Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pescole G.,

RASARSH Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pavesi G.,

RASARSH Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pavesi G.,

RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sensa L., Sheng Y.,

Raberling S., Stupka E., Sugiuta K., Sullena R., Yananishi H., Zabarovsky E., Zhu S., Kai C., Yagi K., Teasdale R., Sullena R., Sullena R., Wananishi H., Zabarovsky E., Zhu S., Kai K., Yananishi H., Zabarovsky E., Zhu S., Kai K., Rananoci-Katayama M., Sulvki M., Aoki J., Arakawa T.,

Rawashima R., Kanamoci-Katayama M., Sulvki M., Aoki J., Arakawa T.,

Rawashima T., Kojiama M., Koto T., Kawaji H., Kawagashira N., Rawashima T., Kojiam M., Sulvaki M., Sulvaki M., Rawashima T., Kojiam M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUB=Thymus;
MEDLINE=99279253; PubMed=1049636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:C920021M21 product:muscleblind-like 1 (Drosophila),
                                                                                                                                                                                                                                                                                                                                                                          11-OCT-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                            11-0CT-2005, sequence version 1. 07-FEB-2006, entry version 5.
                                                                                                                                                                                                                                                                                           PRELIMINARY;
1 AAMAAAAAAA 12
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                                                                              18 SAAAAAAAAMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       full insert sequence.
Name=Mbnll;
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K MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

K Awai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fhkuda S.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fhkuda S.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Alzawa K., Izawa M., Nishi K., Gojobori T., Bono H., Kasukawa T., Saito R.,

K Adota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

A Robinan M., Gaasterland T., Gissi C., King B., Kochiwa H.,

R Pleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

Saki K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Bake J., Boffelli D., Bojunga N., Carnincia M., Wagner L., Washio T.,

Bronstein M.J., Bult C., Fletcher C., Fullita M., Gariboldi M.,

By Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoco N.,

Asaaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Wanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Hayashizaki V., V.
                                                                                                                                                      CYRAINCESTIBL/GST.

WEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

WEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

WEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

MIKAIGO I., OSATO N., SAITO R., SUZUKI H., Yamanaka I., Kiyosawa H.,

Nikaido I., Comaro Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Baldarelli R., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Balake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Balake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Gasterland T., Gariboldi M., Gisel C., Forrest A., Frazer K.S.,

Anai A., Kawasawa Y., Kedzierski R.M., King B.L.,

Kanai A., Kawasawa Y., Kedzierski R.M., King B.L.,

Kanai A., Kawasi H., Marchionni L., Miki H.,

RA Nagashima T., Numaca K., Okido T., Pavan W.J., Pertea G., Pescol G.,

RA Rasis T., Reed J.C., Reed D.J., Reid J., Ramachandran S.,

Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

Sandelin A., Schneider C., Semple C., Watanabe Y., Watlan M.,

RA Yana C., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

Shiraki T., Waki K., Kawai J., Aizawa Y., Shinagawa T., Fukuda S.,

Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

Hara A., Hashizume W., Waterston R., Lander E.S., Rogers J.,

Bananishi A., Yashiao M., Zhiaka, Y.,

Hara K., Hara K., Lander Y., Lander E.S., Rogers J.,

Bananishi A., Yashiaoki Y., Shibata K., Shinagawa J.,

Bananishi A., Sakai V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-C57BL/6J; TISSUE=Thymus; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itch M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., In Muramatsu M., Hayashizaki Y., Itch M., Okomalization and subtraction of cap-trapper-selected cDNAs to prepare full-length CDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Birney E., Hayashizaki Y.; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                  PubMed=16141073; DOI=10.1126/science.1112009; RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium; "Antisense Transcription in the Mammalian Transcriptome."; Science 309:1564-1566(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection.";
    STRAIN=C57BL/6J; TISSUE=Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 409:685-690(2001).
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                                                                                                                                              NUCLEOTIDE SEQUENCE
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Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Natawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Mateumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwak S., Inoue K., Togawa Y., Izawa M., Ohara B., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Rike integrated sequence analysis (RISA) system-384-format Sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K., Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S., Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N., Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D., Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A., Muramatsu M., Hayashizaki Y.;
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21-FEB-2006, entry version 6.
Regulatory protein, LysR:LysR substrate binding domain precursor.
ORFNames=BproDRAFT_3748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome and assembly of Polaromonas sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Comamonadaceae; Polaromonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41; DB 2; Length 254;
Pred. No. 4.1e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Muramatsu M., Hayashizaki Y.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGI; MGI:1928482; Mbn11.

GO; GO:0005737; C:cytoplasm; IDA.
GO; GO:0005737; C:cytoplasm; IDA.
GO; GO:0005737; P:mxNa splice site selection; IMP.
InterPro; IPR000571; Znf CCCH.
InterPro; IPR005571; Znf CCCH.
SMART; SM00356; Znf C3HI; Z.
SMART; SM00356; Znf C3HI; Z.
SEQUENCE 254 AA; Z6605 MW; 3030142F792FAAE3 CRC64;
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US DOE Joint Genome Institute (JGI-ORNL);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AK153848; BAE32210.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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nes 10; Conservative
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Larimer F., Land M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
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Q4B1F7;
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RRITAR RR

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Ensembl; ENSMUSG0000045179; Mus musculus.

MGI; MGI:98365; Sox3.

MGI; MGI:98365; Sox3.

GO; GO:0005634; C:nucleus; RCA.

GO; GO:0005700; F:transcription factor activity; RCA.

GO; GO:0006325; P:establishment and/or maintenance of chromat. . .; RCA.

GO; GO:0030900; P:forebrain development; IMP.
                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                            , Transcription; Transcription regulation.
Transcription factor SOX-3.
/FTIG=FRO_0000048721.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tanaka S., Kamachi Y., Tanouchi A., Hamada H., Jing N., Kondoh H.; "Interplay of SOX and POU Factors in Regulation of the Nestin Gene in Neural Primordial Cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41; DB 1; Lengtn 5.2.
Pred, No. 5.76+02;
  SIMILARITY: Contains 1 HMG box DNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2A8477A10A517FEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=15456859; DOI=10.1128/MCB.24.20.8834-8846.2004;
                                                                                            EMBL; X94125; CAA63845.1; -; Genomic_DNA.
HSSP; P48432; 1GT0.
SMR; P53784; 67-145.
Ensembl; ENSWUSG0000045179; Mus musculus.
MG1; MG1: 98365; SOX3.
GO; GO:0030900; P: forebrain development; IMP.
GO; GO:0010900; P: forebrain development; IMP.
InterPro; IPROGOSI0; HMG 12_box.
Pfam; PF00505; HMG box; 1.
SMART; SM00398; HMG; 1.
PROSITE; PS50118; HMG; 1.
DNA-binding; Nuclear protein; Transcription; TracCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2003, integrated into UniProtKB/TrEMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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Poly-Ala.
Poly-Pro.
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HSSP; P48432; IGT0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2003, sequence version 1. 07-FEB-2006, entry version 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37858 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.0%;
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les 10; Conservative
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2223
223
259
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293
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164
2119
252
269
282
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COMPBIAS
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Q80XF1_MOU
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                                                                                                                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96189340; PubMed=8625802; Collignon J., Sockanathan S., Hacker A., Cohen-Tannoudji M., Nortis D., Rastan S., Stevanovic M., Goodfellow P.N., Lovell-Badge R.; "A comparison of the properties of Sox-3 with Sry and two related genes, Sox-1 and Sox-2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Purnellary, S. Bell D., Casey E.S., Harland R., Lovell-Badge R.;
"Expression of Sox3 throughout the developing central nervous system is dependent on the combined action of discrete, evolutionarily conserved, regulatory elements.; submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELDULAR LOCATION: Nucleus.
-!- TISSUE SPECIFICITY: Mainly in the developing central nervous system. Expressed in developing urogenital ridge.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                            US DOE Joint Genome Institute (JGI-PGF);

Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israni S., Pitluck S., Richardson P.;

Hammon N., Israni S., Pitluck S., Richardson P.;

Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.

-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                EMBL, AARQ02000004, EAM39845.1; -; Genomic DNA.
GO; GO:0003700; F:transcription factor activity, IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent, IEA.
GO; GO:0006350; P:reanscription; IEA.
InterPro; IPR000847; HTH LysR.
Pfam; PF00126; HTH 1; 1.
Pfam; PF00146; IysR ubbstrate; 1.
PROSITE; PS50931; HTH LYSR.
PROSITE; PS50931; HTH LYSR; 1.
SNA-binding; Signal; Transcription; Transcription regulation.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
  sp. JS666.";
                                                                                                                                                                                                                     preliminary data.
SIMILARITY: Contains 1 HTH lysR-type DNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.0%; Score 41; DB 2; Length 331; 100.0%; Pred. No. 5.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
"Annotation of the draft assembly of Polaromonas sp. JS(
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              331 AA; 36159 MW; 2A4B7BA88EC46B78 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE (GENOMIC DNA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.00,
100.0%; Pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996, sequence version 1. 07-FEB-2006, entry version 35. Transcription factor SOX-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Development 122:509-520(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=Sox3; Synonyms=Sox-3;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
10s 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 AAMAAAAAA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AAMAAAAAA 10
                                                       NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=129/Sv;
                                                                            STRAIN=JS666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOX3 MOUSE
P53784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                     Buell R.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
-!- DOMAIN: The RING-type zinc finger domain is essential for
-!- ubiquitin ligase activity. It coordinates an additional third zinc
ion (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Mus.
NCBI_TaxID=10090;
                                             Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                               Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M., Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S., Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M., "Oryza sativa chromosome 3 BAC OsJNBa0065F09 genomic sequence."; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6; TISSUE=Brain;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.0%; Score 41; DB 2; Length 417; 83.3%; Pred. No. 6.2e+02; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gramene; Q75KP;...
Gramene; Q75KP;...
GO; G0:0005634; C:unucleus; IEA.
GO; G0:000151; C:ubiquitin ligase complex; IEA.
GO; G0:00046812; F:metal ion binding; IEA.
GO; G0:0004842; F:ubiquitin-protein ligase activity; IEA.
GO; G0:0016567; F:zinc ion binding; IEA.
GO; G0:0016567; P:protein ubiquitination; IEA.
InterPro; IRRO1841; Znf. RING.
PF00097; zf-C3HC4; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00184; RING; 1.
PROSITE; PS50089; ZF RING 2; 1.
Metal-binding; Woclear protein; Zinc; Zinc-finger.
SEQUENCE 417 AA; 42736 MW; 7CC9F220D3B7B83E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Contains 1 RING-type zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2005, integrated into UniProtKB/TrEMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AC099323; AAR87274.1; -; Genomic_DNA
             Putative RING-H2 zinc finger protein.
Name=OSJNBa0065F09.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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07-FEB-2006, entry version 3.
Sox3 protein (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 83...
Best Local 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 AAVAAAAAAFA 112
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                         NCBI_TaxID=39947;
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Q4VBD8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=Sox3;
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ð
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leu H.-L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP clade,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                  Gaps
                 GO; GO:0006355; P:regulation of transcription, DNA-dependent; RCA. GO; GO:0048515; P:regulation of transcription; IMP.
InterPro; IPR000910; HMG 12_box.
Pfam; PF00505; HMG box; 1.
PRART; SM00398; HMG; 1.
PROSITE; PS50118; HMG; 1.
SEQUENCE 375 AA; 37789 MW; 3E117E20D40BFE34 CRC64;
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Wu H.-P. P., Shaw J.-P.;

Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41; DB 2; Length 403;
Pred. No. 6e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                  82.0%; Score 41; DB 2; Length 375; 83.3%; Pred. No. 5.7e+02; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase, Hypothetical protein.
SEQUENCE 403 AA, 42774 MW; 30722980A480A479 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0006725; P:aromatic compound metabolism; IEA.
InterPro; IPR003089; AB.hydrolase.
InterPro; IPR000073; AB.hydrolase_1.
InterPro; IPR000379; Ser_estrs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-NOV-2004, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                           403 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AC137623; AAV25643.1; -; Genomic_DNA Gramene; Q60DW4; -.
    GO:0009887; P:organ morphogenesis; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-NOV-2004, sequence version 1.
OY-FBB-2006, entry version 10.
Hypothetical protein P0426G01.8.
Name=P0426G01.8,
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                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                     284 AAAAAAAAAAAS 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                  10; Conservative
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Best Local Similarity
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Q75KP7 ORYSA
Q75KP7;
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Q60DW4;
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RESULT 22 Q75KP7 ORY ID Q75KP AC Q75KP DT 05-JU

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Hum. Mol. Genet. 2:2013-2018(1993).
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COMPBIAS
COMPBIAS
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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Brownerch A., Schein J.E., Jones S.J.M., Marra M.A.;
F. "Generation and initial analysis of more than 15,000 full-length human
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MGI; MGI: 98365; Sox3.

GO; GO:0005634; C:nucleus; RCA.

GO; GO:0005700; F:transcription factor activity; RCA.

GO; GO:0005325; P:establishment and/or maintenance of chromat. . .; RCA.

GO; GO:0009807; P:orebrain development; IMP.

GO; GO:0009807; P:regulation of transcription, DNA-dependent; RCA.

GO; GO:00048515; P:spermatid differentiation; IMP.

InterPro; IPRO00010; HMG 12_box.

PFam; PF00505; HMG box; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.0%; Score 41; DB 2; Length 436; 83.3%; Pred. No. 6.4e+02; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOX2 HUMAN STANDARD,
P41225; P35714; Q9NR49;
01-FEB-1995, integrated into UniProtKB/Swiss-Prot.
07-UNN-2004, sequence version 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; BC096018; AAH96018.1; -; mRNA.
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MEDLINE=94154672; PubMed=8111369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50118; HMG_BOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6; TISSUE=Brain;
NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    345 AAAAAAAAAAS 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcription; Transcription regulation. Transcription factor SOX-3. /FTId=PRO_0000048720.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                         NUCLEOTIDE SEQUENCE OF 150-203.
MEDLINE=22310933; PubMed=1614875;
MEDLINE=2310933; PubMed=1614875;
MEDENDY P., Swift S., Brand N., Dabhade N., Barton P., Ashworth A.;
"A conserved family of genes related to the testis determining gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 1; Length 446; Pred. No. 6.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HGNC; HGNC:11199; SOX3.

Mi; 313430; gene.

MGO; GO:0003677; F:DNA binding; TAS.

GO; GO:0007417; F:DNA binding; TAS.

GO; GO:0007417; P:Central nervous system development; TAS.

HGCFPFO; IPRO00910; HMG 12_box.

PFONO:00098; HMG box; T.

SMART; SM00398; HMG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                   Gorry M.C., Hart P.S., Sashi V., Hart T.C.; "Clarification of the genomic sequence for human SOX3."; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L -> Q (in Ref. 3).
D -> E (in Ref. 3).
E -> D (in Ref. 3).
Missing (in Ref. 2).
F79E79C2D16BB929 CRC64;
                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Nucleus.
-!- SIMILARITY: Contains 1 HMG box DNA-binding domain.
-!- CAUTION: Was originally (Ref.3) termed SOX-9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAY 2005, integrated into UniProtKB/TrEMBL 10-MAY-2005, sequence version 1. 07-FEB-2006, entry version 2. 07-FEB-2006, entry version 7. Name-SOX3; ORFNames=RPI1-51C14.3-001;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X71135; CAA50465.1; -; Genomic_DNA.
EMBL; AF264713; AAF73059.1; -; Genomīc_DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X65665; CAA46616.1; -; mRNA.
PIR; 138239; 138239.
PIR; S22942; S22942.
HSSP; P8432; 1GTO.
SMR; P41225; 137-215.
TRANSFAC; T04916; -.
Ensembl; ENSG00000134595; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Poly-Gly.
Poly-Ala.
Poly-Pro.
Poly-Ala.
Poly-Ala.
Poly-Ala.
Poly-Ala.
                                                                                                                                                                                                                               Nucleic Acids Res. 20:2887-2887(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSS0118; HMG_BOX_2; 1.
ing; Nuclear protein; T
1 446 Tr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.0%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QSJWI3 HUMAN PRELIMINARY;
QSJWI3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      355 AAAAAAAAAAS 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AAMAAAAAAA 12
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159
176
202
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NUCLEOTIDE SEQUENCE.
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Best Local Similarity
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234
234
3324
3353
1159
1176
202
297
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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QSRKWO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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Q5RKW0 MOU
1D Q5RKW
AC Q5RKW
DT 21-DE
DT 21-DE
DT 07-FE
DE NAME
ON NAME
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                                                                                                                                                      Richards R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altsusner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Anderder G.F., Barefer C.F., Bara N.K., Anderder C.F., Bara N.K., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Haieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.B., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Webwan D.J., McKernan K.J., Malek J.A., Gunarane P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Mathing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Schmutz J., Mysers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Rand M.D., Shein J.E., Jones S.J.M., Marra M.A.; Rand M.D., Smailus D.E., Tand Monse C.D., Bernerch A., Schein J.E., Jones S.J.M., Marra M.A.; Rand M.D., Smailus D.E., Tand Monse C.D., Bernerch A., Schein J.E., Jones S.J.M., Marra M.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
  Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000910; HMG 12_box.
Pfam; PF00505; HMG_box; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                             MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.0%; Score 41; DB 2; Length 446; 83.3%; Pred. No. 6.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                      Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00398; HMG; 1.
PROSITE; PS50118; HMG BOX 2; 1.
SEQUENCE 446 AA; 45210 MW; F79E79C2D16BB929 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             448 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL121875; CAB87584.1; -; Genomic_DNA.
EMBL; BC093865; AAH93865.1; -; mRNA.
EMBL; BC093863; AAH93863.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMR; Q5JWI3; 137-215.
Ensembl; ENSG0000134595; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004, sequence version 1. 07-FEB-2006, entry version 13. Sox3 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      355 AAAAAAAAAAAS 366
                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.
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nes 10; Conservative
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                                                            NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                  NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH MGC Project;
                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QEP564_MOUSE
QEP564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=Sox3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q6P564
ID Q6
AC Q6
DT Q5
DT 07
DD SQ GN NA
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Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Alausner R.D., Collins F.S., Wagner L., Shemen C.W., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Appkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Rha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Rochards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Radiques S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rhiting W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Rochneration and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; 0005634; C:nucleus; RCA.
GO; GO:0005534; C:nucleus; RCA.
GO; GO:0003700; F:transcription factor activity; RCA.
GO; GO:0003700; F:establishment and/or maintenance of chromat. . .; RCA.
GO; GO:0003090; P:forebrain development; IMP.
GO; GO:0009887; P:oregulation of transcription, DNA-dependent; RCA.
GO; GO:0046515; P:spermatid differentiation; IMP.
InterPro; IPR000910; HMG 12_box.
Ffam; PF00505; HMG 2box; I.
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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   448 AA; 45157 MW; BC567C0808CA64C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-DEC-2004, integrated into UniProtXB/TrEWBL.
21-DEC-2004, sequence version 1.
07-FEB-2006, entry version 10.
Sox3 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         449 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; BC063061; AAH63061.1; -; mRNA.
SMR; Q6P564; 140-218.
Ensembl; ENSMUSG00000045179; Mus musculus.
MGI; MGI:99365; Sox3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00398; HMG; 1.
PROSITE; PS50118; HMG_BOX_2; 1.
Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                        STRAIN=C57BL/6; TISSUE=Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.
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                                                                                                       NUCLEOTIDE SEQUENCE.
                      NCBI_TaxID=10090;
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SEQUENCE
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                                                                                                                                             MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;
Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., WcKernan K.J., Malek J.J., Hulyk S.J.,
Rhebs S.S., Loquelland N.A., Sodergren B.J., Lu X., Gibbs R.A.,
Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Generation and initial analysis of more than 15,000 full-length human
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GO; GO:0005700; F:transcription factor activity; RCA.
GO; GO:0003700; F:transcription factor activity; RCA.
GO; GO:0006325; P:establishment and/or maintenance of chromat. . .; RCA.
GO; GO:0030990; P:forebrain development; IMP.
GO; GO:0006855; P:regulation of transcription, DNA-dependent; RCA.
GO; GO:00048515; P:spermatid differentiation; IMP.
InterPro; IPR000910; HMG_12_box.
Pfam, PF00005; HMG_box; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
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13-SEP-2004, sequence version 1.
07-FEB-2006, entry version 8.
CG4928 (Fragment).
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Ensembl; ENSMUSG00000045179; Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; BC052024; AAH52024.1; -; mRNA.
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Q6BCZS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6; TISSUE=Brain;
Director MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 83.3"
....hes 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.
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                                                                                                                                NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AY665388; AAT76555.1; -; mRNA.
InterPro; IPR010291; DUF895_euk.
Pfam; PF05978; DUF895; 1.
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                                                                                                                                                                                                  Swanson W.J., Wong A., Wolfner M.F., Aquadro C.F.; "Evolutionary expressed sequence tag analysis of Drosophila female reproductive tracts identifies genes subjected to positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name-CG7687, ORFNames-CG31122;
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=51159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 82.0%; Score 41; DB 2; Length 524; Best Local Similarity 83.3%; Pred. No. 7.5e+02; Matches 10; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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FlyBaae; FBGN0051122; CG31122.
SEQUENCE 524 AA; 57365 MW; A43288FD17FC3DC0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             515 AA; 56186 MW; 77FBDDA7864EF077 CRC64;
                                                                                                                                                                             PubMed=15579698; DOI=10.1534/genetics.104.030478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB 2; L
Pred. No. 7.4e+02;
1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2002, sequence version 1. 07-FEB-2006, entry version 9.
                                                                                                                                                                                                                                                                                                                       Genetics 168:1457-1465(2004).
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83.3%;
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Best Local Similarity 83.3
Marches 10, Conservative
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                                                                                                                                               NUCLEOTIDE SEQUENCE
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QBMQJS;
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Celniker S.;
                                                                                                                                                                                                                                                                                               selection.";
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SEQUENCE

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"Anopheles gambiae re-annotation.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                NUCLEOTIDE S
STRAIN=PEST;
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                                                      05-JUL-2004, sequence version 1.
07-MAR-2006, entry version 16.
Hypothetical protein P0597G07.116.
Name=P0597G07.116,
Oryza sativa (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryzea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
Anophelinae; Anopheles.
                                                                                                                                                                                                                                                    Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                Sasaki T., Matsumoto T., Yamamoto K.; "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00271; DnāJ; 1.

PROSITE; PS50076; DNAJ 2; 1.

Chaperone; Hypothetical protein; Inner membrane; Membrane; Protein transport; Translocation; Transmembrane; Transport SEQUENCE 603 AA, 64186 MW; 949D42CFD9143639 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41, DB 2; Length 603;
Pred. No. 8.4e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                  Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                            70; 001016021; C:integral to membrane; IEA.
70; GO:0016021; C:membrane; IEA.
70; GO:0019866; C:organelle inner membrane; IEA.
70; GO:001986; F:binding; IEA.
70; GO:001072; F:heat shock protein binding; IEA.
70; GO:005489; F:unfolded protein binding; IEA.
70; GO:006695; P:protein folding; IEA.
70; GO:0066695; P:protein targeting; IEA.
70; GO:0015031; P:protein targeting; IEA.
70; GO:0015031; P:protein targeting; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-2003, integrated into UniProtKB/TrEMBL. 07-DEC-2004, sequence version 2. 07-FEB-2006, entry version 8. 07-FEB-2006, entry version 8. 08-SNACP0000016550 (Fragment). ORFNames=ENSANGG0000014161;
                                              05-JUL-2004, integrated into UniProtKB/TrEMBL
                        603 AA.
                                                                                                                                                                                                                                                                         EMBL; AP004316; BAC83507.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=PEST;
The Anopheles gambiae Sequence Committee;
                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001623; DnaJ N.
InterPro; IPR011990; TPR-like_helical.
InterPro; IPR013105; TPR_2.
Pfam; PF00226; DnaJ; 1.
Pfam; PF00719; TPR_2; 1.
                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                        PRELIMINARY;
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Best Local Similarity 83...
The 10, Conservative
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                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=180454;
                                                                                                                                                NCBI_TaxID=39947;
                        Q7F010_ORYSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q7PV80_ANOGA
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              ORYSA
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  RESULT 30
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RADILINE-20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Stetchards S.E., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., R.A. Brandon R.C., Baxter E.G., Helf G., Nelson C.R., Miklos G.L.G., R.A. An H.-G., Andrews-Pfannkoch C., Baldwin D., R.A. Ballew R.M., Basu A., An H.-G., Andrews-Pfannkoch C., Baldwin D., R.A. Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Botchan D.A., Butler H., Cadieu E., Center P., Botchan M.R., Buck J., Brokstein P., Brottler P., Borkova D., Botchan M.R., Buller H., Cadieu E., Center P., Butlis K.C., Busam D.A., Butler H., Cadieu E., Center P., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Dunkov B.C., Dunn P., Butlis K.C., Busam D.A., Bengan R.O., Dew I., Dietz S.M., A de Pablos B. Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Plukov B.C., Dunn P., Dodson K., Gabrielian A.E., Garg N.S., Glan P., Harris M.L., Harrey D.A., Heiman T.J., Hernandez J.R., Houck J., R.A. Hostin D., Houston K.A., Howland T.J., Wei M.-H., T. Degwam C., Alasie R. Jalali M., Kalush F., Karpen G.H., Kravitz S., Kulp D., Lai Z., Alasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Markel B., Molina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., R.A., Nelson D.R., Nelson D.R.
                                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
The Anopheles gambiae Sequence Committee;
Submitted (ARF-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 635;
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Pred. No. 8.7e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      635 AA; 71145 MW; 860CC8CFEC3D541C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                EMBL; AAAB01008986; EAA00301.3; -; Genomic_DNA.
InterPro; IPR004343; Plus-3.
Pfam; PF03126; Plus-3; 1.
SMART; SM00719; Plus3; 1.
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Matches 10; Conservative
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Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasaarman D.A., Weinstock G.M., Weissenbach J., Walliams S.M., Woodage T., Wulley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao G., Zheng K., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Zheng E.M., Rubin G.M., Venter J.C.; The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22456070; PubMed=12537573; Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.; "The transposable elements of the Drosophila melanogaster euchromatin: a genomics perspective."; Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
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MBDLINE=224456069; Pubmed=12537572;
MBDLINE=224456069; Pubmed=12537572;
Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayrakraroglu L., Berman B.P.,
Bettencourt B.R., Cellniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith
Yu C., Rubin G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9VJU5:BG:DS00180.10; NDExp=1; IntAct=EBI-94009, EBI-163876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9WIK2:CG12491; NDExp=1; IntAct=EBI-94009, EBI-137341; Q8IQII:CG17666; NDExp=1; IntAct=EBI-94009, EBI-139867; Q9VDW9:CG3517; NDExp=1; IntAct=EBI-94009, EBI-175797; P17917:mus2009; NDExp=1; IntAct=EBI-94009, EBI-148806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0005515; F:protein binding; IPI.
SEQUENCE 642 AA; 70834 MW; 7F54E6806E05C487 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE003722; AAF55560.3; -; Genomic_DNA
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FlyBase; FBgn009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20231739; PubMed=10767535; DOI=10.1016/S0378-1119(00)00064-0; Davis T. Kurihara J., Yamamoto D.; Genomic organization and charaterization of the neural sexdenomic organization and fruitless (fru) in the Hawaiian species Drosophila
                                                    Gaps
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Length 642;
                                                 1; Indels
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Pfam; PF00051, BTB, 1.
Pfam; PF00096; zf-C2H2; 1.
SMART; SM00225; BTB; 1.
PROSITE; PS50097; BTB; 1.
PROSITE; PS00028; ZINC FINGER C2H2 1; 1.
PROSITE; PS01029; ZINC FINGER C2H2 2; 1.
Metal-binding; Nuclear protein; Zinc; Zinc-finger.
SEQUENCE 698 AA; 75481 MW; 1C7D73C4B3EA8E78 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF051664; AAF61178.2; -; Genomic_DNA.
EMBL; AF051662; AAF61178.2; JOINED; Genomic_DNA.
FlyBaes; F990029402; Dhet\fru.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0006634; C:nucleus; IEA.
GO; GO:000876; F:metal ion binding; IEA.
GO; GO:0008515; F:protein binding; IEA.
InterPro; IPR000210; BTB.
InterPro; IPR013069; BTB.
InterPro; IPR013069; BTB.
InterPro; IPR0070817; Znf_C2H2.
InterPro; IPR0070817; Znf_C2H2.
Score 41; DB 2; I
Pred. No. 8.8e+02;
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                                                                                                                                                                                                                                                                              698 AA.
                                               1; Mismatches
                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila heteroneura (Fruit fly)
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Q9NJZ3;
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                                                 10; Conservative
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Matches 10; Conservative
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Query Match
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Q7KSD2;
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RESULT 35
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                                                                                                                       NUCLECTIDE SEQUENCE.

RADINUE-2019606; PubMed=10731132; DDI=10.1126/science.287.5461.2185; Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adamstides P.G., Scherer S.E., It in the M.D. Ashburner M., Henderson S.N., Brandon R.C., Rogers R.A., Lewis S.E., Richards S., Ashburner M., Hederson S.N., Brandon R.C., Rogers Y.-H.C., Blazej K.G., Chang Q., Chen L.X., M. Brand M. Basu M. M. Bardin J. F. Botchan M.R., Bouck J. Experiently D., Bolshakov S., Burtis N. Botchan M.R., Buller H., Cadieu E., Center A., Chadra I., Rabandari D., Bolshakov S., Burtis N. Cawley S., Dahlke C., Perraz C., Ferriaz C., Perriag C., Perraz C., Perriag C., Perrag C., Perra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDILINE=22426065; PubMed=12537568; MEDILINE=22426065; PubMed=12537568; MEDILINE=22426065; PubMed=1 D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren B.J., Sviraks R., Tabor P.E., wan K., Stapheron M., Sutron G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finishing a whole-genome shotgun: release 3 of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
              Name=fru; ORFNames=Dmel_CG14307;
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Biol. 3: RESEARCH0084.1-RESEARCH0084.20(2002)
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Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                               Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
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Science 287:2185-2195(2000)
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   CG14307-PK, isoform K.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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Svirskas R., Smith E.
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E. Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B. Betencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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                                                                                                                                                                                                                                                                                                                                                                     Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E.,
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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SMART; SM00355; ZnF C2H2; 1.
PROSITE; PSS0097; BTB; 1.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
Metal-binding; Nuclear protein; Zinc; Zinc-finger.
SEQUENCE 705 AA; 76675 MW; F2D99E279741D9EE CRC64;
                                                                                                                                                                                                                                                                       Genome Biol. 3: RESEARCH0083.1-RESEARCH0083.22 (2002)
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Pred. No. 9.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AE003722; AAS65172.1; -; Genomic_DNA. FlyBase; FBgn0004652; fru. GO; GO:0005634; C:mucleus; IEA. GO; GO:0004687; F:mucleus; IEA. GO; GO:0003676; F:mucleic acid binding; IEA. GO; GO:0005515; F:protein binding; IEA. GO; GO:0008270; F:zinc ion binding; IEA.
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InterPro; IPR013069; BTB_POZ.
InterPro; IPR007087; Znf_C2H2.
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Pfam; PF00096; zf-C2H2; 1.
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Matches 10; Conservative
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MEDLINE-22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Featingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B. A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brapleton M., Soares M.B., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Ugdin T.B., Toshiyuki S., Garninci P., Prange C.,
Brownstein M.J., WcKernan N.J., Malek J.A., Gunarathe P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettemman M., Madan A., Rodrigues S., Sanchez A.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
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Gennerth A., Schein J.E., Jones S.J.M., Marra M.A.;
Generation and initial analysis of more than 15,000 full-length human
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XY Pubmed-14702039; DOI-10.1038/ng1285;

Ota T. Suzuki Y. Nishikawa T., Otsuki T., Sugiyama T., Irie R.,

Bubmed-14702039; DOI-10.1038/ng1285;

Ota T. Suzuki Y. Nishikawa T., Otsuki T., Shibahara T., Tanaka H.,

Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,

Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,

Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

Abe K., Kamihara K., Kateuta N., Saro K., Tanikawa M., Yamazaki M.,

Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,

An Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,

Ono Y., Takaguchi S., Watanabe M., Hiraoka S.,

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Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,

Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,

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Taylor T.D., Whittaker C.A., Chang J.L., Cuomo C.A., Dewar K.,

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Garber M., Ghirke A., Hafez N., Hall J.L., Norman C.H., Itch T.,

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Mikkelsen T.S., Naylor J.W., Nicol R., Nguyen C., Noguchi H.,

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Totoki Y., Toyoda A., Wain H.M., Young S.K., Zeng Q., Zimmer A.R.,

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"DNA sequence and analysis of human chromosome 18.";
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Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;
"Construction of expression-ready cDNA clones for KIAA genes: manual curation of 330 KIAA clones.";
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DNA Res. 5:31-39(1998).
                                                                                                                                                                                                                                                                                                      MEDLINE=98290545; PubMed=9628581; DOI=10.1093/dnares/5.1.31;
                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 349-1717.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O., Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., Yamazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., Pujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T., Rawabaka A., Hikiji T., Robatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R., Nakamura Y., Ohara O., Isogai T., Sugano S., Makai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S., Complete sequencing and characterization of 21,243 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              apoptosis, and suppresses tumor growth.";
Mol. Cell 18:13-24(2005)
-!- FUNCTION: Protein phosphatase that specifically mediates
dephosphorylation of Ser-473 of AKTI, a protein that regulate the
balance between cell survival and apoptosis through a cascade that
primarily alters the function of transcription factors that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           act as a negative regulator of K-Ras signaling in the membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regulate pro- and antiapoptotic genes. Dephosphorylation of Ser-473 of AKT1 triggers apoptosis and suppression of tumor growth.
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PubMed=15808505; DOI-010.016/j.molcel.2005.03.008;
Gao T., Furnari F., Newton A.C.;
"PHI.PP: a phosphatase that directly dephosphorylates Akt, promotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: A phosphoprotein + H(2)0 = a protein +
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EMBL; AC022046; -; NOT_ANNOTATED_CDS; Genomic_DNA.
EMBL; AC02753; -; NOT_ANNOTATED_CDS; Genomic_DNA.
EMBL; BC01178; BAA2553.2; -; mRNA.
EMBL; BC01178; BAH10706.1; -; mRNA.
EMBL; BC014927; AAH1927.2; -; mRNA.
EMBL; BC041653; AAH1953.1; -; mRNA.
EMBL; BC065159; AAH6753.1; -; mRNA.
EMBL; BC082244; AAH63519.1; -; mRNA.
EMBL; AK001924; AAH63244.1; ALT_TERM; mRNA.
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Ensembl; ENSG0000081913; Homo sapiens.
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Interpro; IPR0015991; LRR typ.
Interpro; IPR001849; PH.
Interpro; IPR001932; PP2C-like.
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   94 AA; 8628 MW;
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Best Local Similarity 83...
Local 10; Conservative
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
Ehrhartoideae; Oryzeae; Oryza
            Pfam; PF00169; PH; 2.
Pfam; PF00481; PP2C; 2.
PRINTS; PR00019; LEURICHEPT.
SMART; SM00332; PP2Cc; 1.
PROSITE; PS50003; PH_DOMAIN; 1.
PROSITE; PS50003; PH_DOMAIN; 1.
Apoptosis; Hydrolase; Leucine-rich repeat; Manganese; Membrane;
Metal-binding; Protein phosphatase; Repeat.
CHAIN 1 1717 PH domain leucine-rich repeat-containing
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Lee J.-Y.K., Hodges T.K.;
Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
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                                                                                               protein phosphatase.
/FIId=PRO_000057781
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01-NOV-1996, sequence version 1.
07-FEB-2006, entry version 23.
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1; Mismatches
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Poly-Ala.
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      Pfam; PF00560;
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Liu F., Lu J., Hu W., Wang S.-Y., Cui S.-J., Chi M., Yan Q.,

Liu F., Lu J., Hu W., Wang S.-Y., Cui S.-J., Zhang X.-L., Wang Z.-Q.,

Wang X.-R., Song H.-D., Xu X.-N., Wang J.-J., Zhang X.-L., Wang Z.-Q.,

Xue C.-L., Brindley P.J., McManus D.P., Yang P.-Y., Feng Z., Chen Z.,

Han Z.-G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (Rice).
Bukarych; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                            29-MMR-2005, integrated into UniProtKB/TrEMBL.
29-MAR-2005, sequence version 1.
07-FEB-2006, entry version 4.
SJCHGC07588 protein.
Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Plaryhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomat.
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                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The full-length cDNA sequences of Schistosoma japonicum genes."; Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "New Perspectives on Host-parasite Interplay by Comparative
Transcriptomic and Proteomic Analyses of the Human Blood Fluke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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83.3%; Pred. No. 2.8e+02;
ive 1; Mismatches 1; Indels
Length 94;
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McCombie W.R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schistosoma japonicum.";
Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 109 AA; 10655 MW; ZEA7EF32B06A6CEF CRC64;
   Score 40; DB 2; I
Pred. No. 2.5e+02;
0; Mismatches 1;
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Search completed: September 9, 2006, 23:00:26
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                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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SEQUENCE 156 AA; 16458 MW; 2EA5CBB33370E61C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "An integrated gene annotation and transcriptional profiling approach towards the full gene content of the Drosophila genome."; Genome Biol. 5:RESEARCH0003.1.FESEARCH0003.1.7(2003).
-!- MISCELLANBOUS: The sequence shown here is derived from an EMBL/GenBank/DDBJ third party annotation (TPA) entry.
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Eukaryota; Metazoa; Arthropoda; Myriapoda; Diplopoda; Pentazonia;
Glomerida; Glomeridae; Glomeris.
NCBL_TaxID=62006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=14709175; DOI=10.1186/gb-2003-5-1-r3;
Hild M., Beckmann B., Haas S.A., Koch B., Solovyev V., Busold C.,
Fellenberg K., Boutros M., Vingron M., Sauer F., Hoheisel J.D.,
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                               80.0%; Score 40; DB 2; Length 149; 75.0%; Pred. No. 3.6e+02; Live 2; Mismatches 1; Indels
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                                                                                                                                                                               Gramene; Q94102; -.
Hypothetical protein.
SEQUENCE 149 AA; 14809 MW; E9125D3203F934A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004, integrated into UniProtKB/TrEMBL. 05-JUL-2004, sequence version 1. 07-FEB-2006, entry version 8.
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QGILHG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 AA.
                                                                                                                                                   EMBL; AC022352; AAK51587.1; -; Genomic_DNA
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Q7YTA3;
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Best Local Similarity 83.33,
Best Local 10; Conservative
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Matches 9; Conservative
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60 AALAAAAAVALA 71
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MEDLINE=22767835; PubMed=12885558; DOI=10.1016/S0012-1606(02)00217-3; Prpic N.M., Tautz D.; Prpic N.M., Tautz D.; Prpic N.M., Tautz D.; 
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GO; GO:0005634; C:nucleus; IEA.

GO; GO:0003100; F:transcription factor activity; IEA.

GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR001356; Homeobox.

InterPro; IPR012287; Homeodomain-rel.
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NON TER 1 163
NON TER 163 A3, 17588 MW; 87BBECD9F5421697 CRC64;
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Pfam; PF00046; Homeobox; 1.
ProDom; PD000010; Homeobox; 1.
PROSITE; PS50071; HOMEOBOX_2; 1
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And 10; Conservative
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Run δ

Sequence:

Searched:

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ADD87412
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AEA10631
AEA10633
AEB56003
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Adr 29007 Human MHC
Adr 98917 Lung spec
Adv 92213 Plant ful
Abo58367 Human gen
Abg15501 Novel hum
Abg15501 Novel hum
Abb65204 Drosophil
Abb65204 Drosophil
Abb65207 Drosophil
Abg18917 Novel hum
Abb6918917 Human SEC
Ado61835 Transcrip
Abb65077 Hypoxia-i
Amm25623 Human pro
Abb68274 Human pro
Abb59750 Drosophil
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Abb79719 Drosophil
Abb71877 Drosophil
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          GenCore version 5.1.9
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Minimum I Maximum I

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Result Š.

Adh73564 Mouse POS Adr38267 Murine PO Ads3428 POSH proct Adt77904 Mouse POS Adu6897 Mouse POS Adu68997 House POS Adu68997 Mouse POS Adu68997 Mouse POS Adu68997 Mouse POS Adu68999 Novel hum Abb58985 Drosophil Abb58989 Drosophil Adb58999 Drosophil Add56773 Human Can Adi26773 Human Can Adi26773 Human Can Adr38361 Human Can Abr38361 Human Can Abr38361 Human Can Abr38361 Human Can Abr38363 Cell atta Adv78591 Cell atta Adv89595 Cell

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The present invention describes an isolated WHC class II compound (I) comprising: (a) an WHC class II component comprising at least a portion of an WHC class II alpha chain and at least a portion of an WHC class II beta beta chain, such that the WHC class II alpha chain and MHC class II beta chain form a peptide binding groove; (b) a spaceholder molecule; and (c) an effector component, where the effector component is linked to the MHC class II component, Also described; (i) a pharmaceutical composition comprising the MHC class II compound; (3) a method of directly identifying producing an MHC class II compound; (3) a method of directly identifying an antigen-specific T cell; (4) a method of tregulating an immune response as unsubject; (5) a method of regulating an immune disorder in a subject; (6) a method of treating an immune disorder in a subject; and (7) a method of treating an immune disorder ex vivo in a subject; and (7) a method of treating an immune disorder ex vivo in a subject; (1) has vivicies, and can be used in gene therapy. The MHC class II compound (1) can be used for preparing a composition for treating immune activities, and can be used in gene therapy. The MHC class II compound infections, parasitic disease, autoimmunity or treating immune sequence represents a spaceholder molecule peptide, which can be used in sequence represents a spaceholder molecule peptide, which can be used in the present invention.
                                                                                                                                                                                                                                                                                                                                                                 MHC class II compound; MHC class II component; MHC class II alpha chain; MHC class II beta chain; peptide binding groove; spaceholder molecule; effector component; immune response; immune disorder; virucide; antibacterial; antiparastic; cytostatic; immunosuppressive; gene therapy; viral infections; bacterial infection; parasitic infection; neoplastic disease; autoimmunity; toxicity; human.
Cell adhe
Wound dre
Auxiliary
Auxilliar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New MHC class II compound, useful for preparing a composition for treating immune disorders e.g. viral infections, bacterial infections, parasitic infections, neoplastic disease, autoimmunity or toxicity.
 Aeb23103 (
Aed01242 V
Aee05648 A
                                                           Aee01614
                                                                                                                                                                                                                                                                                                                             Human MHC class II compound spaceholder molecule SEQ ID NO:3.
                                                                                                                    ALIGNMENTS
                     AED01242
AEE05648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; SEQ ID NO 3; 92pp; English
                                                           AEE01614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DAND ) DANA FARBER CANCER INST INC.
     AEB23103
                                                                                                                                                                                                                   ADI29007 standard; peptide; 13 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-JUL-2002; 2002US-0395494P.
22-JUL-2002; 2002US-0397893P.
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                                                                                                                                                                                                                                                                                              (first entry)
     044040
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   88.7
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Synthetic.
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744
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The invention relates to a new isolated lung specific nucleic acid molecule (I) comprising any of 113 fully defined nucleotide sequences of given in the specification, their encoded protein sequences.

C given in the specification, their encoded protein sequences care sequences at least 60% identity to the nucleotide sequences. The methods and car least 60% identity to the nucleotide sequences. The methods and compositions of the present invention are useful for identifying, classing, imaging and treating lung cancer and non-concernous diseases of the lung. They are also used for identifying lung crisus, monitoring and identifying and/or designing entagonists of the polypeptide of the invention, gene therapy, production of transgenic polypeptide of the invention of engineered lung tissue for treatment and creasarch. Lung specific genes (LSGS) were identified by a systematic research. Lung specific genes (LSGS) were identified by a systematic caragarch. Lung specific genes (LSGS) were identified by a systematic canalysis of gene expression data in the LIFESEQ Gold database using the data mining software package candidate lead automatic search program (CLASP). Genes were grouped into gene bins where each bin is a cluster of sequences grouped together where they share a common contig.

C percentage level in the targeted tissue versus all the other tissues. The common result is utissue libraries associated with tumour or disease. This sequence reparted the invention of the inventio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated human lung specific nucleic acid molecule, useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous diseases of the lung.
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic; gene therapy; vaccine; lung; diagnosis; cancer; non-cancerous lung disease; lung tissue; antagonist; gene therapy; transgenic animal; splice variant.
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Score 53; DB 8; Length 13;
Pred. No. 0.24;
                                              0; Indels
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                                                 Mismatches
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06-DEC-2002; 2002US-0431510P.
06-DEC-2002; 2002US-0431516P.
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                        100.08;
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                                                                                               1 AAMAAAAAAAAA 13
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Query Match 100.
Best Local Similarity 100.
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                  ADR98917;
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Sequence 278 AA;

Sequence 13 AA;

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polypeptide that can be used in the recombinant DNA construct of

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The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, ignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
                                                                                               Gaps
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                                  8; Length 278;
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                               Score 53; DB 8
Pred. No. 4.2;
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                                                                                                                                                                                                                                                                                                                                                                  ADY09213 standard; protein; 646 AA
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                               100.0%;
100.0%;
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05-NOV-2001; 2001US-00985678.
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ZHOU Y.
KOVALIC D K.
SCREEN S E.
TABASKA J E.
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(CAOY/) CAO Y.
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(SCRE/)
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                                                                                                                                                                                                                                                                                                                                                                    plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; heat tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; yalatcomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; protein content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            recombinant DNA construct, useful for improving plant tolerance to 1, heat, drought, herbicides, extreme osmotic conditions, pathogens s, for conferring increased resistance to plant disease, or for
                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cao Y;
                                                                        Length 646;
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                                                                                                                                                                                                                                                                                                                                            Plant full length insert polypeptide seqid 47812.
                                                                       8;
                                                                   100.0%; Score 53; DB 8
100.0%; Pred. No. 9.3;
                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 47812; 15pp; English.
                                                                                                                                                                                                                                       ADX78446 standard; protein; 333 AA.
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                                                                                        Best Local Similarity
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                                           Sequence 646 AA;
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21-APR-2005
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                invention.
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                                                                       Query Match
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(ZHOU/)
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(CAOY/)
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(SCRE/)
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ADX78446
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         recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert polypeptide that can be used in the recombinant DNA construct of the
lignin or plant growth regulators, for increasing the rate of homologous
                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                       Revised record issued on 23-MAR-2006 : Corrected organism line
                                                                                                                                                                                                                                                   Length 333;
                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                   Score 50; DB 8;
Pred. No. 13;
1; Mismatches
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                                                                                                                                                                                                                                                     94.3%;
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les 12; Conservative
                                                                                                                                                                                                                 Sequence 333 AA;
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157 SAMAAAAAAAAA 169
1 AAMAAAAAAAAA 13
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ABO58367 standard; protein; 109 AA. ABO58367; RESULT

Human genome derived single exon protein #4601. (first entry) 29-JUL-2004

Human, gene expression, single exon probe, microarray, alternative splicing event, genomic alteration.

Homo sapiens.

US2003194704-A1.

16-OCT-2003.

03-APR-2002; 2002US-00029386

03-APR-2002; 2002US-00029386

(PENN/) PENN S G. (RANK/) RANK D R. (HANZ/) HANZEL D K.

Penn SG, Rank DR, Hanzel DK,

WPI; 2004-119264/12.

New human genome-derived single exon nucleic acid probes useful for hume gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for surveying tissues.

Claim 45; SEQ ID NO 32001; 80pp; English.

The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human gene expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of measuring human gene expression, a method of 

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contiguous amino acids of any of the above- mentioned amino acid sequences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing human gene expression data by subscription, and a computer-readable catoriac medium which contains a database having a plurality of records catoriac medium which contains a database having a plurality of records catoriac medium which contains a database having a plurality of records catoriac medium which contains a database having a plurality of records catoriac methods and apparatus are useful in gene cypression analysis. The probes may be used as tools for surveying cited above. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterising calternative splicing events, in detecting and characterising calterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic a human construction format directly from USPYO at this patent did not form part of the printed specification, but was consider and process and a part of the printed specification, but was near a contain the surface of the printed specification, but was near and the process and the process and the process and the printed specification, but was near the process and the process and the printed specification, but was near the process and the process and the printed specification, but was near the process and the 
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Pred. No. 6.3;
1; Mismatches 0; Indels
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Matches 12; Conser
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Novel human diagnostic protein #15492. ABG15501 standard; protein; 112 AA. (first entry) 18-FEB-2002 ABG15501; ABG15501 RESULT

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder. 30-MAR-2001; 2001WO-US008631. WO200175067-A2. Homo sapiens. 11-OCT-2001. 

31-MAR-2000; 2000US-00540217 23-AUG-2000; 2000US-00649167 Tang YT, WPI; 2001-639362/73. Drmanac RT, Liu C, (HYSE-) HYSEQ INC.

N-PSDB; AAS79688

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

Claim 20; SEQ ID NO 45860; 103pp; English

The invention relates to isolated polynucleotide (I) and polypeptide (II)

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reaction (PCR) primers, oligomers, and for chromosome and gene mapping, reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed sequence. (I) is useful in gene therapy techniques to restore normal cativity of (II) or torreat disease states involving (II). (II) is useful in gene therapy techniques to restore normal cativity of (III) or torreat disease states involving (II) (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical inaging of sites expressing (II). (I) and (II) are useful for treating disorders in classics, generate protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in displacement of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG3037 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in the full of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences
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Gaps

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0; Indels

Mismatches

Score 49; DB 4; Length 112; Pred. No. 6.5;

91 AAVAAAAAAAAA 103

AAO16493 standard; protein; 252 AA AA016493; RESULT 7 AA016493 

(first entry) 01-MAY-2003

Spider silk; spider silk protein; fabric; suture; medical covering; high-tech clothing; rope; reinforced plastic. Zorocrates fibronin 1 protein.

Zorocrates sp.

WO200299082-A2.

12-DEC-2002

06-JUN-2002; 2002WO-US018256

06-JUN-2001; 2001US-0296184P.

(UYWY-) UNIV WYOMING.

Roth DA, Lewis RV;

WPI; 2003-140616/13. N-PSDB; AAL51692. Expressing spider silk protein in a higher plant, by contacting a plant cell with silk protein encoding a gene linked to a gene that confers resistance to selection agent, and selecting cells that survive when incubated with the agent.

Claim 52; Fig 11; 114pp; English.

The invention comprises a method for expressing spider silk in a higher plant (e.g. arabidopsis, tobacco, tubers, sunflower, canola, alfalfa, soybean, maize, sorghum, wheat, cotton, small grains and rice). The method is useful for expressing spider silk in a higher plant. The silk

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produced is useful in the production of fabrics, sutures, medical coverings, high-tech clothing, rope, reinforced plastics, and other applications in which various combinations of strength and elasticity are required. The present amino acid sequence represents a spider silk-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sutures used in surgical procedures, including eye surgery, vascular closure, bowel surgery, cosmetic surgery, reconstructive surgery (e.g. nerve or tympanic membrane reconstruction) and central nervous system surgery. Natural and synthetic spider silk fibers are also used in the generation of antibiotic impregnated sutures and implant material and matrix material for reconstruction of bone and connective tissue. Spider
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spider silk protein; flagelliform-like spider silk protein; FLAG; MaSp; major ampullate spidroin; fabric; medical covering; clothing; parachute; rope; relinforced plastic; suture; aerial device wing; sail; hand glider; implantation biomaterial; resin product; fiber-reinforced plastic; thermal injected plastic; fibroin 1.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                       AAE36894 standard; protein; 252 AA.
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92.3%;
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                                                                                                                   Sequence 252 AA;
                                                                             related protein
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fibroin and different spider silk proteins. Synthetic spider silk fibers may be mixed with various plastics and/or resins to prepare a fiber-reinforced plastic and/or resin product. They are useful as structural reinforcement material in thermal injected plastics. The present sequence is Zorocrates species fibroin I protein. This sequence is used in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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Pred. No.
                                                                                                                                                                                                                                                                                                                                              ABB65204 standard; protein; 285 AA.
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                                                                                                                                        Sequence 252 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pharmaceutical
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed control of (II) is useful in gene therapy techniques to restore normal activity of (II) is useful in gene therapy techniques to restore normal consectul for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of polypeptide and polynucleotide sequences have applications in collapsed and polynucleotide sequences have applications of mutations capponshible for genetic disorders or other traits to assess blodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in collectronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                      Human, chromosome mapping, gene mapping, gene therapy, forensic; food supplement, medical imaging, diagnostic, genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID NO 49276; 103pp; English.
                                                                                                                                                                                                                                                  Novel human diagnostic protein #18908.
                                                                                                                                  ABG18917 standard; protein; 316 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                  189 AAIAAAAAAAA 201
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Query Match Best Local Similarity Matches 12; Conserv

92.5%; Score 49; DB 4; Length 285; 92.3%; Pred. No. 16;

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell in development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA aequences (ABL16175) and the encoded proteins (ABB2737-ABB372072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                 detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; secreted protein; SECP; cell proliferative disorder; cirrhosis;
                                                                                                             Drosophila; developmental biology; cell signalling; insecticide;
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Pred. No. 18;
1; Mismatches 0; Indels
                                                                                   Drosophila melanogaster polypeptide SEQ ID NO 35523
                                                                                                                                                                                                                                                                                                                                            Myers EW;
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ABB69577 standard; protein; 337 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid genes from Drosophila and interactions.
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                                                                                                                                                        Drosophila melanogaster,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 337 AA;
                                                                                                                                                                                  WO200171042-A2
                                                                                                                            pharmaceutical
                                                       26-MAR-2002
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                           ABB69577;
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proteins, useful for Huntington's disease; stroke; dementia; Parkinson's disease; anxiety; amyotrophic lateral sclerosis, schizophrenic disorder; mental disorder; mental disorder; recorder; recorder; quoting autoimmune disorder; mode; AIDS; inflammatory disorder; acquired immunodeficiency syndrome; allergy; ARDS; abdlt respiratory distress syndrome; diabetes mellitus; crohn's disease; asthma; autoimmune thyroiditis; glomerulonephritis; theumatoid arthritis; atopic dermatitis; ulcerative colitis; trauma; cardiovascular disorder; atherosclerosis; seizure disorder; renal tubular acidosis; anaemia; cataract; sensorineural hearing loss; neurological disorder; epilepsy; ischaemic cerebrovascular disease; Alzheimer's disease; Pick's disease; infection; congestive heart failure; heart disease, angina pectoris; myocardial infarction; myocarditis; transgenic animal; gene therapy; transgenic; vaccine; virucide; antibacterial; fungicide; antiparasitic; cancer; arteriosclerosis; hepatitis; psoriasis; developmental disorder; Novel human secreted proteins and genes encoding the proteins, useful treating, diagnosing and preventing cell proliferative, autoimmune/inflammatory, cardiovascular, developmental or neurological Yue H, Lee EA, Becha SD, Baughn MR, Yao MG, Tang YT;
Au-Young JK, Lal PG, Warren BA, Duggan BM, Tran UK, Xu Y;
Thangavelu K, Richardson TW, Bandman O, Jones KA, Yang J;
Emerling BM, Swarnakar A, Luo W, Walia NK, Azimzai Y, Khan FA;
Lu DAM, Griffin JA, Lee SY, Burford N, Elliott VS, Honchell CD;
He A, Mason PM, Li JX, Hafalia AJA, Gururajan R; .. .48 'label= Signal\_peptide\_#1 .ocation/Qualifiers 2001US-0293728P. 2001US-0297019P. 2001US-0299297P. 21-MAY-2002; 2002WO-US016234 2001US-0300537P 2001US-0301936P. 2002US-0362439P. 2002US-0363649P. 2002US-0366041P. (INCY-) INCYTE GENOMICS INC. WPI; 2003-129519/12. N-PSDB; AAD54316. WO200297035-A2. protozoacide. Homo sapiens 22-JUN-2001; 29-JUN-2001; 25-MAY-2001; 19-JUN-2001; 06-MAR-2002; 19-MAR-2002; 05-DEC-2002 disorders Peptide Peptide Protein

The present invention relates to novel human secreted proteins (SECP) and polynucleotides encoding such proteins. SECP sequences are useful for diagnosing, treating and preventing cell proliferative disorders including cancer (e.g. arteriosclerosis, cirrhosis, hepatitis, psoriasis and atherosclerosis), developmental disorders (e.g. seizure disorders, renal tubular acidosis, anaemia, cataract and sensorineural hearing 10ss), meurological disorders (e.g. epilepsy, ischaemic cerebrovascular disease, Alzheimer's disease, Pick's disease, Huntington's disease, stroke, dementia, Parkinson's disease, amyotrophic lateral sclerosis, schizophrenic disorders, mental disorders including mood and anxiety, Tourette's disorder and muscular dystrophy), autoimmune/inlammatory disorders (e.g. acquired immunodeficiency syndrome (AIDS), allergy, adult respiratory distress syndrome (ARDS), asthma, autoimmune thyroiditis, Claim 85; Page 168-169; 192pp; English.

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Gaps

Gaps

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diabetes mellitus, Crohn's disease, glomerulonephritis, rheumatoid arthritis, atopic dermatitis, ulcerative colitis, trauma and viral, bacterial, fungal, parasitic, protozoal and helminthic infections) and cardiovascular disorders (e.g. congestive heart failure, ischaemic heart disease, angina pectoris, myocardial infarction, hypertensive heart disease, congenital heart disease and myocarditis). They are useful for creating knocking humanised animals or transgenic animals to model human diseases. Sequences of the invention are useful in somatic or germline gene therapy and in diagnostic purposes. They are also used as vaccines. The present sequence is human SECP-30 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant; transcription factor; transgenic plant; abiotic stress tolerance; osmotic stress tolerance; cold tolerance; heat tolerance; low nitrogen tolerance; low phosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.
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Sherman BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 373;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 49; DB 6;
Pred. No. 20;
1; Mismatches (
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Riechmann JL, Haake V, Dubell AN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADO61835 standard; protein; 377 AA.
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17-DEC-2002; 2002US-0434166P.
24-APR-2003; 2003US-0465809P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                   Sequence 373 AA;
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Reuber TL;

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Companies conditions, increased tolerance to disease, including fungal disease and particularly Erysiphe, Fusarium and Botrytis, correased tolerance to multiple fungal pathogens, increased resistance to increased colerance to multiple fungal pathogens, increased resistance to glyphosate, increased sensitivity to ABA, reduced sensitivity to ABA, reduced sensitivity to ACC, altered sugar sensing, increased tolerance to sugars, altered carbon/nitrogen sensing, increased tolerance (to sugars, altered carbon/nitrogen sensing, altered branching pattern, altered stem morphology, altered velopment, altered branching pattern, altered stem morphology, altered velopment, altered branching pattern, altered trichome structure, altered seed trichome structure, altered seed trichome structure, altered seed ripening, altered seed avoidance, altered seed trichome structure, altered seed cipening, altered seed call proliferation, altered seed cipening, altered seed call proliferation, altered cell expansion, altered bhase change, altered sensescence, abnormal embryo development, altered plants, increased plants, lathality when overexpressed, altered necrosis patterns, increased plants, lathality when overexpressed, altered necrosis patterns, increased plants, lathality, altered seed size, altered seed coloration, altered seed size, altered seed coloration, altered seed size, altered seed seed oil content, altered seed protein content, increased leaf fatty acids, altered seed oil content, altered seed protein content, altered seed protein content, increased anthocyanin levels, and decreased anthocyanin levels, and decreased anthocyanin levels. Note: The sequence data for this patent did content form part of the printed specification, but was obtained in celectronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytostatic; vasotropic; tranguiliser; antiatherosclerotic; gene therapy; antiinflammatory; vulnerary; gynecological; ophthalmological; vaccine; hypoxia; tumourigenesis; angiogenesis; apoptosis; cancer; ischaemic condition; reperfusion injury; retinopathy; neonatal stress; preeclapmsia; atherosclerosis; inflammatory condition; wound healing; inflammatori erythropoiesis; hair loss; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP65077 standard; protein; 378 AA.
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08-FEB-2001; 2001GB-00003156.
25-OCT-2001; 2001GB-00025666.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypoxia-induced protein #17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 12; Conserv
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21-JAN-2000; 2000US-00488725
25-APR-2000; 2000US-00552317
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AAE35774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
antinflammatory, antirheumatic; antiarthritic; immunosuppressive;
antiadererial; endocrine; cardiant; central nervous system; virucide;
anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;
dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
w genetic disease; hematopoietic disorder; platelet disorder; asthma;
thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
allergic rhinitis; diabetes; multiple sclerosis; depression;
Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
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                                                                                                                                The present invention relates to methods for identifying genes and proteins that are implicated in a specific disease or physiological condition. The method comparing the transcriptored-proteome of a specialised cell type implicated in a disease or condition with that of second specialised cell type, under two experimental conditions, and identifying a gene that is differentially regulated in the two specialised cell types under experimental conditions, and specialised cell types under experimental conditions ABN77873-ABY78116 and ABP65061-ABP65257 were identified using the methods of the invention. The coding sequences and proteins are useful for treating a disease in a patient, for manufacture of a medicament for treating hypoxia-regulated conditions, and for regulating tumourigenesis, anglogenesis, apoptosis, biological response to hypoxia conditions, or hypoxic-associated
                                                                                                                                                                                                                                                                                                                      pathology in a patient. The coding sequences and proteins are also useful for monitoring the therapeutic treatment of a disease or physiological condition, such as cancer, ischaemic conditions, reperfusion injury, retinopathy, neonatal stress, preeclapmsia, atherosclerosis, inflammatory conditions, wound healing, inflammation, erythropoiesis or hair loss
                            Identifying a gene involved in disease for treating hypoxia-regulated conditions, comprises comparing the transcriptome/protecome of two cell types under different conditions and identifying a differentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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                                                                                                        Claim 13; Page 281; 538pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 92.3
les 12; Conservative
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WPI; 2002-627238/67.
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 378 AA;
                                                                            regulated gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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AAM25963. The proteins can have activities based on the tissues and cells they are expressed in. such as: antiinities based on the tissues and cells they are expressed in. such as: antiinitiammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiovascular; antiamemic; antiagoregant; heamostatic; vulnerary; cardiovascular; antiamemic; antiagoregant; heamostatic; vulnerary; antidabetic; detemacological; antiallergic; antiasthmatic; antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; cantidabetic; cytostatic; neuroprotective; antidepressant; nootropic; cording them can be used in gene therapy, antisense therapy and vaccine concing them can be used in gene therapy, antisense therapy and vaccine cording them can be used in gene therapy, antisense therapy and vaccine cording them can be used in gene trivity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, candemia, placelet disorders, thrombocytopaenia, wounds, burns, ulcers, costeoporosis, severe combined immunodeficiency, eczema, allergic rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, challed sease, parkinson's disease, neurodegenerative and corders and corders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infection, congestive heart failure, heart disease, angina pectoris, myocardial infarction, myocarditis, transgenic animal, gene therapy; transgenic, vaccine, virucide, antibacterial, fungicide, antibarasitic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer; arteriosclerosis; hepatitis; psoriasis; developmental disorder; atherosclerosis; saizure disorder; renal tubular acidosis; anaemia; cataract; sensorineural hearing loss; neurological disorder; epilepsy; ischaemic cerebrovascular disease; Alzheimer's disease; Pick's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; secreted protein; SECP; cell proliferative disorder; cirrhosis;
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                                                                                                                                                                                                                                                                                                                                                                      Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection.
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; Page 236; 1217pp; English.
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                                                                                                       Tang YT, Liu C, Drmanac RT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human SECP-26 protein.
                                                                                                                                                                                                              2001-457603/49.
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(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                    N-PSDB; AAH99564.
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protozoacide

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The present invention relates to novel human secreted proteins (SECP) and polynucleotides encoding such proteins. SECP sequences are useful for diagnosing, treating and preventing cell proliferative disorders including cancer (e.g. arteriosclerosis, cirrhosis, hepatitis, psoriasis and atherosclerosis), developmental disorders (e.g. seizure disorders, cand atherosclerosis), developmental disorders (e.g. seizure disorders, cand tubular acidosis, anaemia, cataract and sensorineural hearing consistence. Alzheimer's disorders (e.g. epilepsy, ischaemic cerebrovascular disorders mentia, Parkinson's disease, Huntington's disease, Schizophrenic disorders, mental disorders including mood and anxiety, correcte's disorder and muscular disorders including mood and anxiety, disorders (e.g. acquired immunodeficiency syndrome (ADS), allergy, adult crespiratory distress syndrome (ARDS), asthma, autoimmune thyroiditis, disorders mellitus, Crohn's disease, glomerulonephritis, rheumatorid arthritis, atopic dermatitis, ulcerative colitis, trauma and viral, bacterial, fungal, parasitic, protozoal and helminthic infections) and cardiovascular disorders (e.g. congestive heart failure, ischaemic heart disease, angina pectoris, myocardial infarction, hypertensive heart disease, congenital heart disease and myocarditis). They are useful for creating knocking humanised animals or transgenic animals to model human ciseases, Sequences of the invention are useful in somatic or germiline con the present sequence is human SECP-26 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human secreted proteins and genes encoding the proteins, useful for treating, diagnosing and preventing cell proliferative, autoimmune/inflammatory, cardiovascular, developmental or neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yue H, Lee EA, Becha SD, Baughn MR, Yao MG, Tang YT;
Au-Young JK, Lal PG, Warren BA, Duggan BM, Tran UK, Xu Y;
Thangavelu K, Richardson TW, Bandman O, Jones KA, Yang J;
Emerling BM, Swarnakar A, Luo W, Walia NK, Arimzai Y, Khan FA;
Lu DAM, Griffin JA, Lee SY, Burford N, Elliott VS, Honchell CD;
He A, Mason PM, Li JX, Hafalia AJA, Gururajan R;
                                                                                                                                                                                                                                                                                                                                                                                         /note= "Mature SECP-26 protein"
                                                                                                                                                                                                                                                                         27. .47
/note= "Transmembrane domain"
49. .394
                                                                                                                    l. .48
/label= Signal peptide_#1
                                                                                                                                                                                                                                /label= Signal_peptide_#2
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                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-JUN-2001; 2001US-0297019P.
19-JUN-2001; 2001US-0299297P.
22-JUN-2001; 2001US-030937P.
29-JUN-2001; 2001US-0301936P.
06-MAR-2002; 2002US-0362439P.
08-MAR-2002; 2002US-0363649P.
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Emerling BM, bww..
Tam. Griffin JA, bee
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N-PSDB; AAD54312.
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Homo sapiens
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                                                                                                            Peptide
                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                             Domain
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The invention discloses a polymuclectide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel comparities that all the polymetrides a polymetride encoded by the polymetrides of the polymetride of the polymetride by contacting the polymetride or peptide or peptide of the polymetric of the polymetride by contacting the polymetride or peptide or peptide or peptide by contacting the polymetride or peptide or peptide or peptide or peptide of the polymetride of the polymetrial peptide or proteins are useful as pharmaceutical agents and many disease-related proteins peptide of genes may be included in them, for developing a diagnostic marker or medicines for regulation of their expression and activity or as targets of generation. Membrane proteins, disease-related proteins, disease-related proteins, creameration and genes or encoding them can be used as indicators for diseases (e.g. osteoporosis, encoding them can be used as indicators for diseases (e.g. osteoporosis, concert, the activity or expression of the encoded protein to treat diseases. The sequence presented is a protein of the invention. Note: Some of the
                                                                                                                                                                                                                                                                                                                                                                                                          Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration; cell regeneration; membrane protein; signal transduction-related protein; transcription-related protein; osteoporosis; neurological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or
                                                  Gaps
                                                  ;
0
          Length 394;
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             9
                                                                                                                                                                                                                                                                                                                                                                     Human protein encoded by clone OCBBF20120950.
                                                  Mismatches
             Score 49;
Pred. No.
                                                                                                                                                                                                                                               ADB64824 standard; protein; 512 AA.
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(REAS-) RES ASSOC BIOTECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-NOV-2001; 2001JP-00379298.
25-JAN-2002; 2002US-00350978.
                                                                                                                                                                                                                                                                                                                                  04-DEC-2003 (first entry)
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Query Match
Best Local Similarity 92.3<sup>7</sup>
....hes 12; Conservative
                                                                                               1 AAMAAAAAAAA 13
                                                                                                                       Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-450961/43.
N-PSDB; ADB62854.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer; tumour
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Homo sapiens.
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                                                                                                                                                26-JUN-2001
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Ishii S,
                                                                                                           AAB92956;
                         RESULT 19
                                                 4AB92956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL1617-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                        Gaps
                         the
sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             developmental biology; cell signalling; insecticide;
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                                                                                                                           Score 49; DB 7; Length 512;
Pred. No. 27;
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                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster polypeptide SEQ ID NO 6042.
                                                                                                                                                                      1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                         ABB59750 standard; protein; 578 AA.
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11-JUL-2000; 2000US-00614150.
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                                                                                                                             92.5%;
                                                                                                                                                                                                                                                      136 AAVAAAAAAAA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                     Query Match
Best Local Similarity 92.5-
Best Local 2; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster.
                                           European Patent Office.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-656860/75.
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                                                                                      Sequence 512 AA;
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pharmaceutical
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                                                                                                                                                                                                                                                                                                                  RESULT 18
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The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dr primer and an oligonucleotide complementary to the
complementary strand of a polymucleotide which comprises one of the 5602
nucleotide sequences defined in the specification, where the
complementary strand of a polymucleotide which comprises one of the 5602
complementary strand of a polymucleotide which comprises a 5'-end
complementary strand of a polymucleotide which comprises a 5'-end
complementary strand of a polymucleotide which comprises a 5'-end
complementary strand of a polymucleotide which comprises a 5'-end
complementary strand of a polymucleotide which comprises a 5'-end
complementary strand of a polymucleotide which comprises a 5'-end
complementary strand of a polymucleotide which comprises a 5'-end
complementary strand of a polymucleotide complementary to a
polymucleotide comprises a 1 least 15 nucleotides and the combination of
the 5'-end sequence/3'-end sequence is selected from those defined in the
specification. The primer sets can be used in antisense therapy and in
complementary full-length cDNAs. The primers are also useful for the
detection and/or diagnosis of the abnormality of the proteins encoded by
the full-length cDNAs. The primers allow obtaining of the full-length
conditionally without any specialised methods. AAH03165 to AAH13628 and
AAH13631 to AAH13632 represent human anino acid sequences; and AAH3629 to AAH3622 represent
colligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                     Human; primer; detection; diagnosis; antisense therapy; gene therapy.
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Otsuki T;
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A, Nagai K,
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                                                                                                                                                                                                                              Human protein sequence SEQ ID NO:11642.
AAB92956 standard; protein; 708 AA.
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Sugiyama T, Wakamatsu
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11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
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                                                                                                                                                      (first entry)
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hes 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
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                                                                                                                                                                                                                                                                                                              Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                Drosophila melanogaster polypeptide SEQ ID NO 38289.
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                                                          ABB70499 standard; protein; 815 AA.
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11-JUL-2000; 2000US-00614150.
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The present invention describes a nucleic acid sequence and its encoded polypeptide, which are part of at least one signalling pathway in insects and vertebrates. The nucleic acid sequence is the daughter of legless (dail) gene, as well as its homologues, fragments, derivatives, or functional or structural analogues. The polypeptide is the daughter of ediess (DOLL) procein, as well as its homologues, fragments, derivatives, or controlly and can be used in gene therapy. The daughter of derivatives, or functional or structural analogues. Doll sequences have cycostatic activity, and can be used in gene therapy. The doll nucleic acid, DOLL protein, or their homologues, derivatives or fragments can be used for developing a therapeutic and diagnostic compound (e.g. used for developing a therapeutic and diagnostic compound (e.g. arrinded RNA, or themical or naturally occurring compounds interfering cut differentiation or proliferation. Fragments of the doll DNA compounds interfering capter, differentiation or proliferation. Fragments of the doll DNA compounds interfering treatment or diagnosis of the doll DNA compounds interfering main doll sequences includes human tumours, (pre-) neophastic, compound interfering compounds includes human tumours, (pre-) neophastic, compounds interfering the present invention interfering the present invention interfering compounds includes human tumours, includes human tumours, includes human tumours in the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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1; Mismatches
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                                                                                                                                                          01-FEB-2002; 2002WO-CH000063
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                   Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                       Kramps
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a POSH (plenty
                                                                                                  The present invention relates to a method of identifying an antiproliferative agent, comprising providing a POSH (plenty of SH3 domains) polypeptide and a test agent, and identifying the test agent that interacts with the POSH polypeptide. The POSH protein is a ubiquitin ligase enzyme. The method is useful for identifying agents for treating a neoplastic condition, preferably cancer selected from thyroid carcinoma, liver cancer (hepatocellular cancer), lung cancer, cervical cancer, ovarian cancer, renal cell carcinoma, lymphoma, osteosacoma, liposarcoma, leukaemia, breast carcinoma and breast adenocarcinoma. The present sequence is a protein sequence shown in the exemplification of the
 neoplasia,
identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid encoding a POSH (plen of SH3 domains) polypeptide. The polypeptide sequence additionally comprises a RING domain. The nucleic acid mitigates a POSH loss of function phenotype in a cell. The POSH loss of function phenotype is a decrease in HIV virus like particle production. The method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Virucide, ligase inhibitor; gene therapy; POSH; plenty of SH3 domains; RING domain, envelop virus; retroid virus; RNA virus; retrovirus; rhabdovirus; lentivirus; filovirus.
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Identifying an anti-proliferative agent, useful for treating comprises providing a POSH polypeptide and a test agent, and the test agent that interacts with the POSH polypeptide.
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Pred. No. 45;
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                                                                      2; Fig 15; 151pp; English
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15-MAR-2002; 2002US-0364530P.
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                                                                                                                                                                                                                                                                                        invention
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                                                                        Claim
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                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL186176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, fruit fly, mouse, POSH, plenty of SH3 domains, ubiquitin ligase,
cell proliferation, enzyme, cytostatic, cancer.
                                                                                                                                                                                                                                New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 41523; 21pp + Sequence Listing; English.
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                                                                                                                                           Myers EW;
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                                                                                                                                           PWD,
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26-JUN-2002; 2002US-0391629P.
27-NOV-2002; 2002US-0429916P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.5%;
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                23-MAR-2001; 2001WO-US009231.
                                                  23-MAR-2000; 2000US-0191637P.
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                                                                                                                                           Venter JC, Adams M,
                                                                                                                                                                            2001-656860/75
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                                                                                                       (PEKE ) PE CORP NY
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N-PSDB; ABL15680
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                                                                                                                                                                                                                                                                     interactions.
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invention involves producing a recombinant POSH polypeptide. Also disclosed is a method for identifying an antiviral or antiapoptotic agent, comprising providing a POSH polypeptide and a test agent, and identifying a test agent that interacts with the POSH polypeptide. The POSH polypeptide comprises an SH3 or RING domain, where the test agent binds. The test agent is a polypeptide, an antibody, a small molecule or a peptidomimetic. The test agent that interacts with POSH decreases the maturation of a virus containing the PTAP or PPEY motif. The interaction with POSH and decreases the interaction between POSH and Gap polypeptide. Alternatively, identifying an antiviral agent comprises providing a POSH nucleic acid and a test agent, and identifying a test agent that binds to the POSH nucleic acid. The test agent is a contained of a ribozyme. The nucleic acids, polypeptides, compositions and enzyme or a ribozyme. The nucleic acids, polypeptides, compositions and methods of the invention are useful for treating virtual disorders, and and a test agent is a compositions and methods of the invention are useful for treating virtual disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      particularly disorders caused by envelop viruses, retroid viruses and RNA viruses, including retroviruses, rhabdoviruses, lentiviruses and filoviruses. The current sequence represents the mouse POSH protein
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Sequence 892 AA;

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Gaps
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92.5%; Score 49; DB 7; Length 892; 92.3%; Pred. No. 45; o; Indels ive 1; Mismatches 0; Indels
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419 AAVAAAAAAAA 431
                                                                      1 AAMAAAAAAAA 13
                     Best Local Similarity 92.3
Matches 12; Conservative
       Query Match
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ADR89697 standard; protein; 892 AA. (first entry) 18-NOV-2004 ADR89697; RESULT 25
ADR89697
XX
AC ADR89
XX
DT 18-NO
XX
MULIN
XX
MOUSE
XX
MUS 8
OS MUS 8
OS WUS 8
OS WUS 8
OS WUS 9
OS WUS 8
OS WUS 9
OS WUS 1
OS WU

Mouse; POSH; plenty of SH3 domains; virucide; anti-HIV; cytostatic; Murine POSH (Plenty of SH3 domains) coding sequence. vaccine.

Mus sp.

WO2004073609-A2.

02-SEP-2004.

05-FEB-2003; 2003US-0445534P. 03-MAR-2003; 2003US-0451437P. 21-APR-2003; 2003US-0464285P. 16-SEP-2003; 2003US-0503931P.

05-FEB-2004; 2004WO-US003600.

(PROT-) PROTEOLOGICS INC

Taglicht DN, Reiss Y, Yaar L, 2004-635468/61. Alroy I,

N-PSDB; ADR89696

Tuvia S;

New complex comprising a Plenty Of SH3 (POSH) polypeptide and a POSH-associated kinase (POSH-AK) or its subunit, useful in preparing a composition for treating or preventing a POSH associated cancer.

Disclosure; SEQ ID NO 9; 163pp; English

The present sequence is the protein sequence of murine Plenty Of SH3 domains (POSH). The invention provides novel complexes of POSH

polypeptides and POSH associated kinases (POSH-AKB). An isolated, countied or recombinant complex comprising a POSH polypeptide and a POSH-AK but of a POSH-AK is claimed. The complex is used in methods for identifying agents that modulate an activity of POSH or POSH-AK by disrupting a complex of POSH and POSH-AK. These modulator agents can be used as antiviral agents, or as anti-apoptotic or anti-cancer agents in which a modulator agent will decrease the proliferation or survival of a POSH-associated cancer cell. The modulator agents may also inhibit thraftixing of a protein through the servetory pathway. An inhibitor of POSH, e.g. an agent that inhibits a POSH-AP, or an agent that inhibits posh, e.g. an agent that inhibits a POSH-AP, or an agent that inhibits complex containing and thence to treat a JMK pathway-associated disease. A posh or understain of the protein kinase (JMK) pathway in a coll and hence to treat a protein kinase A (PKA) associated disease. A method of enhancing interaction of a POSH polypeptide with a second protein in a cell comprises contacting the cell with an agent that inhibits phosphorylated POSH by PKA. An isolated, purified or crecombinant phosphorylated POSH polypeptide is claimed, which is phosphorylated POSH polypeptide is claimed, the sequence K/R-R-X-S/T-hydrophobic or R-X-X-S/T-hydrophobic. Also claimed is a portion of a POSH polypeptide including a consensus PKA possphorylation site and compensation at least one modified amino acid or postpidomimetic moiety, which inhibits PKA phosphorylation of POSH. ô cytostatic; nootropic; neuroprotective; antiparkinsonian; anticonvulsant; antiviral; neuroleptic; central nervous system; POSH polypeptide; POSH-associated protein; POSH-AP; HERPUDI; Ubiquitin ligase; antiviral agent; anti-apoptotic agent; anti-cancer agent; neurological disorder progression disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; schizophrenia; Gaps ö Score 49; DB 8; Length 892; Pred. No. 45; 1; Mismatches 0; Indels ADS34245 standard; protein; 892 AA. POSH protein associated protein #4. 03-MAR-2003; 2003US-0451437P. 05-MAR-2003; 2003US-0452284P. 19-MAR-2003; 2003US-0455760P. 20-MAR-2003; 2003US-0456640P. 03-APR-2003; 2003US-0460526P. 04-APR-2003; 2003US-0460792P. 21-APR-2003; 2003US-046428FP. 09-MAY-2003; 2003US-0469462P. 92.5%; 92.3%; 02-MAR-2004; 2004WO-US006308 ||:|||||||||| 419 AAVAAAAAAAAA 431 02-DEC-2004 (first entry) 1 AAMAAAAAAAA 13 Local Similarity 92.3 Niemann-Pick's disease WO2004078130-A2. Sequence 892 AA; Homo sapiens. 16-SEP-2004. ADS34245; Query Match Matches RESULT 26 ADS34245 %\$GGGGGGGGGGGGGGGGGGGGGGGGG ò 유

Taglicht DN;

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The present sequence is the protein sequence of murine POSH (plenty of SH3 domains), a ubiquitin ligase. The invention relates to POSH and to the discoverty of novel interactions between POSH and POSH and to proteins, especially HERPUDI. Methods are provided for modulating a process in which POSH participates by targeting HERPUDI or the POSH participates by targeting a process in which HERPUDI participates of EOSH and hence the POSH-mediated ubiquitination. The neurological disorder is selected from: Alzheimer's disease, Parkinson's disease, Huntington's disease, Pick's disease, Niemann-Pick's disease, Huntington's disease, depression and schizophrenia. The modulator agent is a short interfering RNA (siRNA) construct, a small molecule, an antibody or an antisense construct.
                                                                                                                                                                                                                                                                                                                                                              New complex of POSH polypeptides and POSH-associated protein (POSH-AP) useful for identifying an agent for treating neurological disorder e.g. Alzheimer's disease, Parkinson's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.5%; Score 49; DB 8; Length 892; 92.3%; Pred. No. 45; ive 1; Mismatches 0; Indels
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                                                                                               03-APR-2003; 2003US-0460526P.
03-JUN-2003; 2003US-0475825P.
02-MAR-2004; 2004WO-US006308.
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20-MAR-2003; 2003US-0456640P.
09-MAY-2003; 2003US-0469462P.
                                                     05-APR-2004; 2004WO-US010582
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                                                                                                                                                                                                                                             Yaar L, Alroy I, Reiss Y,
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                                                                                                                                                                                               (PROT-) PROTEOLOGICS INC
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                                                                                                                                                                                                                                                                                         WPI; 2004-748573/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                  N-PSDB; ADT77903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 892 AA;
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    21-OCT-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated, purified or recombinant complex (I) comprising a PoSH polypeptide and a PoSH-associated protein (POSH-AP) (a) or HERPUDI and a Ubiquitin ligase (b). Methods using (I), (a) or (b) are useful for identifying an agent that modulates an activity of a POSH polypeptide or POSH-AP, for identifying an antiviral agent, an anti-apoptotic agent, an anti-cancer agent, an agent that inhibits trafficking of a protein through the secretory pathway, an agent that inhibits the progression of a neurological disorder, an agent that modulates a POSH function, an agent that modulates a HERPUDI function. The methods can be used for treating a viral infection, for inhibiting an activity of a POSH-associated disease is viral infection, POSH-associated cancer or POSH-associated disease is viral infection, POSH-associated cancer or POSH-associated neurological disorder. The methods are useful for treating or preventing POSH-associated neurological disorder. The methods are useful for treating or preventing POSH-associated neurological disorder in a subject e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease, schizophrenia, Niemann-Pick's disease. This sequence corresponds to a protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated, purified or recombinant complex, useful for identifying an antiviral, anti-apoptotic or anti-cancer, comprising POSH polypeptide and POSH-associated protein (POSH-AP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse, POSH, plenty of SH3 domains, ubiquitin ligase, enzyme, neuroprotective, nootropic, antiparkinsonian, anticonvulsant, cerebroprotective, CNS-gen.; antidepressant, neuroleptic, gene therapy.
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Pred. No. 45;
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                                                                                                                                                                                                                                                                                                                                                              Yaar L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 9; 374pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADT77904 standard; protein; 892 AA
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                                                                                                                   19-JUN-2003; 2003US-0480376P.
08-AUG-22003; 2003US-0493860P.
28-AUG-2003; 2003US-04938634P.
16-SEP-2003; 2003US-0503931P.
10-NOV-2003; 2003WO-US035712.
05-FB-2004; 2004WO-US035600.
                                              2003US-0475825P.
2003US-0479317P.
2003US-0480215P.
    2003US-0472327P.
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Best Local Similarity
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20-MAY-2003; 2
30-MAY-2003; 2
03-JUN-2003; 2
                                                                    17-JUN-2003;
19-JUN-2003;
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Gaps

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niemann pick disease; prion infection; inflammation; autoimmune disease; diabetes mellitus; glycosylation; liver tumor; hepatocellular carcinoma; lung tumor; cervical dysplasia; colorectal tumor; ovary tumor; renal carcinoma; lymphoma; osteosarcoma; prostate tumor; leukemia; breast tumor; thyroid tumor; cancer.

us-10-617-568-3.rag

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                                                                                                                                                                                                                                                         The present sequence is the protein sequence of mouse POSH. The invention relates to novel associations between Cbl-b and POSH. Cbl-b and POSH are involved in viral maturation, including the production, post-translational processing, assembly and/or release of proteins in a viral particle. Viral infections may be ameliorated by inhibiting an activity (e.g. ubiquitin ligase activity or target protein interaction) of POSH or cbl-b. The virus is a retroid virus, an RNA virus or an envelope virus, especially a human immunodeficiency virus. A claimed method of identifying an antiviral agent comprises identifying a test agent that disrupts a complex of a Cbl-b polypeptide and a POSH polypeptide. A claimed method of treating a viral infection comprises administering an agent that inhibits the expression activity of Cbl-b. The agent is preferably an siRNA construct ADU73816 that inhibits especial
                                                                                                                                                                                                                                                                                                                                                                                                                                                 of human Cbl-b, an antisense construct, an antibody, a polypeptide or a small molecule. Also claimed are: methods of identifying and evaluating agents that modulate a Cbl-b or PoSH function by measuring the effect of the agent on Cbl-b-mediated or PoSH-mediated builduitination or on budding, release, infectivity or reverse transcriptase activity of a virus or virus-like particle; methods of identifying an anti-apoptotic agent, an anti-cancer agent or an agent that inhibits progression of a neurological disorder, where the agent disrupts a complex comprising Cbl-b and PoSH (or a CBl-b-associated protein such as POSH); and methods of
                                                                                                                                                          New isolated, purified or recombinant complex comprises a Cbl-b polypeptide, a POSH polypeptide, useful for treating Cbl-associated diseases, e.g. cancer, viral infection, disorders of the immune system,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treating or preventing a POSH-associated cancer, POSH-associated neurological disorder or POSH-associated viral disorder using an agent that inhibits the expression or an activity of a Cbl-b polypeptide.
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Pred. No. 45;
1; Mismatches 0; Indels
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                                                                                        Barr
                                                                                        Tuvia S,
                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 9; 190pp; English.
                                                                                        Alroy I,
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 15-MAY-2003; 2003US-0471378P.
19-JUN-2003; 2003US-0480215P.
19-JUN-2003; 2003US-0480376P.
                                                                                                                                                                                          diseases, e.g. cancer, vire or neurological disorders.
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Matches 12; Conservative
                                                          (PROT-) PROTEOLOGICS INC
                                                                                        Reiss Y, Taglicht DN,
                                                                                                                    WPI; 2004-805123/79.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 892 AA;
                                                                                                                                     N-PSDB; ADU73760
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or SH3

Modulating activity or localization of trans-Golgi network (TGN)-associated protein useful, eg, for inhibiting Beta amyloid production reducing virus infectivity comprises modulating activity of plenty of

Example 22; SEQ ID NO 9; 248pp; English.

domains protein (POSH)

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Tuvia S,

Alroy I, Reiss Y, Taglicht DN,

WPI; 2004-833580/82.

N-PSDB; ADU68996

(PROT-) PROTEOLOGICS INC.

11-NOV-2002; 2002EP-00257796. 12-NOV-2002; 2002US-0029365. 29-JAN-2003; 2003US-0043495P. 02-JUN-2003; 2003US-045387P. 01-AUG-2003; 2003US-0491891P.

10-NOV-2003; 2003WO-US035712

WO2004098492-A2 Mus musculus.

18-NOV-2004

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The invention relates to a novel method for modulating the activity or localization of a trans-Golgi network (TGN) -associated protein. The method involves modulating the activity of one or more TGN-associated or proteins chosen from plenty of SH3 domains protein (PoSH), a POSH-pathway CC proteins chosen from plenty of SH3 domains protein (PoSH), a POSH-pathway polypeptide, a PoSH-associated polypeptide or a POSH binding protein. The method of the invention demonstrates neuroprotective, nootropic, contidiabletic, antinflammatory, virucide, antibacterial, antiparsitic, immunosuppressive, antiparkinsonian, anticonvulsant, neuroleptic, cytostatic and CNS-Gen applications. The method of the invention may be cytostatic and CNS-Gen applications. The method of the invention may be cytostatic and CNS-Gen applications. The method of the invention may be cytostatic and CNS-Gen applications. The method of the invention may be cytostatic processing of a protein associated with a neurological disorder, of a viral, bacterial, parasitic or microbial protein, and for inhibiting cardiovascular disease or immunological disorder, in the subject, where the subject exhibits a neurological disorder chosen from Alzheimer's disease and prion-associated disease, parkinson's disease and prion-associated disease, preferably con immunological disorder chosen from an inflammatory disease or an autoimmune disease, such as diabetee or a disease associated with a neoplastic impunological disorder plycosylation, where the improper glycosylation is N-linked cylycosylation in a subject having cancer. The cancer is chosen from thyroid cancer, only a protein such as a myristylated protein, and for inhibiting cancer, nepatocellular cancer, lung cancer, cervical cancer, hepatocellular cancer, lung cancer, cervical cancer, hepatocellular cancer, lung cancer, colorectal cancer, hepatocellular secured cancer, lung cancer, colorectal cancer, protein secured cancer, lung cancer, colorectal cancer, protein serviced protein protein serviced cancer, lungman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        carcinoma and breast adeno-carcinoma, preferably breast cancer or colorectal cancer. The current sequence is that of a POSH protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Length 892;
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92.5%; Score 49; DB 92.3%; Pred. No. 45; iive 1; Mismatches 12; Conservative Local Similarity Matches

1 AAMAAAAAAAA 13

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protein secretion; protein localization; golgi apparatus; plenty of SH3 domains protein; POSH; neuroprotective; nootropic; antidiabetic; antiinflammatory; virucide; antibacterial; antiparasitic; immunosuppressive; antipartinsonian; anticonvulsant; neuroleptic; cytostatic; CNS-Gen.; cardiovascular disease, viral infection; bacterial infection; bacterial infection; microbial protein; neurological disease; immune disorder; Alzheimers disease; parkinsons disease;

House mouse plenty of SH3 domains (POSH) protein.

(first entry)

10-FEB-2005

ADU68997 standard; protein; 892 AA.

ADU68997

a

0; Indels

Gaps ö

POSH inhibitor; ubiquitin ligase inhibitor; APP; cell proliferation; amyloid precursor protein; viral infection; neurological disease; Huntingtons chorea; Alzhelmers disease; parkinsons disease; pick's disease; major depressive disorder; schizophrenia; cancer; cytostatic; virucide; anti-HIV; neuroprotective; nootropic; anticonvulsant; antiparkinsonian; cerebroprotective; antidepressant; ADW87412 standard; protein; 892 AA Mouse POSH protein SEQ ID NO 9. 419 AAVAAAAAAAA 431 (first entry) WPI; 2005-132260/14. N-PSDB; ADW87411 WO2005007141-A2. 07-APR-2005 neuroleptic 27-JAN-2005 ADW87412; cancers Mus sp. RESULT 30 셤 

This invention describes a novel small molecule inhibitor of a POSH polypeptide chosen from human Cbl-b polypeptide, a human PEM-3-like polypeptide, a SIAH1 polypeptide or a TTG3 polypeptide, comprising a RING domain. The POSH polypeptide is ARIN2, AFESA1, BANP1, BAT3, BARN1, BAT3, BCAR1, BCB9, BIA2, BRD4, CLK2, COLTA1, DAP, DDX31, DKF2P434B1231, DKF2P76LA052, CIC, CL25084, CLK2, COLTA1, DAP, DDX31, DKF2P434B1231, DKF2P76LA052, DLG5, DNM2, DRP2, EEFIA1, EGLN2, EIFAB121, DKF2P76LA052, CIC, CL25084, CL313479, FU31474, FST11, GC20, GLU1, HEBP2, CLJ13131, KLA1391, LAMA5, LOC118987, LOC20987, MADH6, MAP1A, MBD2, MRP136, MT2A, NAP4, NQO2, NUMA1, OPTN, PA1-RB1, PAWK, PCBP1, CRN22, PCN22, PCN22, RPS20, RPS20, SETDB 1, SF3A2, SETDB 1 New small molecule inhibitor of a POSH polypeptide useful e.g. to inhibit ubiquitin ligase activity of polypeptide, to treat viral infections, neurological disorder e.g. Alzheimer's disease, and to treat or prevent Levi-Hacham O; Claim 45; SEQ ID NO 9; 171pp; English. 11-JUL-2003; 2003US-0486730P.
24-JUL-2003; 2003US-0489755P.
10-NOV-2003; 2003US-04897512.
02-MAR-2004; 2004US-US065308.
05-MAR-2004; 2004WO-US066519.
05-ARR-2004; 2004WO-US066619. Alroy I, Tuvia S, Reiss Y, 09-JUL-2004; 2004WO-US021900 28-MAY-2004; 2004WO-US016865 (PROT-) PROTEOLOGICS INC

ö transport of amyloid precursor protein (APP) in a cell or cell proliferation or amyloid polypeptide production in a cell and also for the treatment of a viral infection (an envelope, a retroviral or a human immunodeficiency viral infections) or neurological disorder (Alzheimer's disease, Parkinson's disease, Huntington's disease, Pick's disease, depression or schizophrenia). The inhibitor is also useful in the treatment and prevention of cancer, in a method of inhibiting ubiquitin ligase activity of a polypeptide, for maturation of a virus in a cell, for transport of APP and is capable of targeting one or more proteins. The products of the invention have cytostatic, virucide, anti-HIV, cerebroprotective, nootropic, anticonvulsant, antiparkinsonian, cerebroprotective, antidepressant and neuroleptic activity. This sequence represents a mouse POSH protein. This sequence represents a mouse ubiquitin (Ub) ligase, plenty of SH3 domains (POSH). The composition of the invention comprises a human POSH polypeptide and a POSH-associated protein (POSH-AP), or a polypeptide comprising a domain that is 90% indentical to a POSH SH3 domain and a POSH involved in many cellular processes, including viral maturation, stimulating ubiquitinylation of certain proteins, vesicular trafficking, regulating Rac or JNK signaling pathway, etc. An antibody which is rimmunoreactive with the epitope of human POSH amino acid sequence, where the antibody disrupts the interaction between a POSH polypeptide and a POSH-AP may be used for inhibiting viral infection. The POSH-AP comprises Isolated, purified or recombinant complex useful for identifying antiviral agent and anti-apoptotic agent, comprises plenty of SH3 domains POSH polypeptide and POSH-associated proteins POSH-AP. Gaps Virucide, human; ubiquitin ligase; Ub; plenty of SH3 domains; POSH; POSH-associated protein; POSH-AP; SH3 domain; viral maturation; ubiquitinylation; vesicular trafficking; viral infection; enzyme. ö 9; Length 892; 0; Indels Score 49; DB 9 Pred. No. 45; 1; Mismatches Disclosure; SEQ ID NO 9; 171pp; English ADZ66429 standard; protein; 892 AA. 92.5%; 18-OCT-2004; 2004WO-US034498. 17-OCT-2003; 2003US-0512046P. ||:|||||||| 419 AAVAAAAAAAA 431 (first entry) 1 AAMAAAAAAAA 13 12; Conservative (PROT-) PROTEOLOGICS INC. WPI; 2005-322863/33. Query Match Best Local Similarity Sequence 892 AA; N-PSDB; ADZ66428 WO2005038007-A2 14-JUL-2005 28-APR-2005. Mouse POSH ADZ66429; Reiss Y; Mus sp. Matches RESULT 31 ADZ66429 g ò

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The invention relates to a novel method for identifying a protein substrate for an E3 protein comprising expression of an E3 protein, a bait fusion protein and a prey fusion protein in a cell, where the E3 protein that is a protein substrate of the bait protein to a prey protein that is a protein substrate of the E3 protein. The physical protein inmediated proteins induces an output signal which is detected. The ubiquitin-mediated proteolysis system is the major pathway for the selective, controlled degradation of intracellular proteins in eukaryotic cells. The process of degradation is catalyzed by a ubiquitin-activating enzyme (E1) and a ubiquitin-conjugating enzyme (E2), but may also require auxiliary substrate recognition proteins (E3s). The method of the continum may be useful for identifying a protein substrate for an E3 protein, which is subsequently useful for mediating ligation of ubiquitin or ubiquitin-like proteins. The current sequence is that of the murine POSH (plenty of SH3 domains) protein of the invention.
                                                                                                                                                                                      ö
BE2, which is chosen from UBC13, UBC5a, UBC5c and UBC6. The UBC13 is in a heterodimeric complex with a Ub conjugating enzyme variant (UBV) protein eg. UBV1a. The composition of the invention is useful for identifying an anti-viral agent and an anti-apoptotic agent, which involves identifying a test agent that disrupts the compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful to allow
of an E3 protein, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein degradation; protein interaction; POSH; plenty of SH3 domains.
                                                                                                                                                                                      Gaps
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                                                                                                                                                   DB 9; Length 892;
                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying a protein substrate for an E3 protein, modulation of ubiquitination, comprises expression bait fusion protein, and a prey protein in a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine POSH (plenty of SH3 domains) protein.
                                                                                                                                                 Score 49; DB 9
Pred. No. 45;
1; Mismatches
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                                                                                                                                                   92.5%;
92.3%;
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Best Local Similarity 92.3
Matches 12; Conservative
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REFSEQ; NP_067481.1.
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DB 9; Length 892; 45;

Score 49; Pred. No.

92.5%;

Best Local Similarity

Query Match

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The invention relates to a method for identifying an agent that modulates
an activity of a HERPUDI polypeptide. The method comprises identifying an
agent that modulates a complex comprising a HERPUDI
colypeptide, where an agent that modulates a complex comprising a HERPUDI
colypeptide and a Nef polypeptide is an agent that modulates an activity
of the HERPUDI polypeptide. Also described: (1) a method of inhibiting a
contining the progression of AIDS in a subject infected with HIV; (3) an
colypeptide and a Nef polypeptide; (4) a method of inhibiting a
colypeptide and a Nef polypeptide; (4) a method of identifying an
activity an enter, (5) a method of inhibiting viral replication in a cell;
colypeptide; and (8) a Nef polypeptide. The methods are useful for
colypeptide; and (8) a Nef polypeptide. The methods are useful for
colypeptide; and (8) a Nef polypeptide. The methods are useful for
collibiting a Nef-mediated process in a cellinfected with HIV, and
cinhibiting a progression of AIDS in a subject infected with HIV, and
conhibiting the progression of AIDS in a subject infected with HIV. The
control of collibiting a viral infected with HIV, and
collibiting the progression of AIDS in a subject infected with HIV. The
collibiting a Nef-mediated process in a cell infected with HIV. The
collibiting a Nef-mediated polypeptide in a subject infected with HIV. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying agent that modulates activity of HERPUDI polypeptide, by identifying agent that modulates a complex comprising HERPUDI and Nef polypeptide, where agent that modulates the complex modulates activity of HERPUDI polypeptide.
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                                                                                                                                                                                                                                                                                                                        viral maturation inhibition; viral replication; viral infection; antiviral; anti-HIV; POSH.
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Pred. No. 45;
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, SEQ ID NO 9; 141pp; English
                                                                                                                                                                       AEC94736 standard; protein; 892 AA.
                                                                                                                                                                                                                                                                                        Mouse POSH protein SEQ ID NO:9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAR-2005; 2005US-00070332.
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19-JUL-2004; 2004US-0589261P.
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419 AAVAAAAAAAAA 431
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Best Local Similarity 92.3.
Best Local 21 Conservative
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12; Conservative
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N-PSDB; AEC94735.
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RESULT 35

419 AAVAAAAAAAA 431

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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain creation (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed control of (II) is useful in gene therapy techniques to restore normal cativity of (II) in or to treat disease states involving (II). (II) is useful in gene therapy techniques to restore normal conspicul for generating antibodies against it, detecting or quantitating a polyment. (II) and its binding partners are useful in medical imaging of supplement. (II) and its binding partners are useful in medical imaging of supplement. (II) and (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in colyppeptide and polymucleotide sequences have applications in colyppeptide for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this gratem tid not appear in the printed specification, but was obtained in colfpection int/pub/published_pct_esquences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy, forensic, food supplement; medical imaging; diagnostic; genetic disorder.
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Pred. No. 50;
1; Mismatches
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                                                                                                            Novel human diagnostic protein #5900.
ABG05909 standard; protein; 992 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT;
                                                                                                                                                                                                                                                                                                                      30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                            31-MAR-2000; 2000US-00540217, 23-AUG-2000; 2000US-00649167,
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                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-639362/73
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                            WO200175067-A2
                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           biodiversity.
                                                                         13-FEB-2002
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                                    ABG05909;
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                 developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 24801; 21pp + Sequence Listing; English
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                                                                                                     Drosophila melanogaster polypeptide SEQ ID NO 24801.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster polypeptide SEQ ID NO 2271.
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              ABB66003 standard; protein; 1184 AA.
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                                                                                                                                                                                                                                                                        23-MAR-2001; 2001WO-US009231
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11-JUL-2000; 2000US-00614150
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                                                                         (first entry)
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                                                                                                                                                                               Drosophila melanogaster.
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                                                                                                                                   Drosophila; dev
pharmaceutical.
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                                                                                                                                                                                                                                          27-SEP-2001.
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                                           ABB66003;
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ABB58493
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ABB6600
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The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed can dispuse therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful in generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating a useful for spencating and its binding partners are useful in medical imaging colypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diaponostics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 49; DB 4; Length 1444;
Pred. No. 71;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster polypeptide SEQ ID NO 3747.
                                                                                                                                                                                   Claim 20; SEQ ID NO 46026; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB58985 standard; protein; 1937 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            782 AAIAAAAAAAA 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AAMAAAAAAAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-656860/75
               WPI; 2001-639362/73.
N-PSDB; AAS79854.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1444 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200171042-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB58985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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ABB58985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher elucatores for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, chromosome mapping, gene mapping, gene therapy, forensic; food supplement, medical imaging, diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 2271; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 49; DB 4; Length 1235; Pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                            Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human diagnostic protein #15658.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG15667 standard; protein; 1444 AA.
                                                                                                                                                                                                                                                                              PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang YT;
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23-AUG-2000; 2000US-00649167.
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                                                                                                                           23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                    23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AAMAAAAAAAA 13
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  Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu C,
                                                                                                                                                                                                                                                                                                                   WPI; 2001-656860/75.
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                                                                                                                                                                                                                                   (PEKE ) PE CORP NY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1235 AA;
                                                                                                                                                                                                                                                                                                                                           N-PSDB; ABL02596
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                                             WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                           interactions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-FEB-2002
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                                                                                    27-SEP-2001
                                                                                                                                                                                                                                                                            Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG15667;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher useryers for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proreins (ABB37737-ABB32072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, p53 pathway, therapeutic, angiogenic disorder, apoptotic disorder, chromodomain helicase DNA binding protein, CHD, cancer, gene therapy, cell proliferative disorder, chromatin organisation modifier domain;
                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                               Disclosure; SEQ ID NO 3747; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "Conserved C-terminal domain"
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Pred. No. 93;
1; Mismatches
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739. .1035
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1100. .1174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE36107 standard; protein; 1944 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; 2001US-0328605P.
; 2001US-0338733P.
; 2002US-0357253P.
; 2002US-0357600P.
                                                                                                                                                                                                                                                                                                                                                                                                               92.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                330 AAVAAAAAAAAA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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nes 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EXEL-) EXELIXIS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-156840/15.
                                                                                                                                                                                                                                                                                                                                                                        Sequence 1937 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200298899-A2
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22-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lioubin MN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE36107;
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
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The present invention relates to a method for identifying candidate p53 pathway modulating agents. The method involves contacting an assay system comprising purified chromatin organisation modifier (chromo) domain helicase DNA binding proteins (CHD), nucleic acids, their functionally active fragments or derivatives, with a test agent under conditions where, but for the presence of the test agent, the system provides a reference activity. The methods are useful for identifying modulators of the p53 pathway as therapeutic targets for disorders associated with defective p53 function, such as anglogenic disorders, apoptotic disorders or cell proliferative disorders, e.g. cancer. The modulators are useful as research reagents, diagnostics and therapeutics. The invention is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antiinflammatory, Antiarteriosclerotic, Antipsoriatic, Gynaecological, Vasotropic, Vulnerary, Hypotensive, Antianginal; Cardiant, Osteopathic, gene therapy, antiangiogenic, tumour vascularisation, retinopathy: rheumatoid arthritis, Crohn disease, atherosclerosis, ovarian hyperstimulation; psoriasis, endometriosis, neovascularization, restenosis, cardiovascular disease; hypertension; Raynaud disease; muscular degeneration; osteoporosis, human; CHD3.
Identifying a candidate p53 pathway-modulating agent as therapeutic targets for disorders related to defective p53 function e.g. cancer by contacting an assay system having purified CHD polypeptide or nucleic acid, with a test agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful in gene therapy. The present sequence is human chromodomain
helicase DNA binding protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 49; DB
Pred. No. 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 94;
1; Mismatches
                                                                                                                                                                                                Claim 13; Page 207-215; 278pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92.5%;
92.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-MAR-2002; 2002FR-00003655
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Claim 5; SEQ ID NO 34; 110pp; French.

atherosclerosis; ovarian hyperstimulation; psoriasis; endometriosis associated with neovascularization; restenosis (arterial or after balloon angioplasty); overgrowth of cells in wound healing; peripheral vascular disease; hypertension; vascular inflammation; Raymaud disease; aneurysm; thrombophlebitis; lymphedema; ischaemia; angina; myocardial infarct; ofronic heart disease; (congestive) cardiac insufficiency; age-related muscular degeneration and osteoporosis. This sequence is chromodomain helicase DNA binding protein 3 (CHD3). The present invention relates to antiangiogenic pharmaceutical compositions. The compositions comprise, as active ingredient, one or more of: nucleic acid (I; ADI26740-ADI26744 and ADI2676-ADI26769) from an endothelial cell gene the expression of which is induced by an angiogenic agent, or its complement or fragment; polypeptide (II; ADI26745-ADI26749 and ADI26770-ADI26773) encoded by (I), or its fragment; an antisense nucleic acid (III; ADI26773) encoded by (I), or its fragment; expression of (I); or an antibody (Ab) that binds (II). The compositions are used for treating a wide range of angiogenic diseases: tumour vascularisation; retinopathy; rheumatoid arthritis; (rohalicialicialism) 

Sequence 1944 AA;

; Gaps ; Query Match

92.5%; Score 49; DB 7; Length 1944;
Best Local Similarity 92.3%; Pred. No. 94;
Matches 12; Conservative 1; Mismatches 0; Indels

1 PAMAAAAAAAA 13

||:||||||||| 207 AAVAAAAAAAAA 219

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9, 2006, 22:48:07 Search completed: September Job time : 101.418 secs

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Result Š. repair protein hypothetical protein hypothetical protein to pro-neural achaete hypothetical prote hypothetical prote conserved hypothet hypothetical prote sugar ABC transpor probable ABC trans probable glutamate acyl CoA dehydroge probable acyl coen probable acyl coen probable potassium nonstructural prot hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote genome polyprotein genome polyprotein polyprotein - deng hypothetical prote aryl sulfottansfer T24D18.18 protein probable membrane probable phosphoes probable 2,3-bisph fumarate hydratase hypothetical prote ATP-dependent prot DNA helicase II (E ribonucleoside-dip hypothetical prote cobyric acid synth cobyric acid synth ribosomal protein NADH-ubiquinone ox carbon-monoxide de hypothetical prote hypothetical prote genome polyprotein proteinase (EC 3.4 proteinase (EC 3.4 probable two compo sensor protein Cpx nypothetical prote protein-tyrosine-p vitellogenin vit-2 vitellogenin vit-1 CT365 hypothetical conserved hypothet hypothetical prote conserved hypothet phosphoribosylglyc hypothetical prote r-cell surface pro hypothetical prote hypothetical prote DNA repair protein hypothetical prote conserved hypothet genome polyprotein negative modulator negative modulator protein vit-2 [imp hypothetical prote protein C34G6.6 protein C86115
AB0024
AB0024
BE96671
E96671
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GNWYUB
AG1081
AG2021
F89528
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F89528
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F89528
F89528 G75435 T22143 R5MUL9 D82822 A56279 S46805 D71288 I41124 A34866 JC5000 F86295 AD0994 T24660 B90186 D87510 T20851 C70868 S76229 T20850 T26238 C82194 AI0467 D70309 T13593 C87789 T13592 E83233 S74394 

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class II histocompatibility antigen-associated gamma chain Ii, 41K splice form - mouse N,Alternate names: Ia-associated invariant chain Ii41; invariant-chain proteoglycan core N,Contains: class II histocompatibility antigen-associated gamma chain Ii, 31K splice fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Note: the authors translated the codon AAC for residue 70 as Asp
R,Singer, P.A.; Lauer, W.; Dembic, Z.; Mayer, W.E.; Lipp, J.; Koch, N.; Hammerling, G.;
EMBO J. 3, 873-877, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 47-191,256-279 <SIN>
A;Cross-references: UNIPARC:UPI000016CEFA; GB:X00496; NID:g53102; PIDN:CAA25191.1; PID:
R;Eades, A.M.; Litfin, M.; Rahmsdorf, H.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-25 - READ-
A; Residues: 1-25 - READ-
A; Cross-references: UNIPARC: UPI0000089341; GB:M35872; NID:g194129; PIDN:AAA37897.1; PID
R; Stone, J.; Perry, R.; Todd, J.A.; McDevitt, H.O.
R; Stone, J.; Perry, R.; Todd, J.A.; March 1988
A; Reference number: S03099
A; Reference number: S03099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPARC:UP1000016CE3B; EMBL:X07129; NID:g52637; PIDN:CAA30141.1; PII R;Zhu, L.; Jones, P.P.
Nucleic Acids Res. 17, 447-448, 1989
A;Title: Complete sequence of the murine invariant chain (Ii) gene.
A;Reference number: S09284; MUID:89098406; PMID:2492095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Structure of the murine Ia-associated invariant (Ii) chain as deduced from A;Reference number: A02244; MUID:84207946; PMID:6327293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Immunol. 144, 4399-4409, 1990
A;Title: The IRV-gamma response of the murine invariant chain gene is mediated by
A;Reference number: A43530; MUID:90257363; PMID:2111346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Mus musculus (house mouse)
C;Species: 17-Mar-1987 #sequence revision 12-Apr-1996 #text change 09-Jul-2004
C;Accession: B27866; A27866; Ā02244; A43530; S03099; S09284; A28956
R;Koch, N.; Lauer, W.; Habicht, J.; Dobberstein, B.
EMBO J. 6, 1677-1683, 1987
A;Title: Primary structure of the gene for the murine Ia antigen-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Molecule type: DNA
A,Residues: 1-279 <KOC>
A,Cross-references: UNIPROT:P04441; UNIPROT:O19452; UNIPARC:UPI000017382A
                                                                                                                                                                                                                                                                                                                                                                                                                          #status predicted
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A;Note: the authors translated the codon AAC for residue 70 as Asp
A;Accession: A27866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 216;
                                           A map position: 5q31-5q33

A; Introns: 26/2; 84/1; 110/3; 131/3; 163/3; 193/1; 214/1
C; Superfamily: Lhyroglobulin type I repeat homology
C; Keywords: glycoprotein; transmembrane protein
F;1-30/Domain: intracellular #status predicted <INT>F;31-56/Domain: extrassmembrane #status predicted <INT>F;71-216/Domain: extracellular #status predicted <INT>F;71-516/Domain: extracellular #status predicted <INT>F;71-216/Domain: extracellular #status predicted <INT>F;71-216/Domain: extracellular #status predicted <INT>F;71-216/Domain: extracellular #status predicted <INT>F;114,120/Binding site: carbohydrate (Asn) (covalent) #st
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 73; DB 1; 100.0%; Pred. No. 2.7e-06; ive 0; Mismatches 0;
A; Cross-references: GDB:119846; OMIM:142790
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A;Cross-references: UNIPARC:UP1000003E32
A;Experimental source: strain AKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87 PVSKMRMATPLLMQA 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15; Conservative
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Matches 15; Conserv
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A; Residues: 1-58 <STO
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A; Residues: 81-104 cRIB>
A; Cross-references: UNIPARC:UP100002F1B4
A; Cross-references: UNIPARC:UP100002F1B4
B; Strubin, M.; Mach. B.; Long, E.O.
EMBO J. 3, 869-872, 1984
A; Title: The complete sequence of the mRNA for the HLA-DR--associated invariant chain re
A; Residues: WHENENSEREDQKEV, 1-216 <STR>
A; Cross-references: UNIPARC:UP100002AB09; EMBL:X00497; NID:932130; PIDN:CAA25192.1; PID
A; Residues: WHENENSEREDQKEV, 1-4 <STR>
A; Cross-references: UNIPARC:UP100000895C2
A; Residues: WHENENSEREDQKEV, 1-4 <STR2>
A; Residues: WHENENSEREDQKEV, 1-4 <STR2>
A; Residues: WHENENSEREDQKEV, 1-4 <STR2>
A; Residues: WHENENSEREDQKEV, 1-100000895C2
A; Residues: WHENENSEREDQKEV, 1-100000895C2
A; Residues: WHENENSEREDQKEV, 1-100000895C3
A; Reference number: 846255; MUID:94326933; PMID:8050579
A; Contents: annotation
A; Ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.Note: some conclusions in this reference are based on the assumption, with no experime C;Comment: Class II antigens are associated with the invariant gamma chain during intract a chains become independently integrated into the plasma membrane.

C;Comment: Both cell-free translation experiments and the consensus sequence for the initian additional sixteen residues upstream of the initiator, but this region is not I
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A; Residues: 1, XXXXXX, 14, X, 16-17 < CL2>
A; Residues: 1, XXXXX, 7, XXXXXX, 14, X, 16-17 < CL2>
A; Cross-referencés: UNIPARC: UPI0000173828
A; Cross-referencés: UNIPARC: UPI0000173828
A; Kudo, J.; Chao, L.Y.; Narni, F.; Saunders, G.F.
A; Kudo, J.; Chao, L.Y.; Narni, F.; Saunders, G.F.
A; Title: Structure of the human gene encoding the invariant gamma-chain of class II hist
A; Reference number: A93602; MUID:86093681; PMID:3001652
                                                                                                                                                                                                                                                                            class II histocompatibility antigen-associated gamma chain - human
N;Alternate names: CD74 antigen; HLA-DR antigen-associated invariant chain; MHC class II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-216 <CL1>
A;Cross-references: UNIPROT:P04233; UNIPROT:O19685; UNIPARC:UPI000016AA48; GB:K01144; NT
A;Accession: B93981
                                                                                                                                                                                                                                                                                                                                                                                         C'Species: Homo sapiens (man)
C'Species: Homo sapiens (man)
C'Date: O4-Dec-1906 #sequence revision 26-Jan-1996 #text change 31-Dec-2004
C'Accession: A93881; B93981; A93602; A94103; S28903; S07182; A33234; A02243; A27551; A30
R;Claesson, L.; Larhammar, D.; Rask, L.; Peterson, P.A.
R;Claesson, L.; Larhammar, D.; Rask, L.; Peterson, P.A.
A;Title: CDNA clone for the human invariant gamma chain of class II histocompatibility a A;Title: CDNA clone for the human invariant gamma chain of class II histocompatibility a A;Reference number: A93981; MUID:84170234; PMID:6324166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: A93602
A;Molecule type: DNA
A;Residues: 'MHRRSRSCREDOKPV',1-150,'T',152-216 <KUD>
                     ALIGNMENTS
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A; Status: preliminary
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antigen-associated invariant ch

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N;Contains: class II histocompatibility antigen-associated gamma chain, short splice for C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C;Accession. S04362; S02182
R;McKnight, A.J; Mason, D.W.; Barclay, A.N.
Nucleic Acids Res. 17, 3983-3984, 1989
Nucleic Acids Res. 17, 3983-3984, 1989
A;Fitler: Sequence of a rat MHC class II-associated invariant chain cDNA clone containing A;Reference number: S04362; MUID:89282409; PMID:2499873
                                                                                                                                                                                                                                                                                                                                                          A,Molecule type: mRNA
A,Residues: 1-280 <MCK>
A,Residues: 1-280 <MCK>
A,Residues: 1-280 <MCK>
A,Cross-references: UNIPROT:P10247, UNIPARC:UPI000012C6BC, EMBL:X14254; NID:956652; PIDI
R;Henkes, W.; Syha, J.; Reske, K.
Nucleic Acids Res. 16, 11822, 1988
A;Title: Nucleotide sequence of rat invariant gamma chain cDNA clone pLR-gamma-34.3.
A;Reference number: S02182; MUID:89098337; PMID:3264906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-192,257-280 <hEN>
A; Cross-references: UNIPARC:UPI00002AB0A; EMBL:X13044; NID:956497; PIDN:CAA31450.1; PII
A; Cross-references: UNIPARC:UPI000002AB0A; EMBL:X13044; NID:956497; PIDN:CAA31450.1; PII
A; Cross-references: UNIPARC:UPI0000000 ATC for residue 17 descriptions translated the authors translated the compatibility antigen-associated gamma chain; thyroglobulin C; Keywords: alternative splicing; transmembrane protein
F;197-255/Domain: thyroglobulin type I repeat homology <THY1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-127 < STO>
A, Cross-references: UNIPARC: UPI00005502CC, GB:AE002093; NID:g6598626; PIDN:AAF18659.1;
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A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
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C;Decies: Jana-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T44583
R;Summer, B.J.; McCaffery, M.W.; Cline, K.
submitted to the EMBL Data Library, April 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 24-Aug-2001
C;Accession: G84420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80.8%; Score 59; DB 2; Length 280;
85.7%; Pred. No. 0.0017;
iive 1; Mismatches 1; Indels
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Pred. No. 3.4;
3; Mismatches 1; Indels
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C,Superfamily: conserved hypothetical protein H10188
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Best Local Similarity 66.7.,
Best Local Similarity 61.7.,
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Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecule type: mRNA
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: UNIPARC:UP1000017382C
A;Note: proof by site-directed mutagenesis that the sole chondroitin sulfate glycosaminc
C;Genetics: 26/2; 83/1; 109/3; 130/3; 161/3; 192/1; 256/1; 277/1
A;Introns: 26/2; 83/1; 109/3; 130/3; 161/3; 192/1; 256/1; 277/1
C;Superfamily: class II histocompatibility antigen-associated gamma chain; thyroglobulin
C;Reywords: alternative splicing; glycoprotein; transmembrane protein
F;1-29/Product: class II histocompatibility antigen-associated gamma chain Ii,
F;1-29/Domain: intracellular #status predicted <CYT>
F;30-55/Domain: transmembrane #status predicted <TYM>
F;56-279/Domain: thyroglobulin type I repeat homology <THY1>
F;36-279/Domain: thyroglobulin type I repeat homology <THY1>
F;13,119,239,253/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;265/Binding site: carbohydrate (Ser) (covalent) #status experimental
A; Molecule type: DNA
A; Residues: 1-9, "M',11-112, 'Q',114-228,'STG',232-279 <ZHU>
A; Residues: 1-9, "M',11-112, 'Q',114-228,'STG',232-279 <ZHU>
A; Crose-references: UNIPARC:UP1000017382B
B; Miller, J.; Hatch, J.A.; Simonis, S.; Cullen, S.E.
Proc. Natl. Acad. Sci. U.S.A. 85, 1359-1363, 1988
A; Title: Identifization of the glycosaminoglycan-attachment site of mouse invariant-chain A; Reference number: A28956; MUID:88144436; PMID:3422739
A; Accession: A28956.
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F; 12-15/Region: endosomal/lysosomal sorting signal
F; 31-56/Domain: transmembrane #status predicted <TMM>
F; 57-204/Domain: extracellular #status predicted <EMM>
F; 81-104/Region: class II associated invariant chain CLIP motif
F; 81-104/Region: class II associated invariant chain CLIP motif
F; 112,118/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A, Cross-references: UNIPROT: Q29630, UNIPARC: UPI000008774C; DDBJ: D83962, NID: g1374680, PI
C, Comment: This is a type II intracellular membrane glycoprotein. It binds major histocc II expression and its function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   intracellular membrane glycoprotein type II invariant chain Ii - bovine (rSpecies: Bos primigenius taurus (cattle) (cj. 2004-11995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004 (cj. 2004-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004 (cj. 2004-1996 #s. Niimi, M.; Nakai, Y.; Aida, Y. Biochem Biochem Biochem Biochem Biochem Biochem Biochem Biochem Biochem: Judylys. Res. Commun. 222, 7-12, 1996 // Ajtile: Identification of bovine invariant chain (Ii) gene by nucleotide sequencing. AjReference number: JC4796; MUID:96212904; PMID:8630076
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Pred. No. 0.00069;
2; Mismatches 0; Indels
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PMSQMRMATPMLMRA 101
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Best Local Similarity 85.7
Matches 12; Conservative
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Best Local Similarity
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S04362 class II histocompatibility antigen-associated gamma chain, long splice form - rat

enterica serovar Typhi (strain C

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Cjaccession: AG0918
R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, R.Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Dowd, L.; White, N.; Farrar, J.; Moule, S.; O'Gaora, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P. Mature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; MUID:21534947; PMID:11677608
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C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
                                                                                                                               C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology C;Superfamily: human cytochrome P450 cytochrome P450 homology cP45> P;341-500/Domain: cytochrome P450 homology cP45> F;478/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                  Length 543
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14;
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19;
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2; Mismatches
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Pred. No.
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Best Local Similarity 66...
8; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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              T20D16.18; At2g23190
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C,Superfamily: helicase
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Matches 8; Conser
                                                        A; Map position: 2
A; Introns: 211/3; 339/3
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A;Molecule type: DNA
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A;Cross-references: UNIPROT:022188; UNIPARC:UPI00000A8D78; EMBL:AC002391; NID:g2642427;
A;Experimental source: cultivar Columbia
A;Experimental source: cultivar Columbia
R;Inin, X; Kaul, S; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M; Koo, H; Moffat, K.S; Cronin, L.A.; Shen, M; VanAken, S.E.; Umayam, L.; Tallon, L.
avs., D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
A;Tele: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUD:20083487; PMID:10617197
A;Residues: 1-543 «TOOD»
A;Residues: 1-540 «TOOD»
A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable poly(3-hydroxyalkanoate) polymerase - Rhodobacter capsulatus
C;Species: Rhodobacter capsulatus
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T03471
R;Vlcek, C.; Paces, V.; Maltese, N.; Paces, J.; Haselkorn, R.; Fonstein, M.
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
A;Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB1003
A;Reference number: Z14955; MUID:97404404; PMID:9256491
A; Description: An Arabidopsis homolog of TatC/YCF43.
A; Reference number: 222800
A; Reference number: 222800
A; A; Accession: T44583
A; Ascession: T44583
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residuas: 1-340 < SUM-A
A; Residuas: 1-340 < SUM-A
A; Cross-references: UNIPROT: 09SJV5; UNIPARC: UP1000003CA3E; EMBL: AF145045; PIDN: AAD33946.
C; Superfamily: conserved hypothetical protein H10188
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C;Genetics:
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Pred. No. 3.5;
3; Mismatches 1; Indels
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A,Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 2.2;
2; Mismatches
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A,Molecule type: DNA
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Best Local Similarity 66.7%;
Matches 8; Conservative
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314 PVTQMLLATPLL 325
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Best Local Similarity
8; Conserva
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C;Species: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T4346
R;Blum, H; Bauersachs, S; Mewes, H;W; Gassenhuber, J; Wiemann, S.
aubmitted to the Protein Sequence Database, December 1999
A;Reference number: 222517
                                                         Gaps
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A;Cross-references: UNIPROT:Q9UNNS; UNIPARC:UPI000016AC9D; EMBL:AL133631
A;Experimental source: adult testis; clone DKFZp434P1723
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Length 720;
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                                                         Indels
                                                                                                                                                                                                                                                                                                           hypothetical protein DKFZp434P1723.1 - human (fragment)
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A;Residues: 1-17 <COL>
A;Cross-references: UNIPARC:UP1000172EBA; GB:M38257
C;Comment: The gene that codes for this protein is induced during the SOS response; the
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A,Note: expression is induced by DNA-damaging agents, e.g. nalidixic acid or mitomycin (
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C; Superfamily: helicase II
C; Keywords: ATP; DNA binding; DNA repair; DNA replication; hydrolase; nucleotide binding
F; 29-36/Region: nucleotide-binding motif A (P-loop)
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A.Hitle: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen A;Reference number: A99629; MUID:21156231; PMID:11258796
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A;Cross-references: UNIPROT:Q8X8P5; UNIPARC:UPI0000D08F3; GB:BA000007; PIDN:BAB38166.1.
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                         A; Molecule type: DNA
A; Residues: 1-47, X', 43-91, X', XY, 100-720 cDAN>
A; Residues: 1-47, X', 49-91, X', 49-91, XX, 100-720 cDAN>
A; Cross-references: UNIPARC: UPIO000172EB9; EMEL: M87049
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1992
B; Colloms, S.D.; Sykora, P.; Szatmari, G.; Sherratt, D.J.
B; Bacteriol. 172, 6979-6980, 1990
A; Title: Recombination at ColEl cer requires the Escherichia coli xerC gene product, a A; Reference number: A37841; MUID: 91072248; PMID: 2254268
A;Title: Analysis of the Escherichia coli genome: DNA sequence of the region from 84.5 A;Aeference number: $30660; MUID:9238234; PMID:1379743 A;Accession: $30703 A;Accession: $30703 A;Status: nucleic acid sequence not shown; translation not shown
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C;Species: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
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B8606B
DNA-dependent ATPase I and helicase II [imported] - Escherichia coli (strain O157:H7,
C;Species: Escherichia coli
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Pred. No. 29;
2; Mismatches
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Mismatches
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Pred. No.
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653 PVSHQRMGTPMV 664
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Best Local Similarity
7; Conserve
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nes 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: E37841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: G91221
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Best Local &
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A,Experimental source: strain K-12, substrain MG1655
B,Yamamoto, Y.; Ogawa, T.; Shinagawa, H.; Nakayama, T.; Matsuo, H.; Ogawa, H.
J. Blochem. 99, 1579-1590, 1986
A,Title: Determination of the initiation sites of transcription and translation of the uA,Reference number: A92004; MUID:86304220; PMID:2943729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-437,'R', 439-720 <YAM>
A;Residues: 1-437,'R', 439-720 <YAM>
A;Cross-references: UNIPARC:UPIO00016F607; GB:D00069; GB:N00069; NID:g216672; PIDN:BAA00
A;Cross-references: L-24 were confirmed by protein sequencing
R;Finch, P.W.; Emmerson, P.T.
Nucleic Acids Res. 12, 5789-5799, 1984
A;Title: The nucleotide sequence of the uvrD gene of Escherichia coli.
A;Reference number: A93528; MUID:84272253; PMID:6379604
A;Accession: A93528
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R;Daniels, D.L.; Plunkett III, G.; Burland, V.; Blattner, F.R.
Science 257, 771-778, 1992
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A;Cross-references: UNIPARC:UPI000016F606; GB:X00738; GB:K01148; GB:X00225; NID:g43296;
R;Easton, A.M.; Kushner, S.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HJECDZ

DNA helicase II (EC 3.6.1.-) [validated] - Escherichia coli (strain K-12)

N;Contains: adenosinetriphosphatase (EC 3.6.1.3)

C;Species: Escherichia coli
C;Date: 17-Mar-1987 #sequence revision 10-Oct-1997 #text_change 09-Jul-2004

C;Accession: F65185; JS0014; A93528; A93498; S30703; E37841; A03549

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; (A.; Rose, D.J.; Mau, B.; Shao, Y.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli is controlled by the lexA PMID:6324092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-650 <RYU>
A;Cross-references: UNIPROT:Q9UNN5; UNIPARC:UP100001698CA; GB:AF106798; NID:g5805207;
                                                                                                                                                                                                                                                                                                                                                              associated factor 1, hFAF1
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                                                                                                                     Fas associated factor 1 - human ("Species: Homo sapiens (man) ("Species: Homo sapiens (man) ("Species: Homo sapiens (man) ("Date: 0.3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 ("Spacession: JC7093 ("S.K.; Lee, K.J.; Kim, E. R.Ryu, S.W.; Chae, S.K.; Lee, K.J.; Kim, E. Biochem. Biophys. Res. Commun. 262, 388-394, 1999 A.Title: Identification and characterization of human Fas associated factor A.Reference number: JC7093; MUID:99393315; PMID:10462485
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A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-720 <BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Length 650,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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A;Title: Transcription of the uvrD gene of
A;Reference number: A93498; MUID:84169504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Experimental source: HeLa cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 70.0
Matches 7; Conservative
476 PVSKLRIRTP 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||||:|: ||
PVSKLRIRTP 581
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A;Residues: 1-258 <EAS>
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A; Molecule type: mRNA
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셤 8

C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004

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Nibuchrieser, C.; Rusmiok, C.; Couve, E.; Frangeul, L.; Billault, A.; Kunst, F.; Carniel submitted to the EMBL Data Library, October 1998
A; Description: DNA sequence of the 102 kbases unstable region of Yersinia pestis.
A; Reference number: 224348
A; Accession: T47054
A; Accession: preliminary; translated from GB/EMBL/DDBJ
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-168 cBUC>
A; Residues: 1-168 cBUC>
A; Residues: 1-168 cBUC>
A; Cross-references: UNIPARC: UNIPARC: UNIPARC: UNIPARC: UNIPARC: EMBL: AL031866; PIDN: CAA21397.
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Cjaccesion: AD0222

R; Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Jl, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001

A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A; Reference number: AB0001; MUID:21470413; PMID:11586360
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R,Fetherston, J.D.; Bertolino, V.J.; Perry, R.D.
Mol. Microbiol. 32, 289-299, 1999
Mol. Microbiol. 32, 289-299, 1999
A,Title: YbtP and YbtQ: two ABC transporters required for iron uptake in Yersinia pestif A,Reference number: Z18782; MUID:99248409; PMID:10231486
A,Accession: T17446
A,Status: preliminary; translated from GB/EMBL/DDBJ
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C;Species: Yersinia pestis
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                      hypothetical protein [imported] - Yersinia pestis
C;Species: Yersinia pestis
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004
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C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein YPO1905 [imported] - Yersinia pestis (strain CO92)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 52.1%; Score 38; DB 2; Length 168; Best Local Similarity 63.6%; Pred. No. 9.8; Matches 7; Conservative 1; Mismatches 3; Indels
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Local Similarity 63.6%;
Los 7; Conservative
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A; Residues: 1-184 <FET>
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T17446
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                                                  RESULT 16
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A;Molecule type: genomic RNA
A;Molecule type: genomic RNA
A;Residues: 1-3390 <cos.
A;Cross.references: UNIPROT:P27915; UNIPARC:UPI0000131DFE; GB:M93130; NID:g323468; PIDN:
C;Suyuerfamily: hepatitis C virus genome polyprotein
C;Seywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein;
C;Seywords: ATP; capsid protein #status predicted <CAP>
F;1-14/Product: membrane protein precursor #status predicted <MEP>
F;15-205/Domain: transmembrane protein #status predicted <MEM>
F;206-280/Product: membrane protein #status predicted <MEM>
F;206-280/Product: membrane protein #status predicted <MEM>
F;206-280/Product: envelope protein #status predicted <MEM>
F;207-771/Domain: transmembrane #status predicted <TM>
F;7115-205/Domain: transmembrane #status predicted <TM>
F;724-746/Domain: transmembrane #status predicted <TM>
F;733-771/Domain: transmembrane #status predicted <TM>
F;7115-1134/Product: nonstructural protein NS21 #status predicted <NS1>
F;1185-1143/Product: nonstructural protein NS21 #status predicted <NS2>
F;1185-1147-2092/Product: nonstructural protein NS2 #status predicted <NS3>
F;167-1674/Region: nucleotide-binding mocif A (P-loop)
F;715-175/Poduct: nonstructural protein NS3 #status predicted <NS3>
F;167-1674/Region: nucleotide-binding mocif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genome polyprotein - dengue virus type 3
N;Contains: capsid protein; envelope protein; membrane protein; nonstructural protein NS
N;Contains: capsid protein; envelope protein; membrane protein; nonstructural protein NS5
c;pate: 30-dun-1992 #sequence_revision 30-dun-1992 #text_change 31-Dec-2004
C;Accession: A34774
R;Osatoni, K.; Sumiyoshi, H.
Virology 176, 643-647, 1990
A;Title: Complete nucleotide sequence of dengue type 3 virus genome RNA.
Cincesion: B6608
Riperna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, B.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: B86068
A;Accession: B86068
A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-720 <420>
A;Residues: 1-720 <420>
A;Residues: 1-720 <420>
A;Residues: 1-720 <420
A;Residues: 1-720 <420
A;Residues: 1-720 <40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39; DB 2; Length 720;
Pred. No. 29;
2; Mismatches 3; Indels
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Best Local Similarity 58.39
The Conservative
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653 PVSHQRMGTPMV 664
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Best Local Similarity 58.3
Matches 7; Conservative
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GNWVD3
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A,Molecule type: DNA
A,Residues: 1-828 <WIL>
A,Cross-references: UNIPROT:Q20550, UNIPARC:UPI000080941; EMBL:274035; PIDN:CAA98485.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPARC:UP10000080941; EMBL:Z74041; PIDN:CAA98523.1; GSPDB:GN00023;
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C.Accession: T22367; T24409 F.White, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Introns: 62/1; 181/1; 375/2; 420/1; 452/1; 585/2; 662/2; 740/3
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                                                                                                                                                                       A,Reference number: Z19554
A,Accession: T22367
A,Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-828 <WI2>
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Pred. No. 52;
3; Mismatches
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                                                                                                                                    submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: clone F47G9
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312 ISRRRMALPMLAQ 324
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Best Local Similarity 55...
To Conservative
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C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: B91146
B;Haysshi, T; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Reference number: A99629; WUID:21156231; PMID:11258796
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R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A,Cross-references: UNIPROT.Q9ZFZ9; UNIPARC:UP100000CAC1; EMBL:AF091251; NID:g3818595; C;Superfamily: Yersinia pestis hypothetical 21.1K protein
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
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                                                                                                                                                                                                                                                                                                                                                                                                                                   probable integral transmembrane protein [imported] - Escherichia coli (strain O157:H7,
C;Species: Escherichia coli
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C,Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
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                                                                                               Score 38; DB 2; Length 184;
Pred. No. 11;
1; Mismatches 3; Indels
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Pred. No. 39;
4; Mismatches
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Pred. No.
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                                                                                                      52.1%;
63.6%;
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58.3%;
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58.3%;
                                                                    Query Match
Best Local Similarity 63.87
7; Conservative
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109 NKLQLATPLLPQ 120
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109 NKLQLATPLLPQ 120
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112 PISPSRMTTPL 122
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Best Local Similarity
7; Conserve
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Best Local Similarity
Matches 7; Conserv
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A,Molecule type: DNA
A,Residues: 1-628 <HAY>
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-628 <STO>
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Length 1046; Indels

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A;Residues: 1-1046 <STO>
A;Cross-references: UNIPROT:P52002; UNIPARC:UPI000012F022; GB:AE004479; GB:AE004091; NID
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome polyprotein - dengue virus type 1 (strain Singapore S275/90)
N;Contains: capsid protein; envelope protein; membrane protein; nonstructural protein NS
a; nonstructural protein NS4b; nonstructural protein NS5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AttA2-like ABC transporter, permease protein SMa0952 [imported] - Sinorhizobium meliloti C; Species: Sinorhizobium meliloti C; Species: Sinorhizobium meliloti C; Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004 C; Accession: C95326 R; R; Barnett, M.J.; Pisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowe ; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P33478; UNIPARC:UP1000002F845; GB:M87512
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein;
F;1-114/Product: capsid protein #status predicted <CAP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: dengue virus type i
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-2004
C;Accession: A42551
R;Fu, J; Tan, B.H.; Yap, E.H.; Chan, Y.C.; Tan, Y.H.
Virology 188, 933-958, 1992
A;Title: Full-length CDNA sequence of dengue type 1 virus (Singapore strain S275/90).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72094-2243/Product: nonstructural protein NS4a #status predicted <N4A>
7,2244-2492/Product: nonstructural protein N84b #status predicted <NAB>
7,2493-3396/Product: nonstructural protein N85 #status predicted <NS5>
7,183,347,433/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fil5-281/Product: membrane protein precursor #status predicted <MEP>
Fil5-204/Domain: nonterminal signal sequence #status predicted <SIG>
Fil5-204/Domain: nonterminal signal sequence #status predicted <SIG>
Fil505-281/Product: membrane protein #status predicted <MEN>
Fi262-279/Domain: transmembrane #status predicted <MI>Fi753-769/Domain: transmembrane #status predicted <MI>Fi753-769/Domain: transmembrane #status predicted <MI>Fi753-769/Domain: transmembrane protein N321 #status predicted <NS1>Fi134-1137/Product: nonstructural protein N32a #status predicted <NS2>Fi134-1474/Product: nonstructural protein N32a #status predicted <NS2>Fi1475-2093/Product: nonstructural protein N33 #status predicted <NS3>Fi168-1675/Region: nucleotide-binding motif B (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38; DB 1; Length 3396;
Pred. No. 2.3e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                               5;
                                                                                                                                                                                                                                                                                                                                               Score 38; DB 2
Pred. No. 67;
4; Mismatches
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                                                                                                                                                                                                                                           A;Gene: mexB; PA0426
C;Superfamily: acriflavin resistance protein
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58.3%;
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58.3%;
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2327 PISKMDIGVPLL 2338
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Best Local Similarity 58.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109 NKLQLATPLLPQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: genomic RNA
A; Residues: 1-3396 <FUJ>
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                             A, Status: preliminary
A, Molecule type: DNA
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A; Accession:
                                                                                                                                                                                                              C;Genetics:
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C95326
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
R;Stover, CK.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Jory, S.; Olson, M.V.
Asture 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RND multidrug efflux transporter MexB PA0426 [imported] - Pseudomonas aeruginosa (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 23
539630
multidrug-efflux transport protein B - Pseudomonas aeruginosa
multidrug-efflux transport protein B - Pseudomonas aeruginosa
NyAlternate names: multidrug resistance protein B
C;Species: Pseudomonas aeruginosa
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: 839630
R;Poole, K.; Heinrichs, D.E.; Neshat, S.
Mol. Microbiol. 10, 529-544, 1993
A;Title: Cloning and sequence analysis of an EnvCD homologue in Pseudomonas aeruginosa:
A;Reference number: 839630
A;Status: preliminary
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-1046 <POO>
A;Cross-references: UNIPROT:P52002; UNIPARC:UPI000016FC9A; GB:L11616; NID:g438852; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Description: probably involved in secretion of the siderophore pyoverdine A; Description: probably involved in secretion of the siderophore pyoverdine C; Superfamily: acriffavin resistence protein C; Keywords: transmembrane protein; transport protein C; Keywords: transmembrane #status predicted <TM1> F;14-30/Domain: transmembrane #status predicted <TM2> F;343-359/Domain: transmembrane #status predicted <TM3> F;370-386/Domain: transmembrane #status predicted <TM4> F;397-413/Domain: transmembrane #status predicted <TM6> F;42-458/Domain: transmembrane #status predicted <TM6> F;541-557/Domain: transmembrane #status predicted <TM6> F;541-557/Domain: transmembrane #status predicted <TM9> F;898-914/Domain: transmembrane #status predicted <TM9> F;998-914/Domain: transmembrane #status predicted <TM1> F;913-989/Domain: transmembrane #status predicted <TM1> F;914-1030/Domain: transmembrane #status predicted <TM10> F;1014-1030/Domain: transmembrane #status predicted <TM10>
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                                                                                                                                                                                                                                                                                                                 1; Indels
                         F;540-556/Domain: transmembrane #status predicted <TM7>
F;848-890/Domain: transmembrane #status predicted <TM8>
F;898-914/Domain: transmembrane #status predicted <TM8>
F;974-990/Domain: transmembrane #status predicted <TM10>
F;1012-1028/Domain: transmembrane #status predicted <TM10>
   ;472-488/Domain: transmembrane #status predicted
                                                                                                                                                                                                                                           Score 38; DB 2
Pred. No. 66;
4; Mismatches
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Pred. No. 67;
4; Mismatches
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58.3%;
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Best Local Similarity 58.3%;
Matches 7; Conservative
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Best Local Similarity 58...
7; Conservative
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NKLQLATPLLPQ 120
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A,Cross-references: UNIPARC:UPI0000174A76; GB:M10242; NID:g323245
A,Note: the codons given for residues 54-Lys (AAU) and 55-Ile (GUC) are inconsistent wi
C;Superfamily: paramyxovirus nucleocapsid protein
C;Keywords: nucleocapsid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable acyl Co-A dehydrogenase [imported] - Salmonella enterica subsp. enterica serovo cispecies: Salmonella enterica subsp. enterica serovar Typhi hydro: this species has also been called Salmonella typhi cipere of this species has also been called Salmonella typhi cipere of this species has also been called Salmonella typhi cipere of this species has also been called Salmonella typhi cipere of this species has also been called Salmonella traxt_change 18-Nov-2002 Ciperession: Al1050

Exparkhili, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K., A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica seron A; Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-540 - FPRX>
A;Cross-references: UNIPARC:UPI0000CDBCE; GB:AL513382; PIDN:CAD06854.1; PID:g16505502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable exported protein YPO3664 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 31-Dec-2004
C;Accession: AB0446
C;Accession: AB0446
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: UNIPROT: Q8ZAW7; UNIPARC: UPI00000DCE73;, GB: ALS90842; PIDN: CAC93134.1
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Pred. No. 49;
3; Mismatches
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Pred. No. 52;
2; Mismatches
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C,Superfamily: MSHA biogenesis protein MshH
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Best Local Similarity 53.8%;
Matches 7; Conservative
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8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          2 VSKMRMATPLLMQ 14
      A; Accession: A04028
A; Molecule type: genomic RNA
A; Residues: 1-514 <ROZ>
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Best Local Similarity
Matches 8; Conserv
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A;Molecule type: DNA
A;Residues: 1-638 <KUR>
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                                                                                                                           A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: UNIPROT:Q92ZH0; UNIPARC:UPI00000CB0FC; GB:AE006469; PIDN:AAK65173.1;
A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, P-1 Chain, P.; Cohain, P.; Cohain, P.; Cohain, P.; Cohain, P.; Cohain, P.; Cohain, P.; Mones, T.
Science 293, 668-672, 2001
A;Muthors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Weils, D.H.; Wong, K.; Yeh, K.A;Title: The composite genome of the legume symbiont Sinorhizobium mellloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Gontents: annotation
A;Genetics:
A;Genetics:
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sugar ABC transporter, permease protein BMEI10087 [imported] - Brucella melitensis (stra C;Species: Brucella melitensis
C;Species: Brucella melitensis
C;Species: Brucella melitensis
C;Pate: Ol-Reb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AE3520
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
Affile: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilod
A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: C95326
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A;Cross-references: UNIPROT:Q8YDT8; UNIPROT:Q8FXQ8; UNIPARC:UPI000058346; GB:AE008918;
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Cispecies: canine distemper virus
Cispecies: canine distemper virus
Cispecies: canine distemper virus
Cispecies: a0-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 14-Nov-1997
Ciscession: A04028
R;Rozenblatt, S.; Eizenberg, O.; Ben-Levy, R.; Lavie, V.; Bellini, W.J.
J. Virol. S3, 684-690, 1985
A;Fitle: Sequence homology within the morbilliviruses.
A;Fitle: Sequence homology within the morbilliviruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily: spermidine/putrescine transport system permease protein potH
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Pred. No. 28;
3; Mismatches 1; Indels
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C;Superfamily: probable ribose ABC transporter rbsC-2
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Best Local Similarity 63.6
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25 PIASMALVTPLL 36
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18 LRVATPLLLAA 28
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Best Local Similarity
Matches 6; Conserv
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C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S76260
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Kaneko, T.; Sato, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda A.; Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:055605; UNIPARC:UP100000C0F10; EMBL:D64000; GB:AB001339; NID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Definococcus radiodurans
C;Accession: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: G75435
R;White, 0.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ms.; Saith, H.O.; Venter, J.C.; Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-163 «WHI>
A;Cross-references: UNIPROT:Q9RVB7; UNIPARC:UPI00000C1897; GB:AE001961; GB:AE000513; NII
A;Experimental source: strain R1
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                            hypothetical protein slr0770 - Synechocystis sp. (strain PCC 6803)
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A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: S74322; MUID: 97061201; PMID: 8905231
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Pred. No. 14;
3; Mismatches
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R;Kershaw, J.
submitted to the EMBL Data Library, September 1996
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Pred. No. 2
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782 IGDMRRATPKLAQA 795
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Best Local Similarity 53.0
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11 PFSHVRLAGPLLL 23
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Matches 7; Conserv
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C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C.Accession: D96798
C.Accession: D96798
C.M.; Chung, M.K.; Conn, D.; Conway, A.B.; Conway, A.R.; Kraul, S.; White, O.; Alonso, Chin, C.W.; Hughes, B.; Huizar, L.
Anere, 408, B16-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.S.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Attle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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A;Cross-references: UNIPROT:062119; UNIPARC:UP100000784BB; EMBL:277131; PIDN:CAB00857.1;
A;Experimental source: clone C54C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: UNIPARC: UP100000784BB; EMBL: Z46381; PIDN: CAA86520.1; GSPDB: GN00021;
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A;Gene: F22K20.5
A;Map position: 1
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A;Introns: 26/3; 71/1; 234/3; 375/2; 506/3; 539/1; 580/2; 639/2; 687/3; 927/1; 958/2
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                                                                                                                                                                                                          Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cipacession: T20198; T23659
Rilghtning, J.
Submitted to the EMBL Data Library, July 1996
A;Reference number: Z19236
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from A;Residues: 1-980 WIL>
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Pred. No. 1.1e+02;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.7%; Score 37; DB 2; Length 980; 50.0%; Pred. No. 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels

    Caenorhabditis elegans

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, October 1994
A;Reference number: 219778
A;Accession: T21659
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: clone M01F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 57.1%;
Matches 8; Conservative
        7,4
                                     |::| | | ||:||
57 PINKKREWLPLMMQ 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 PVSKMRMATPLL 12
                                                                                                                                                                                          hypothetical protein M01F1.7
        PVSKMRMATPLLMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-1108 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-980 <W12>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C,Genetics:
A,Gene: CESP:M01F1.7
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: D82822
R;anonymous, The Xylalla fastidiosa Consortium of the Organization for Nucleotide SequerNature 406, 15-157, 2000
A;Title: The genome sequence of the plant pathogen Xylalla fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                      A;Reaidues: 1-222 <SIM>
A;Cross-references: UNIPROT:Q9PG16; UNIPARC:UP10000C2382; GB:AE003884; GB:AE003849; NII
                                                                                                                                                                                                                                                                                                                                                                                                                   Rismpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, Bas-Neco, E.; Docean, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohn J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigi chado, M.A.; Madeira, A.M.B.N.; Madeira, H.F.; Marrino, C.L.; Marques, M.V.; Martins, A.A.; Marcins, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, M.C.; palmieri, D.Y.; Rosa, A.J. de M.; da Silva, V.E.; da Silva, A.M.; Silva Jr., W.A.; da Silvain, M.Y.; Sawasal M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Pseudomonas carboxydovorans
C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
C;Accession: A56279; PL0141; A46361
R;Schuebel, U.; Kraut, W.; Moersdorf, G.; Meyer, O.
J. Bacteriol. 177, 2197-223, 1995
A;Title: Molecular characterization of the gene cluster coxMSL encoding the molybdenum-A;Reference number: A56279; MUID:95238294; PMID:7721710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-288 <SCH>
A; Residues: 1-288 <SCH>
A; Cross-references: UNIPROT: P19920; UNIPARC: UPI00011274D; GB:X82447; NID:g809563; PIDN
A; Cross-references: Uniparted as Oligotropha carboxidovorans
B; Kraut, M.; Hugendleck, I.; Herwig, S.; Meyer, O.
R; Kraut, M.; Hugendleck, I.; Herwig, S.; Meyer, O.
A; Krim Microbiol. 152, 335-341, 1989
A; Title: Homology and distribution of CO dehydrogenase structural genes in carboxydotroj
A; Reference number: PL0138; MUID:90055678; PMID:2818128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R. Hugendieck, I.; Meyer, O. Arch. Microbiol. 157, 301-304, 1992
Arch. Microbiol. 157, 301-304, 1992
A; Title: The structural genes encoding CO dehydrogenase subunits (cox L, M and S) in Ps. hicus, conserved in carboxydotrophic bacteria.
A; Reference number: A48361; MUID:92378472; PMID:1510563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        carbon-monoxide dehydrogenase (EC 1.2.99.2) medium chain - Pseudomonas carboxydovorans
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A,Note: although the chemical evidence is good for an amino-terminal Met-Met sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Residues: 1,'PSAR',6-10,'IPGKS',16-29 <HUG>
A;Cross-references: UNIPARC:UP10000178C94; PIDN:AAB22965.1; PID:9253868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: protein
A;Residues: 'M',1-14 <KRA>
A;Cross-references: UNIPARC:UPI0000178C93
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Contents: annotation
                                                                                                                                                                                                                                                    A; Accession: D82822
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
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A;Reference number: Z25454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NADH-ubiquinone oxidoreductase, NQO10 subunit XF0314 [imported] - Xylella fastidiosa (st
C,Species: Xylella fastidiosa
       A;Reference number: Z19523
A;Accession: T22143
A;Accession: T22143
A;Accession: T22143
A;Accession: T22143
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-179 < WILD>
A;Accession: T279 < WILD>
A;Cross-references: UNIPROT: Q93715; UNIPARC: UPI00000825A1; EMBL: Z79755; PIDN: CAB02105.1;
A;Experimental source: clone F43G9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: UNIPROT:P25864; UNIPARC:UPI000001AF8; EMBL:Z11509; NID:g16500; PIDN
A,Accession: S22960
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A;Introns: 51/3; 94/2; 109/3; 142/2; 158/2
A;Introns: 51/3; 94/2; 109/3; 142/2; 158/2
A;Introns: 51/3; 94/2; 109/3; 142/2; 158/2
C;Superfamily: Escherichia coli ribosomal protein L9
C;Keywords: chloroplast; protein biosynthesis; ribosome
F;1-37/Domain: transit peptide (chloroplast) #status predicted <TNP>F;38-197/Product: ribosomal protein L9 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                      A;Introns: 30/3; 80/1; 111/1; 148/1
C;Superfamily: Caenorhabditis elegans hypothetical protein F43G9.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                       49.3%; Score 36; DB 2; Length 179; 87.5%; Pred. No. 25; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.3%; Score 36; DB 1; Length 197; 42.9%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-197 <DEL>
A;Cross-references: UNIPARC:UP1000001AF8; EMBL:AL391254
A;Experimental source: cultivar Columbia; BAC clone F28D10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 PVSKMRMATPLLMQ 14
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Best Local Similarity 87.5
Matches 7; Conservative
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| PVSRMRMA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 PVSKMRMA 8
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Matches 6; Conserv
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A; Residues: 1-197 < TH2>
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A; Residues: 1-197 <THO>
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A; Status: preliminary
                                                                                                                                                                                                                                                 C;Genetics:
A;Gene: CESP:F43G9.2
A;Map position: 1
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9, 2006, 23:01:55

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|: :||| | ||||| 58 PLQRMRMLPPKKRSLLMQ 75
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Job time: 20.0886 secs
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546805
hypothetical protein YHR085w - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C;Accession: $46805
B;PavellO, T.
submitted to the EMBL Data Library, June 1994
A;Description: The sequence of S. cerevisiae cosmid 9205.
A;Accession: $46795
A;Accession: $46795
A;Accession: $46795
A;Accession: $46795
A;Accession: $1-34 < FRV>
A;Accession: $1-34 < FR
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C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Oct-2004
C;Accession: D71288 #sequence_revision 24-Jul-1998 #text_change 05-Oct-2004
C;Accession: D71288 #sequence_revision 24-Jul-1998 #text_change 05-Oct-2004
C;Accession: D71288 #sichardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDc
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281 J75-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: D71288
A;Accession: D71288
A;Accession: D7128
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A;Cross-references: UNIPROT:O83717; UNIPARC:UPI0000D3295; GB:AE001245; GB:AE000520; NID
A;Experimental source: strain Nichols
C;Genetics:
A;Gene: TR073
C;Superfamily: glutamate synthase, small subunit
A; Experimental source: strain OMS, plasmid pHCG3
A; Note: sequence extracted from NCBI backbone (NCBIP:111732); sequence misidentified as A; Genetics coxM; codH
A; Start codon: GTG
C; Complex: heterotrimer of large (see PIR:C56279), medium, and small (see PIR:B56279) ch C; Superfamily: carbon monoxide dehydrogenase medium chain
C; Keywords: heterotrimer; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ï
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49.3%; Score 36; DB 2; Length 518;
Best Local Similarity 50.0%; Pred. No. 77;
Matches 9; Conservative 2; Mismatches 3; Indels
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50.0%; Pred. No. 48;
tive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                  Score 36; DB 2; Length 288;
Pred. No. 41;
2; Mismatches 2; Indels
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A;Cross-references: SGD:S0001127
A;Map position: 8R
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Matches 6; Conservative
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QSUOJ8;
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MEDINE-21388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDINE-21388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MALSCAUL S.P., Teringold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,

Antochia R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Antochia K., Parmer A.A., Rubin G.M., Hong L.,

Branchstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.J.,

Bran S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

N. Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mitchiag M., Madan A., Youchan J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-92375195; PubMed=1380674; DOI=10.1038/35876440; Chicz R.M., Urban R.G., Lane W.S., Gorga J.C., Stern L.J., Vignall D.A., Strominger J.L.; "Predominant naturally processed peptides bound to HLA-DR1 are derived from MHC-related molecules and are heterogeneous in size.";
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                     01-MAY-2000, sequence version 1.
07-FEB-2006, entry version 10.
HLA class II-associated invariant chain II (Fragment).
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25 AA; 2793 MW; 2F80100276A802F4 CRC64;
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01-UUN-2002, sequence version 1.
07-FBB-2006, entry version 15.
                                                                                                             01-MAY-2000, integrated into UniProtKB/TrEMBL
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QBSNAO;
                                                                       25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ensembl; ENSG0000019582; Homo sapiens
                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 358:764-768(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.
nes 15; Conservative
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                                                                       Q9TNQ6_HUMAN
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10-MAY-2005, sequence version 1.
07-FBB-2006, entry version 3.
07-FBB-2006, ent
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
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GO; GO:0006955; P:immune response; IEA.
InterPro; IPR011988; MHCII invariant.
SEQUENCE 232 AA; 26399 MW; 5144439D0FD27C99 CRC64;
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Ensembl; ENSG00000019582; Homo sapiens.
SEQUENCE 160 AA; 18328 WW; 95CB3D7226497DE8 CRC64;
                                                                                                                                                               and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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100.0%; Pred. No. 1.5e-05;
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Ensembl; ENSG0000019582; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; BC024272; AAH24272.1; -; mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 PVSKMRMATPLLMQA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 PVSKMRMATPLLMOA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 PVSKMRMATPLLMQA
                                                                                                                                                                                                                                                                                                                                                                                   IISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
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Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
es 15; Conserv
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Name=Short;
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                                                                                                                                                                                                                                                                                                                                                                                                     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                            TISSUE=Kidney;
The German cDNA Consortium;
Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
Han M., Wiemann S.;
Han M., Wiemann S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-84207945; PubMed-6586420;
Strubin M., Mach B., Long B.O.;
"The complete sequence of the mRNA for the HLA-DR-associated invariant
                                                                                                                                     Pongo pygnaeus (Orangutan).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HG2A HUMAN STANDARD; PRT; 296 AA.
P04233; Q14597; Q29832; Q8WLP6;
20-MAR-1987, integrated into UniProtKB/Swiss-Prot.
16-APR-2002, sequence version 3.
07-MAR-2006, entry version 74.
HLA class II histocompatibility antigen, gamma chain (HLA-DR antigensassociated invariant chain) (Ia antigen-associated invariant chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chain reveals a polypeptide with an unusual transmembrane polarity.";
EMBO J. 3:869-872(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L21
MUCLEOTIDE SEQUENCE.
MEDLINE=86093681; PubMed=3001652;
Kudo J., Chao L.-Y., Narni F., Saunders G.F.;
Kudo J., Chao L.-Y., Narni F., Saunders G.F.;
"Structure of the human gene encoding the invariant gamma-chain of "Structure of the human gene encoding the invariant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 73; DB 2; Length 23
100.0%; Pred. No. 2.3e-05; wiemafches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .l protein.
232 AA; 26411 MW; DE5D7AC72AF7439F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE (ISOFORMS LONG AND SHORT).
                                       21-DEC-2004, integrated into UniProtKB/TrEMBL.
  232 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO, GO:0016020; C:membrane; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR011988; MHCII_invariant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            class II histocompatibility antigens.
Nucleic Acids Res. 13:8827-8841 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; CR857162; CAH89463.1; -; mRNA.
PRT;
                                                          21-DEC-2004, sequence version 1.
07-FEB-2006, entry version 5.
Hypothetical protein DKFZp469K1522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 PVSKMRMATPLLMOA 15
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Name=CD74; Synonyms=DHLAG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
nes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMR; Q5RFJ4; 134-208
                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
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                                                                                                                        Name=DKFZp469K1522;
                                                                                                                                                                                                                    NCBI_TaxID=9600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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OSRFJ4 PONPY
OSRFJ4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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ID HGZA HUMAN
ID 16-APR
DT 20-MARA
DT 07-MARA
DE HLA CARR
DE (Ii) (I) (GN Name=CI
OC EUWARAY
OC HOMO.
OC HOMO.
OC HOMO.
OC HOMO.
OC NAME IJ
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MEDLINE=2038835; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rapleton M.J., Ugdin T.B., Poshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Rodriguez A.C., Grimmood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimmood J., Schmutz J., Myers R.M.,

Rothertield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rothertield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Marra M.A.,

Rothertield W.S., Schein J.E., Jones S.J.M., Marra M.A.;

Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O J. 17:6812-6818(1998).
FUNCTION: Plays a critical role in MHC class II antigen processing by stabilizing peptide-free class II alpha/beta heterodimers in a complex soon after their synthesis and directing transport of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide loading of class II takes place.
SUBUNIT: Nonamer composed of three alpha/beta/gamma heterotrimers.
SUBCELLULAR LOCATION: Membrane; single-pass type II membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cresswell P.;
                                                                                                                                     "Structure of the human Ia-associated invariant (gamma)-chain gene: identification of 5' sequences shared with major histocompatibility complex class II genes."; Proc. Natl. Acad. Sci. US.A. 83:4484-4488(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.75 ANGSTROMS) OF 103-117.
MEDLINE=96085023; PubMed=7477400; DOI=10.1038/378457a0;
Ghosh P., Amaya M., Mellins E., Wiley D.C.;
"The structure of an intermediate in class II MHC maturation: CLIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-93078879; PubMed=1448172; DOI=10.1038/360474a0; Riberdy J.M., Newcomb J.R., Surman M.J., Barbosa J.A., Cresswell I "HLA-DR molecules from an antigen-processing mutant cell line are associated with invariant chain peptides.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claesson L., Larhammar D., Rask L., Peterson P.A.; "CDNA clone for the human invariant gamma chain of class II histocompatibility antigens and its implications for the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complex from the endoplasmic reticulum to compartments where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99059718; PubMed=9843486; DOI=10.1093/emboj/17.23.6812; Jasanoff A., Wagner G., Wiley D.C.; Miley C.C.; Miley cointend a trimeric domain of the MHC class II-associated chaperonin and targeting protein Ii."; EMBO J. 17:6812-6818(1999).
MEDLINE=86233451; PubMed=3459184;
O'Sullivan D.M., Larhammar D., Wilson M.C., Peterson P.A.,
                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM SHORT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 structure.";
Proc. Natl. Acad. Sci. U.S.A. 80:7395-7399(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Long;
IsoId=P04233-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=84170234; PubMed=6324166;
Claesson L., Larhammar D., Rask L.,
"CDNA clone for the human invariant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE OF 27-96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [8]
STRUCTURE BY NMR OF 134-208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN SEQUENCE OF 97-120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences."
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                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Tonsil
                                                                                        Quaranta V.;
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Homo.
NCBI_TaxID=9606;
RESULT 7
Q9MXD5 HORSE
ID . Q9MXD5_HORSE
                                                                                                                                                                                                                                                                                                                                                                                                                               Kalbacher H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                           HUMAN
                                                                                  STRAND
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Matches
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                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00464; THYROGLOBULIN 1_1; 1.
PROSITE; PS51162; THYROGLOBULIN 1_2; 1.
3D-structure; Alternative splicing; Chaperone;
Direct protein sequencing; Glycoprotein; Immune response; Membrane;
Proteoglycan; Signal-anchor; Transmembrane.
CHAIN 1 296 HLA class II histocompatibility antigen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-linked (GlcNAc. .).
N-linked (GlcNAc. .).
O-linked (Xyl. ..) (glycosaminoglycan)
                                                                                                                                                                                                                                                                                                                                                                                                                                                gamma chain.
/FTId=PRO 000067954.
Cytoplasmic (Potential).
Signal-anchor for type II membrane protein (Potential).
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Missing (in isoform Short).
/FTId=VSP_005331.
R -> T (in Ref. 2).
  IsoId=P04233-2; Sequence=VSP_005331;
-!- SIMILARITY: Contains 1 thyroglobulin type-1 domain.
                                               EMBL; KO1144; AAA36304.1; -; MENA.
EMBL; X03339; CAA27046.1; -; Genomic_DNA.
EMBL; X0340; CAA27041.1; -; Genomic_DNA.
EMBL; X00497; CAA25192.1; -; MENA.
EMBL; X00497; CAA25193.1; -; MENA.
EMBL; M1356; AAA36033.1; -; Genomic_DNA.
EMBL; M1355; AAA36033.1; -j Genomic_DNA.
EMBL; M1355; AAA36033.1; JOINED; Genomic_DNA.
EMBL; MAGA; X-ray; C-103-117.
PDB; 1LIE; NWR; A-210-274.
PDB; LL3H; NWR; A-210-274.
PDB; LL3H; NWR; A-210-274.
HGNC; HGNC: L697; CD74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    By similarity.
By similarity.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Potential)
                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00086; Thyroglobulin_1; 1.
SMART; SM00211; TY; 1.
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106
137
149
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250
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TRANSMEM
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Characterization of peptides bound to extracellular and intracellular HLA-DR1 molecules.";
Hum. Immunol. 38:193-200(1993).
                                                                                                                                                                                                                                                                                                                       01-MAY-2000, integrated into UniProtKB/TrEMBL.
01-MAY-2000, sequence version 1.
07-FBB-2006, entry version 10.
HIA-DR1-associated LI peptide.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ensembl; ENSG0000019582; Homo sapiens.
SEQUENCE 20 AA; 2264 MW; D802F7C2C0FAE534 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN SEQUENCE.
MEDLINE=94148715; PubMed=8106277; DOI=10.1016/0198-8859(93)90540-H;
Max H., Halder T., Kropshofer H., Kalbus M., Muller C.A.,
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100.0%; Score 73; DB 1; Length 296; 100.0%; Pred. No. 3e-05; ive 0; Mismatches 0; Indel8
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Local Similarity 100.0%; Pred. No. 9.6e-06;
les 14; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                              Q9TNQ4_HUMAN PRELIMINARY; PRT;
                                                                                                                                           103 PVSKMRMATPLLMQA 117
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                                                                                                          1 PVSKMRMATPLLMQA 15
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                                   Local Similarity 100.
nes 15; Conservative
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Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
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Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Appkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hashe F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldon M.F., Carninci P., Frange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
A Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Broask S.A., McKennan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Nhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Beneration and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                    Būkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
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                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
MEDLINE=20353882; PubMed=10895327;
Tozaki T., Mashima S., Miura N., Tomita M.;
"The equine CD74 gene has a polymorphic (CAG)n repeat in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86.3%; Score 63; DB 2; Length 208; 80.0%; Pred. No. 0.0017; ive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0016620; C:membrane; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR011988; MHCII invariant.
SEQUENCE 208 AA; 23425 MW; 9739F801BE4050F8 CRC64;
                   -OCT-2000, integrated into UniProtXB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2002, integrated into UniProtKB/TrEMBL.
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                                      01-0CT-2000, sequence version 1.
07-FEB-2006, entry version 10.
MHC class II associated invariant chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB032166; BAA92343.1; -; mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2002, sequence version 1.
07-FEB-2006, entry version 14.
Hypothetical protein.
Mus musculus (Mouse).
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| PVSKIRVATPMLMQA 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 PVSKMRMATPLLMOA 15
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Best Local Similarity 80.v.
Best Local 2; Conservative
                                                                                                                                                                                                                                                                                                                             untranslated region.";
                                                                                                              Equus caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P04233; IIIE.
SMR; Q9MXD5; 118-192.
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                                                                                                                                                                                 NCBI_TaxID=9796;
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QBK0S8 MOUSE
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STRAIN=FVB/N; TISSUE=Colon, and Salivary gland;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Strausberg R.L., Feingold E.A., Grouse L.H., Derged J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S.A., Wolly D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
                                                                                                                                                                                                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=Cd74; Synonyms=I;
Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Murcoidea; Muridae; Mus.
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07-FEB-2006, entry version 11.
14-associated invariant Lebin (Adult male kidney cDNA, RIKEN full-length enriched library, clone:0610006B16 product.la-associated invariant chain, full insert sequence) (Cd74 protein).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 84.9%; Score 62; DB 2; Length 208; Local Similarity 73.3%; Pred. No. 0.0027; nes 11; Conservative 4; Mismatches 0; Indels
                                                                                                                                              Strausberg R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein. SEQUENCE 208 AA; 23590 MW; FF36F7835228A596 CRC64;
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                          HSSP, P04233; IIIE.
SMR; QBK0S8; 118-192.
Cop, GO:0016020; C:membrane; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR011988; MHCII_invariant.
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                                                                                                                                                                                                                                                                                                                                                               EMBL; BC030458; AAH30458.1; -; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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87 PLSKMRVATPMMMQA 101
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                                                                       NUCLEOTIDE SEQUENCE.
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QGT22;
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REAL SECURIOR SEQUENCE.

REAL MACEDIANS SEQU
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Magiett D.R., Maltais H., Marchicout L., MKERDIA L., MREMBER L., MRIA B. Magiett D.R., Maltais H., Marchicout L., MKERDIA B. Magiett D.R., Maltais H., Marchicout L., McGod. M. Sinada K., Sandalin A., Sandalin A., Schneidar C., Senpie C.A., Serou M. Sinada K., Sinada M. Sinada M. Sinada M. Sinada M. Sinada M. Sinada R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Manane L., Manane Y., Warlan E., Manane Y., Warlan E., Manane Y., Warlan E., Manane Y., Warlan E., Manane Y., Warlan M. Manane Y., Warlan M. Manane Y., Warlan M. Manane Y., Warlan M. Manane Y., Manane Y., Warlan M. Manane Y., Manane M. Manane

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STRAIN-129; TISSUE-Mammary Stans, (1907-ORM LONG).

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Lischul S.F., Zeeberg B., Buercow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S. I., Wang J., Hsieh F.,

Distribution C.L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

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Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakebley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y., Toya T., Yammura T., Yasunishi A., Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                  Gaps
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"Primary structure of the gene for the murine Ia antigen-associated
invariant chains (Ii). An alternatively spliced exon encodes a
cysteine-rich domain highly homologous to a repetitive sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HG2A_MOUSE STANDARD; PRT; 279 AA.
P04441; 019452;
13-A04-1987, integrated into UniProtXB/Swiss-Prot.
01-NOV-1991, sequence version 3.
01-NAR-2006, entry version 63.
H-2 class II histocompatibility antigen, gamma chain (MHC class II-associated invariant chain) (Ia antigen-associated invariant chain)
                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhu L., Jones P.P.; "Complete sequence of the murine invariant chain (Ii) gene."; Nucleic Acids Res. 17:447-448(1989).
                                                                                                                                                                                                                                                                             Score 61; DB 2; Length 215;
Pred. No. 0.0044;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LONG).
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                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
STRAIN-AKR; TISSUE=Liver;
MEDLINE=89098406; PubMed=2492095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=87275861; PubMed=3038530;
                                                                                                                                                                                                                                                                             83.6%;
                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
STRAIN=FVB/N; TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBO J. 6:1677-1683 (1987).
                                                                                                                                                                                                                                                                                                                                                                                1 PVSKMRMATPLLMQ 14
                                                                                                                                                                                                                                                                                                                                                                                                                            86 PVSQMRMATPLLMR 99
                                                                                                                                                                                                                                                                                                                                  12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Ii) (CD74 antigen).
Name=Cd74; Synonyms=Ii;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                      NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thyroglobulin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=AKR;
                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
HG2A MOUSE
                                                                                                                                                                                                                                                                                                                             Matches
    REARRARA
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-!- FUNCTION: Plays a critical role in MHC class II antigen processing by stabilizing peptide-free class II alpha/beta heterodimers in a complex from the role; synthesis and directing transport of the complex from the endoplasmic reticulum to compartments where peptide loading of class II takes place.
-!- SUBUNIT: Nonamer composed of three alpha/beta/gamma heterotrimers (By similarity).
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=84207946; PubMed=6327293; Singer P.A., Lauer W., Dembic Z., Mayer W.E., Lipp J., Koch N., Singer P.A., Lauer W., Dembic Z., Mayer W.E., Lipp J., Koch N., Hammerling G., Klein J., Dobberstein B.; "Structure of the murine Ia-associated invariant (Ii) chain as deduced from a cDNA clone."
EMBO J. 3:873-877(1984).
                                                                                                                                                                                                                                                                            Stone J., Perry R., Todd J.A., McDevitt H.O.;
"Nucleotide sequences of the murine la-associated invariant chain (Ii)
and I-E (H-2S, Beta) chain expressible cDNA clones.";
Submitted (MAR-1988) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90257363; PubMed=2111346;
Eades A.-M., Litfin M., Rahmsdorf H.J.;
"The IFN-gamma response of the murine invariant chain gene is medie
by a complex enhancer that includes several MHC class II consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (By similarity).
-!- SUBCELLULAR LOCATION: Membrane, single-pass type II membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=88144436; PubMed=3422739;
Miller J., Hatch J.A., Simonis S., Cullen S.E.;
"Identification of the glycosaminoglycan-attachment site of
invariant-chain proteoglycan core protein by site-directed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ensembl; ENSMUSGO000024610; Mus musculus.
MGI; MGI:96534; Ii.
GO; GO:0005783; C:endoplasmic reticulum; IDA.
GO; GO:0009897; C:external side of plasma membrane; IDA.
GO; GO:0005794; C:Golgi apparatus; IDA.
GO; GO:0005764; C:integral to plasma membrane; TAS.
GO; GO:0005764; C:lysosome; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=P04441-2; Sequence=VSP 005332;
-!- SIMILARITY: Contains 1 thyroglobulin type-1 domain.
                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomic_DNA
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EMBL; X07129; CAA30141.1; -; mRNA.
EMBL; X05429; CAA29010.1; -; Genomic_DNA.
EMBL; X05429; CAA29012.1; -; Genomic_DNA.
EMBL; X05430; CAB37297.1; -; Genomic_DNA.
EMBL; X13414; -; NOT_ANNOTATED_CDS;
EMBL; X13414; -; NOT_ANNOTATED_CDS;
EMBL; M35872; AAA37897.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE OF 47-191 AND 256-279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=P04441-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Immunol, 144:4399-4409(1990).
[7]
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SMR; P04441; 117-191, 193-256.
                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE OF 1-58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE OF 1-25
                                                                                                                                cDNA sequences."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein (Potential)
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                                                                                                                                    and mouse
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                               Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Methods Enzymol. 303:19-44(1999).
                                                              NUCLEOTIDE SEQUENCE.
  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=NOD;
                                                                                                                                                                                                                                                                                                 STRAIN=NOD;
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        ö
                                                           P:antigen presentation, IDA.
P:antigen presentation, exogenous antigen via. . .; IMP.
P:antigen processing, exogenous antigen via M. . .; IMP.
P:cell proliferation, ISS.
P:chaperone cofactor dependent protein folding; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gamma chain.

(FTIG=PRO 000067955.

(FTIG=PRO 000067955.

Stracelular (Potential).

Extracelular (Potential).

Thyroglobulin type-1.

N-linked (GlcNAc. .) (Potential).

N-linked (Xyl. .) (GlYcosaminoglycan).

By similarity.

By similarity.

By similarity.

Missing (in isoform Short).

/FTIG+VSP 005332.

/FTIG+VSP 005332.

/FTIG+VSP 005332.

N -> M (in Ref. 1).

N -> M (in Ref. 1).

STG -> RHC (in Ref. 2).

MW; 300A85014F170792 CRC64;
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11-0CT-2005, sequence version 1.
07-FEBS-2006, entry version 5.
NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630001K12 product:Ia-associated invariant chain, full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00484; THYROGLOBULIN 1 1: 1.
PROSITE; PS51162; THYROGLOBULIN 1 2: 1.
Alternative splicing; Chaperone; Glycoprotein; Immune response;
Amenbrane; Proteoglycan; Signal-anchor; Transmembrane.
CHAIN 1 279 H-2 class II histocompatibility antigen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                              GO:0006886; P:intracellular protein transport; IDA.
GO:0043066; P:negative regulation of apoptosis; ISS.
GO:0045581; P:negative regulation of T cell differentiation; IMP.
GO:0045582; P:postive thymic T cell selection; IMP.
GO:0045582; P:postive regulation of T cell differentiation; IMP.
GO:0045059; P:postive thymic T cell selection; IMP.
GO:001516; P:prostaglandin biosynthesis; ISS.
                                                                                                                                                                                                              P:defense response; IMP.
P:humoral defense mechanism (sensu Vertebrata); IMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
0
R GO; GO:0005771; C:multivesicular body; IDA.
R GO; GO:0019955; F:cytokine binding; ISS.
R GO; GO:0019985; P:antigen presentation, IDA.
R GO; GO:0019886; P:antigen presentation, Exception via.
R GO; GO:0019886; P:antigen presentation, exceptions antigen via.
R GO; GO:0010886; P:antigen processing, exceptions antigen via M.
R GO; GO:001085; P:cell proliferation; ISS.
R GO; GO:001085; P:celperone cofactor dependent protein folding
R GO; GO:001086; P:uchaperone cofactor dependent protein folding
R GO; GO:0016064; P:humoral defense mechanism (sensu Vertebrata)
R GO; GO:0049581; P:negative regulation of apoptosis; ISS.
R GO; GO:0045581; P:negative regulation of T cell differentiation
R GO; GO:0045582; P:positive regulation of T cell differentiation
R GO; GO:0045582; P:positive thymic T cell selection; IMP.
R GO; GO:0045059; P:positive thymic T cell selection; IMP.
R GO; GO:0043030; P:regulation of macrophage activation; ISS.
R InterPro; IPR011988; MHCII invariant.
R R RMART; SM00211; TY; II.
R RMART; SM00211; TY; II.
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Pred. No. 0.0058;
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Q3U4Q8;
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Best Local Similarity 85...
Best Local 2; Conservative
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RIKEN Genome Exploration Research Group, and Genome Science Group
(Genome Network Core Team) and the FANTOM Consortium;
"Antisense Transcription in the Mammalian Transcriptome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The transcriptional landscape of the mammalian genome."; Science 309:1559-1563 (2005).
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NUCLEOTIDE SEQUENCE.
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Hayashizaki Y.;
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MGG GO:0005783; C:endoplasmic reticulum; IDA.

GG; GO:0005783; C:endoplasmic reticulum; IDA.

GG; GO:0005784; C:Golgi apparatus; IDA.

GG; GO:0005784; C:Golgi apparatus; IDA.

GG; GO:0005786; C:integral to plasma membrane; IDA.

GG; GO:0005784; C:integral to plasma membrane; TAS.

GG; GO:0005784; C:lysosome; IDA.

GG; GO:000571; C:multivesicular body; IDA.

GG; GO:000571; C:multivesicular body; IDA.

GG; GO:0019882; P:antigen presentation; IDA.

GG; GO:0019882; P:antigen presentation; IDA.

GG; GO:0019882; P:antigen presentation; IMP.

GG; GO:0019885; P:antigen presentation; IMP.

GG; GO:0019886; P:antigen presentation; IMP.

GG; GO:0019886; P:antigen presentation; IMP.

GG; GO:0019886; P:antigen presentation; IMP.

GG; GO:0016686; P:humoral defense mechanism (sensu Vertebrata); IMP.

GG; GO:0016886; P:intracellular protein transport; IDA.

GG; GO:0016886; P:intracellular protein transport; IMP.

GG; GO:0045886; P:intracellular protein; IMP.

GG; GO:0045886; P:protein complex assembly; IDA.

InterPro; IRRO0716; Thyroglobulin_1: 1.

RENDER: PROMO211; TY; 1.
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Distributed under the Creative Commons Attribution-NoDerivs License
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Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
Muramatsu M., Hayashizaki Y.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Bumanla; Butheria; Lauraaiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96212904; PubMed=8630076; DOI=10.1006/bbrc.1996.0689; Niimi M., Nakai Y., Aida Y.; "Identification of bovine invariant chain (Ii) gene by nucleotide
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Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
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; 31557 MW; 300A85014F170792 CRC64;
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Pred. No. 0.0058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004, integrated into UniProtKB/TrEMBL
05-JUL-2004, sequence version 1.
07-FEB-2006, entry version 8.
Invariant chain (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                              EMBL; AK154096; BAE32373.1; -; mRNA.
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Gaps

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RX TISSUBE-Pituitery gland;

RX Straubitus

RX Straubitus

RX Strauberg R.L., Febingold E.A., Grouse L.H., Derge J.G.,

Rausner R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschark E.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rapleton M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

Rapleton M.J., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raples S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robards S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RY, Milalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glibs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rheinguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rad Mederation and initial analysis of more than 15,000 full-length human
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see http://www.uniprot.org/terms
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CD74 antigen (Invariant polpypeptide of major histocompatibility class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                        82.2%; Score 60; DB 2; Length 204; 73.3%; Pred. No. 0.0065; ive 4; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                            204 AA; 23146 MW; 0FD00643BCA82BFA CRC64;
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                                                                                                 EMBL; BC102368; AA102389.1; -; mRNA.
EMBL; BT021489; AAX46336.1; -; mRNA.
PIR; JC4796; JC4796.
HSSP; Q29633; 11IE.
SMR; Q29630; 116-190.
Ensembl; ENSBTAG0000015228; Bos taurus.
                                                                                                                                                                                                                                               GO; GO:0016020; C:membrane; IBA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPRO11988; MHCII_invariant.
SEQUENCE 204 AA; 23146 MW; 0FD006431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                               EMBL; D83962; BAA12156.1; -; mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Conservative
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Name=Cd74;
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Best Local Similarity
Matches 11; Conserv
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07-FEB-2006,
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                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Heaton M.P., Keele J.W., Snelling W.M., Weidmann R.T., Smith T.P.L.,
"Sequencing and analysis of Bos taurus full-length insert CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Japanese Black; TISSUE-Tumorus lymph node;
MEDLINE-S6712904; PubMed-8630076; DOI-10.1006/bbrc.1996.0689;
Niimi M., Nakai Y., Alda Y.;
"Identification of bovine invariant chain (Ii) gene by nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996, sequence version 1.
07-MAR-2006, entry version 26.
Invariant chain (Hypothetical protein MGC127643) (Invariant gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
Pecora, Bovidae, Bovinae, Bos.
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                                                                                                                                                                                                                                                                                                                                         Length 190;
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                                                                                                                                                                                                                                                                                          190 AA; 21660 MW; DA3AD746DCD649FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochem. Biophys. Res. Commun. 222:7-12(1996).
                                                                                                                                                                                                                                                                                                                                         82.2%; Score 60; DB 2; 73.3%; Pred. No. 0.006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996, integrated into UniProtKB/TrEMBL
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                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                            EMBL; D83961; BAA12155.1; -; mRNA.
SMR; Q7JFY1; 109-183.
Ensembl; ENBERGG0000015228; Bos taurus.
G0; G0:0016020; C:membrane; IEA.
G0; G0:0006955; P:immune response; IEA.
InterPro; IPR011988; MHCII_invariant.
          Copyrighted by the UniProt Consortium,
                                    Distributed under the Creative Commons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=MGC127643; Synonyms=CD74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus gene index.";
Mamm. Genome 13:373-379(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q29630 BOVIN PRELIMINARY; Q29630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 PVSKMRMATPLLMQA
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                     190
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                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Pooled
                                                                                                                                                                                                                                                                                                                                                                                           11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res. 16:11822-11822 (1988).

-I-FUNCTION: Plays a critical role in MHC class II antigen processing by stabilizing peptide-free class II alpha/beta heterodimers in a complex soon after their synthesis and directing transport of the complex from the endoplasmic reticulum to compartments where peptide loading of class II takes place.

-I-SUBURIT: Nonamer composed of three alpha/beta/gamma heterotrimers (By similarity) Membrane; single-pass type II membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Henkes W., Syha J., Reske K.;
"Nucleotide sequence of rat invariant gamma chain cDNA clone pLR gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                  McKnight A.J., Mason D.W., Barclay A.N.; "Sequence of a rat MHC class II-associated invariant chain cDNA clone containing a 64 amino acid thyroglobulin-like domain."; Nucleic Acids Res. 17:3983-3984(1989).
                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                         Gaps
                                                                                                                                                                                                                                                  01-FEB-1991, sequence version 2.
07-MAR-2006, entry version 53.
H-2 class II histocompatibility antigen, gamma chain (MHC class II-
associated invariant chain) (Ia antigen-associated invariant chain)
                                                                                                         ..
0
                                                                                 Length 216;
                                                                                                      1; Indels
       SMR; QGGT70; 118-192.
GO; GC:0016020; C:membrane; IEA.
GO; GO:0016955; P:immune response; IEA.
Interbro; IPR011988; MHGII invariant.
SEQUENCE 216 AA; 24503 MW; 33677FA259B84F8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Contains 1 thyroglobulin type-1 domain.
                                                                                                                                                                                                                                       01-JUL-1989, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [MRNA] OF 1-192 AND 257-280.
                                                                               Score 59; DB 2;
Pred. No. 0.011;
1; Mismatches
                                                                                                                                                                                                                 280 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    soId=P10247-2; Sequence=VSP_005333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=P10247-1; Sequence=Displayed;
EMBL; BC059152; AAH59152.1; -; mRNA.
                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X14254; CAA32468.1; -; mRNA.
EMBL; X13044; CAA31450.1; -; mRNA.
BTR; SQ4362; SQ4362.
HSSP; P04233; 11CF.
SWR; P10247; 118-192, 194-257.
                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [MRNA].
STRAIN-PVG X DA; TISSUE-Spleen;
MEDLINE-89282409; PubMed=2499873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=89098337; Pubmed=3264906;
                                                                                80.8%;
ilarity 85.7%;
Conservative
                                                                                                                                            ||| |||||||||
87 PVSPMRMATPLLMR 100
                                                                                                                              1 PVSKMRMATPLLMQ 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein (Potential).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat)
                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                 (Ii) (CD74 antigen).
Name=Cd74;
                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=Short;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Lewis
                                                                                                                                                                                                   HG2A_RAT
ID HG2A_RAT
                                                                                                                                                                                                                           P10247;
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(By
                                                                                                                                                                                                                                                                                                                               gamma chain.

/FTId=FRO 000067956.

/Cytoplasmic (Potential).

Signal-anchor for type II membrane
protein (Potential).

Extracellular (Potential).

Thyroglobulin type-1.

N-linked (GlcNAc. .) (Potential).

N-linked (Xyl. . .) (Glycosaminoglycan) (By gimilarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                         PROSITE; PS00484; THYROGLOBULIN_1 1; 1.
PROSITE; PS51162; THYROGLOBULIN_1 2; 1.
Alternative splicing; Chaperone; Glycoprotein; Immune response;
Membrane; Proteoglycan; Signal-anchor; Transmembrane.
CHAIN 1 280 H-2 class II histocompatibility antigen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa (Pig).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=14681463; DOI=10.1093/nar/gkh037; Uenishi H., Eguchi T., Suzuki K., Sawazaki T., Toki D., Shinkai H., Okumura N., Hamasima N., Awata T.; Eps E. (Pig ST Data Explorer): Construction of a database for ESTs derived from porcine full-length cDNA libraries."; Nucleic Acids Res. 32:D484-D488(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                    GO; GO:0019955; F:cytokine binding; ISS.
GO; GO:0008283; P:cell proliferation; ISS.
GO; GO:0003066; P:negative regulation of apoptosis; ISS.
GO; GO:0001516; P:prostaglandin biosynthesis; ISS.
GO; GO:00043030; P:regulation of macrophage activation; ISS.
InterPro; IPR001988; MHCII invariant.
InterPro; IPR00016; Thyroglobulin_1.
Pfam; PF00086; Thyroglobulin_1.
SWART; SM00211; TY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (in isoform Short).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D935D169A98B5732 CRC64;
ENSRNOG00000018735; Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 59; DB 1;
Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      By similarity.
By similarity.
By similarity.
Missing (in iso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AB116558; BAD06312.1; -; mRNA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR011988; MHCII_invariant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004, sequence version 1. 07-FEB-2006, entry version 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                280 AA; 31642 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87 PVSPMRMATPLLMR 100
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Best Local Similarity 85.7'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234
255
256
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255
114
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266
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                                                                                                                                                                                                                                                                                                                                                                                                                                          57
194
114
120
266
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236
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Q764N1_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=cd74;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLECTIDE SEQUENCE.

Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Etgu P., Lee J.M.,
Toriumi M., Yu G., Brooks S., Chao Q., Chen H., Karlin-Neumann G.,
Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shinn P.,
Southwick A., Davis R. W., Ecker J.R., Theologis A.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Town C.D., Haas B.J., Wu D., Maiti R., Hannick L.I., Chan A.P., Tallon L.J., Rooney T., Utterback T.R., VanAken S.E., Feldblyum T.V., White O., Fraser C.M.; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21417794; PubMed=11526245; DOI=10.1073/pnas.181304598;
Motchashi R., Nagata N., Ito T., Takahashi S., Hobo T., Yoshida S.,
Shinozaki K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=apg2; OrderedLocusNames=At2g01110;
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          z.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
                                                        76.7%; Score 56; DB 2; Length 214; 66.7%; Pred. No. 0.04; ive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Summer E.J., McCaffery M.W., Cline K.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
[9]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Town C.D., Kaul S.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
ES347DE04885524F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        annotation.";
Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                     QSSJVS_ARATH PRELIMINARY; PRT; 340 AA. QSSJVS_QSXVS_QSXVS_1 QSXR14; 01-MAY-2000, integrated into UniProtKB/TrEMBL. 01-MAY-2002, sequence version 2. 07-FEB-2006, entry version 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22088475; PubMed=12093376;
24118 MW;
                                                                                                                                                                                                                                                           PLSKMRVSAPMLMOA 101
                                                                                          66.78;
                                                                                                                                                                                              1 PVSKMRMATPLIMOA 15
                                                                                                                           10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-2000)
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   214 AA;
                                                                                             Best Local Similarity
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Feldmann K.
   SEQUENCE
                                                               Query Match
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Q95JV5 ARR
ID Q95JV5 ARR
ID Q95SJV
DT O1-MA
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Distributed under the Creative Commons Attribution-NoDerivs License
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US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome and assembly of Pelobacter propionicus
DSM 2379.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Larimer F., Land M.;
"Annotation of the draft genome assembly of Pelobacter propionicus DSM
Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
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Pelobacteraceae; Pelobacter.
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Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 340;
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                                                                                                                                                                                               Theologis A.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   340 AA; 37367 MW; 1429C265BFEDB281 CRC64;
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Pred. No. 34;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF360172; AAK25882.1; -; mRNA.
EMBL; AC006837; AAF18659.2; -; Genomic_DNA.
EMBL; AB054096; BAB62074.1; -; mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF145045; AAD33946.1; -; mRNA.
EMBL; AY084784; AAM51351.1; -; mRNA.
EMBL; AY056347; AAL07196.1; -; mRNA.
PIR; T44583; T44583.
TAIR; At2901110; -
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07-FBB-2006, entry version 3.
Hydrophobe/amphiphile efflux-1 HAB1.
ORFNAmes=PproDRAFT_2759;
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PRINTS; PR01840; TATCFAMILY.
TIGRFAMS; TIGR00945; tatC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T., Hammon N., Israni S., Pitluck S., Martinez M., Schmutz J., Larimer F., Land M., Kyrpides N., Ivanova N., Richardson P.; "Complete sequence of Synechococcus sp. CC9902."; Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
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07-MAR-2006, entry version 14.
Hypothetical protein PM0291 precursor.
OrderedLocusNames=PM0291;
Pasteurella multocida.
Bacteria; Proteobbacteria; Gammaproteobacteria; Pasteurellales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-NOV-2005, integrated into UniProtKB/TrEMBL.
22-NOV-2005, sequence version 1.
07-FEB-2006, entry version 3.
YGGT family, conserved hypothetical integral membrane protein.
                                                                                                                                                                                                                                              Score 42; DB 2; Length 1054;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56.2%; Score 41; DB 2; Length 110; 72.7%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                              TIGREAMS; TIGRO0915; 2A0602; 1.
SEQUENCE 1054 AA; 114349 MW; 5F57EC6404F4F839 CRC64;
                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 AA; 12043 MW; A220BA2C0EA9653F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORFNames=Syncc9902 0420;
Synechococcus sp. [strain CC9902).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
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                   Genomic DNA.
                                    GO; GO:0016021; C:integral to membrane; IEA GO; GO:0002515; F:transporter activity; IEA. GO; GO:0006810; P:transport; IEA. InterPro; IPR001036; Acrflvin_res. InterPro; IPR004764; HABI. PFam; PF00973; ACR tran; 1.
                                                                                                                                                                                                                                                                                         4; Mismatches
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GO; GO:0016020; C:membrane; IEA.
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                   EMBL; AAJH01000006; EA036965.1; -;
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109 NKLQLATPLLPQA 121
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                                                                                                                                                                                                                                                                    Best Local Similarity 61.5
Matches 8; Conservative
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Q3AZT7 SYNS9
Q3AZT7;
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Q9CNYO;
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Y291 PASMU
AC 09CNT0,
DT 22-ANG-
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PubMed=15465(10; DOI=10.1073/pnas.0406410101;
PubMed=15465(10; DOI=10.1073/pnas.0406410101;
Ishikawa J., Yamashita A., Mikami Y., Hoshino Y., Kurita H., Hotta K., Shiba T., Hattori M.;
The complete genomic sequence of Nocardia farcinica IFM 10152.";
Proc. Natl. Acad. Sci. U.S.A. 101:14925-14930(2004).
-: SUBCELLUIAR LOCATION: Membrane; multi-pass membrane protein (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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GO; GO:0166221; C:integral to membrane; IEA.
GO; GO:0016020; C:integral to membrane; IEA.
GO; GO:0015520; C:membrane; IEA.
GO; GO:0015520; F:terracycline:hydrogen antiporter activity; IEA.
GO; GO:0015904; P:terracycline transport; IEA.
GO; GO:0015904; P:terracycline transport; IEA.
InterPro; IPR007114; MFS.
InterPro; IPR001411; ICE TECB.
Frans. PF07690; MFS.
Frans. FF07690; MFS.
Frans. FF07690; MFS.
                                                           STRAIN=PMT0;
MEDLINE=21145866; PubMed=11248100; DOI=10.1073/pnas.051634598;
MABLINE=2145866; Li L.L., Paustian M.L., Whittam T.S., Kapur "Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Nocardiaceae; Nocardia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.2%; Score 41; DB 1; Length 238; 57.1%; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein PM0291. /FIId=PRO 0000014174.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete protecome; Membrane; Transmembrane; Transport. SEQUENCE 471 AA; 47603 MW; 7063445CE608F0EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9F507B621AA5B1AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE006064; AAK02375.1; -; Genomic_DNA.
GenomeReviews; AE004439 GR; PM0291.
BioCyc; PMUL747:PM0291-MONOMER; -.
Complete proteome; Hypothetical protein; Signal.
SIGNAL
[1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-NOV-2004, integrated into UniProtKB/TrEMBL. 23-NOV-2004, sequence version 1. 21-FEB-2006, entry version 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  471 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 AA; 26984 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218 PESQQKLATPLLNQ 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OrderedLocusNames=nfa33430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 PVSKMRMATPLLMQ 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR01036; TCRTETB.
PROSITE; PS50850; MFS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Putative transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nocardia farcinica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=37329;
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[2]
NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                              STRAIN=TM1040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q709V4_ANOGA
                                                                           STRAIN=TM1040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=PEST;
                                                      NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANOGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q709V4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 24
Q7Q9V4_ANC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3est
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF010496; AAC16124.1; -; Genomic_DNA.
PIR, T03471; T03471.
InterPro; IFN07208; MxpF_phaF.
Pfam; PF04066; MrpF PhaF; 1.
Antiport; Hydrogen Ton transport; Membrane; Potassium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probable K(+)/H(+) antiporter subunit F./FIId=PRO_0000087745.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Capacinatis Acad. Sci. U.S.A. 94:9384-9388(1997).
-!- FUNCTION: Part of a K(+) efflux system involved in pH adaptation (By similarity).
-!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fonstein M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Belongs to the CPA3 antiporters (TC 2.A.63) subunit
                                                                                                                                                                                                                                                                 07-FEB-2006, entry version 26. Probable K(+//H(+) antiporter subunit F (pH adaptation potassium efflux system protein F) (Pha system subunit F). Name=phaF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORFNames-RoseDRAFT 2168,
Silicibacter sp. TM1040.
Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales,
                                                                                                                                                                                                                                                                                                                                                        Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales,
Rhodobacteraceae, Rhodobacter
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Proc. Natl. Acad. Sci. U.S.A. 94:9384-9388(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40; DB 1; Length 92,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     953B3509FB542A2A CRC64;
                                                                                                                                                                                                                                                                                                                                           Rhodobacter capsulatus (Rhodopseudomonas capsulata)
                                                                                                                                                                                                                        integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-OCT-2005, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                         92 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
 Pred. No. 75;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-00T-2005, sequence version 1, 07-FEB-2006, entry version 3. Inner-membrane translocator precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Potassium transport; Transmembrane;
CHAIN 1 92 Probabl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-SB1003 / St Louis;
MEDLINE-97404404; PubMed-9256491;
                                                                                                                                                                                                                                                  sequence version 1.
                       . 9
                                                                               || ::: ||::||:
269 PVGAIQLVTPMIMQS 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9790 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.8%;
ilarity 57.1%;
Conservative
40.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                        1 PVSKMRMATPLLMQA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VSKMRMATPLLMQA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 VTGMRMGTPFLFEA 66
                     6; Conservative
                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24
57
82
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Best Local Similarity
 Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92 AA;
                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q3QS54_9RHOB
Q3QS54;
                                                                                                                                                                                                                                            01-AUG-1998,
                                                                                                                                                                                                                            30-MAY-2000,
                                                                                                                                                                                         PHAF RHOCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
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                                                                                                                                                                                                           068038;
                                                                                                                                                 RESULT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              930554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Annotation of the draft genome assembly of Silicibacter sp. TM1040.";
Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
Anophelinae; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=TM1040;
US DOE Joint Genome Institute (JGI-PGF);
US DOE Joint Genome Institute (JGI-PGF);
Hammon N., Israni S., Pitluck S., Richardson P.;
Submitted (JUN-2005) to the EMBL/GenBank/DBBJ databases.
-i- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                          Detter C., Glavina T.,
                                                                                                                                               US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Incas S., Lapidus A., Barry K., Detter C., Glavina
Hammon N., Israni S., Pitluck S., Richardson P.,
"Sequencing of the draft genome and assembly of Silicibacter sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Anopheles gambiae re-annotation.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                         Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 Potential.
35328 MW; 3DD256F4FAB77A60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AAFG02000005; EAN56679.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB 2;
Pred. No. 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-2003, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO, GO:0016020; C:membrane; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR001851; Bac_inmem_transp.
Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    350 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                    US DOE Joint Genome Institute (JGI-ORNL);
Larimer F., Land M.;
"Annotation of the draft genome assembly o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The Anopheles gambiae Sequence Committee;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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07-FEB-2006, entry version 12.
ENSANGPO00001807 (Fragment).
ORFNames-ENSANGG0000019318;
Rhodobacteraceae, Silicibacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 54.8%;
Local Similarity 72.7%;
les 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 SKWRMATPLLM 13
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STVRMATPLLL 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preliminary data.
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NUCLEOTIDE SEQUENCE
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                                                                                            SEQUENCE
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NCBI_TaxID=6238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=CBG12444;
                                                                                                                                                                                                                                                                                                                                                                                             Q61DK9_CAEBR
Q61DK9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=AF16;
                                                                                                                                                                                                8,
                                                                                                                                                     Query Match
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UVRD_SALTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OrderedLocusNames=At2g23190;
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Varidiplantae; Streptophyta; Embryophyta; Core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C., Sykes S.M., Kaul S., Mason T.M., Kerlavage A.R., Adams M.D., Somerville C.R., Venter J.C., Submitted (WAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
             The Anotheles gambiae Sequence Committee,
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.8%; Score 40; DB 2; Length 350; 70.0%; Pred. No. 85; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Town C.D., Kaul S.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the cytochrome P450 family.
                                                                                                                                                                                                                                                                                                                                                                                                                   350 AA; 38908 MW; 3DF953760C0688B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AC002391; AAB87112.1; -; Genomic_DNA.
PIR; T00513; T00513.
HSSP, P14779; D1P2.
TAIR; AC2923190; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016020; C:immbrane; IEA.
GO; GO:002037; F:heme binding; IEA.
GO; GO:000566; F:iron ion binding; IEA.
GO; GO:000487; F:metal ion binding; IEA.
GO; GO:000418; P:electron transport; IEA.
INTERPO; IRR001128; Cytochrome_P450.
InterPro; IPR0012401; EP4501.
PANTHER; PTHR19383; Cytochrome_P450; 1.
                                                                                                                                                                                                                EMBL; AAAB01008900; EAA09481.2; -; Genomic_DNA.
GO; GO:0008270; F: sith c ion binding; IEA.
GO: PR002048; EF hand Ca_bd.
InterPro; IPR004181; ZnF_MIZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1998, integrated into UniProtKB/TrEMBL. 01-JAN-1998, sequence version 1. 21-FEB-2006, entry version 31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               543 AA
                                                                                                                                                                                                                                                                                                       Pfam; PF02891; zf-MIZ; 1.
PROSITE; PS00018; EF HAND 1; UNKNOWN 1.
PROSITE; PS51044; ZF SP_RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OZ2188_ARATH PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 PLGKMRMTTP 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 PVSKMRMATP 10
                                                                                                          preliminary data.
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NON TER
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022188 ARA
1D 022188 ARA
DT 01-JAB
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                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=1462427; DOI=10.1371/journal.pbio.0000045; Stein L.D., Bao Z., Blasiar D., Blumenthal T., Brent M.R., Chen N., Chinwalla A., Clarke L., Clee C., Cophlan A., Coulson A., Griffiths-Jones S., Harris T.W., Hillier L.W., Kamath R., Kuwabara P.E., Mardis E.R., Marra M.A., Miner T.L., Minx P., Mullikin J.C., Plumb R.W., Rogers J., Schein J.E., Sohrmann M., Waterston R.H.;
Pfam; PF00067; p450; 1.
PRINTS; PR00463; EP450I.
PRINTS; PR00385; P450.
PROSITE; PS00086; CYTCCHROME P450; UNKNOWN 1.
Heme; Iron; Membrane; Metal-Dinding; Monooxygenase; Oxidoreductase.
SEQUENCE 543 AA; 62777 MW; 06332D6C090FDB12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLOS Biol. 1:166-192(2003).
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The genome sequence of Caenorhabditis briggsae: a platform for comparative genomics.",
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0
                                                                                                                                                                                            Length 543;
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63.6%; Pred. No. 1.7e+02;
1. Indels
                                                                                                                                                                                      Score 40; DB 2; Length 54:
Pred, No. 1.4e+02;
2; Mismatches 2; Indels
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Complete proteome; Hypochetical protein.
SEQUENCE 675 AA; 75900 MW; BF2631230A44B877 CRC64;
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Q05311; Q9L6P3;
01-OCT-1994, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; CAAC01000060; CAE67038.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-NOV-2004, integrated into UniProtKB/TrEMBL 23-NOV-2004, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              675 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO, GO:0008270; F:zinc ion binding; IEA.
InterPro; IPR004181; Znf_MIZ.
Pfam; PF02891; zf-MIZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-FEB-2006, entry version 7. Hypothetical protein CBG12444.
                                                                                                                                                                                      54.8%;
                                                                                                                                                                                                                                                                                                                                                         515 PMAMMRPATPLL 526
                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                    1 PVSKMRMATPLL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis briggsae.
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267 PLSKIRMKTPV 277
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                                                                                                                                                                                                                Local Similarity
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NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAID=ATCC 9150 / SARB42;

STRAID=ATCC 9150 / SARB42;

RY PubMed=1551882;

A MCIelland M., Sanderson K.E., Clifton S.W., Latreille P., McIelland M., Sanderson K.E., Clifton S.W., Latreille P., McLelland M., Porwollik S., Sabo A., Meyer R., Bieri T., Ozersky P., McLellan M., Harkins C.R., Wang C., Nguyen C., Berghoff A., Elliott G., A Harkins C.R., Wang C., Du F., Carter J., Kremizki C., Layman D., Leonard S., Sun H., Fulton L., Nash W., Miner T., Minx P., Delehannty K., Fronick C., Magrini V., Nhan M., Warren W., Florea L., Spieth J., Wilson R.K.;

"Comparison of genome degradation in Paratyphi A and Typhi, human-restricted serovars of Salmonella enterica that cause typhoid.";

Nat. Genet. 36:1268-1274 (2004).
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                              "The genome sequence of Salmonella enterica serovar Choleraesuis, highly invasive and resistant zoonotic pathogen."; Nucleic Acids Res. 33:1690-1698(2005).
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Salmonella paratyph.-a.
Sacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                       Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Salmonella.
                                                                                                                                                                                                                                                                                                   PubMed=15781495; DOI=10.1093/nar/gki297;
Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,
Wang H.-S., Lee Y.-S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE017220; AAX67756.1; -; Genomic_DNA.

QO; GO:0005524; F:ATP binding; IEA.

GO; GO:0005524; F:ATP capendent DNA helicase activity; IEA.

GO; GO:0004367; F:ATP-dependent DNA helicase activity; IEA.

GO; GO:0004386; F:helicase activity; IEA.

GO; GO:0006281; P:DNA repair; IEA.

GO; GO:0006288; P:DNA unvinding during replication; IEA.

InterPro; IPRO05753; UvrD-helicase.

R PANTHER; PTHR11070; UvrD-helicase; 1.

Ffam; PF00580; UvrD-helicase; 1.

Ffam; PF00580; UvrD-helicase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40; DB 2; Length 720;
Pred. No. 1.9e+02;
0; Mismatches 3; Indels
07-FEB-2006, entry version 4.
DNA-dependent ArPase I and helicase II.
Name=uvrb; CoderedLocusNames=SC3850; ORFNames=SCH_3850;
Salmonella choleraesuis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome; Helicase.
SEQUENCE 720 AA; 81953 MW; CBBE8D126B03D80C CRC64;
                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA] .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-JAN-2005, integrated into UniProtKB/TrEMBL.
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07-FEB-2006, entry version 8.
DNA helicase II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QSPKM2_SALPA PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 72.7
Matches 8; Conservative
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                                                                                                                                                                                     NCBI_TaxID=591;
                                                                                                                                                                                                                                                                          STRAIN=SC-B67
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                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=LT2 / SGSC1412 / ATCC 700720;

MEDLINE=21534948; Pubmed=11677609; DOI=10.1038/35101614;

MEDLINE=21534948; Dubmed=11677609; DOI=10.1038/35101614;

MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K., Wilson R.K., "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-93300795; PubMed-814774, Smith R.L., Banks J.L., Snavely M.D., Maguire M.E.; Smith R.L., Banks J.L., Snavely M.D., Maguire M.E.; Squence and topology of the CorA magnesium transport systems of Salmonella typhimurium and Escherichia coli. Identification of a new class of transport protein."; J. B. School R. Sequence and Escherichia coli. Identification of a new class of transport protein."; J. B. School R. School R.
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                                                                                                                                                      Bacteria; Próteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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                                  07-MAR-2006, entry version 41.
DNA helicase II (EC 3.6.1.-).
Name=uvrD; OrderedLocusNames=STM3951; ORFNames=STMD1.39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 720 DNA helicase II.
/FTId=PRO 0000102073.
29 36 ATP (Potential).
720 AA; 81981 MW; CE6D60296392511C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 708-720.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L11043; AAA122795.1; -; Genomic DNA.
HSSP; P09980; IUAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          720 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF233324; AAF33441.1; -; Genomic_DNA.
EMBL; AE008884; AAL22795.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenomeReviews, AE006468 GR; STM3951.
StyGene, SG10414, uvrD.
BioCyc, STYP99287:STM3951-MONOMER, -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro, IPR005753; UvrD.
Interpro; IPR000212; UvrD-helicase.
PANTHER: PTHR11070; UvrD-helicase; 1.
PÉam; PF00580; UvrD-helicase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QC_SALCH
Q57HQ6_SALCH PRELIMINARY; PRT;
Q57HQ6;
            29-AUG-2001, sequence version 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 413:852-856(2001).
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Les 8; Conservative
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                                                                                                                                   Salmonella typhimurium.
                                                                                                                                                                                                                        NCBI_TaxID=602
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SEQUENCE
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SOURCE STANKE WELL TO THE SECOND OF THE SECO

10-MAY-2005, integrated into UniProtKB/TrEMBL. 10-MAY-2005, sequence version 1.

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QZIRQ8_RHOPA
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Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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STRAIN=Ty2 / ATCC 700931;
MEDLINE=22531367; Pubmed=12644504;
DOI=10.1128/JB.185.7.2330-2337.2003;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Bashaman D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin M., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
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Enterobacteriaceae; Salmonella.
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                                                                                              EMBL; CP000026; AAV79568.1; -; Genomic_DNA.

GO; GO:000537; C:cytoplasm; IEA.

GO; GO:000537; C:cytoplasm; IEA.

GO; GO:0004003; F:ATP-dependent DNA helicase activity; IEA.

GO; GO:0004003; F:DNA binding; IEA.

GO; GO:0006281; P:DNA repair; IEA.

GO; GO:0006281; P:DNA unwinding during replication; IEA.

InterPro; IPR00212; UvrD-helicase.

RATHERP PROSESSO; UvrD-helicase; 1.

PFAMT; PF00580; UvrD-helicase; 1.

TIGREAMS; TIGR01075; UvrD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.8%; Score 40; DB 2; Length 720; 72.7%; Pred. No. 1.9e+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
Thomson N.R., Pickar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome, Helicase.
SEQUENCE 720 AA, 81953 MW, CBBEBD126B03D80C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QB23B0 SALTI PRELIMINARY; PRT; 720 AA. QB23B0; Q7C6W2; 01-MAR-2002, integrated into UniProtKB/TrEMBL. 01-MAR-2002, sequence version 1. DYAR-2006, entry version 23. DNA helicase II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=uvrD; OrderedLocusNames=STY3608, t3346; Salmonella typhi.
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EMBL; AE014613; AAO70874.1; -; Genomic_DNA.
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Matches 8; Conservative
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HSSP; P09980; 1UAA
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T., Hammon N., Israni S., Pitluck S., Chain P., Malfatti S., Shin M., Vergez L., Schmutz J., Lariner F., Land M., Hauser L., Pelletier D.A., Kyrpides N., Anderson I., Oda Y., Harwood C.S., Richardson P., "Complete sequence of Rhodopseudomonas palustris HAA2.", Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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07-MAR-2006, sequence version 1.
07-MAR-2006, entry version 1.
Aldehyde oxidase and xanthine dehydrogenase, molybdopterin binding.
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Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Bradyrhizobiaceae, Rhodopseudomonas.
                                                        GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006281; F:DNA repair; IEA.
GO; GO:0006281; P:DNA repair; IEA.
InterPro; IPR00573; UvrD.
InterPro; IPR00573; UvrD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 2; Length 720;
Pred. No. 1.9e+02;
0; Mismatches 3; Indels
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SEQUENCE 720 AA; 82110 MW; 9E926B873D9CE672 CRC64;
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SEQUENCE 755 AA; 79136 MW; 611FD147885CA0F3 CRC64;
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01-JUN-2001, integrated into UniProtKB/TrEMBL.
01-JUN-2001, sequence version 1.
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BioCyc; SENT209261;T3346 MONOMER-; -. BioCyc; SENT90370:STY3608-MONOME-; -.
                                                                                                                                                                                                                                                                                                          PANTHER, PTHR11070; UvrD-helicase; 1.
Pfam; PF00580; UvrD-helicase; 1.
TIGRFAMS; TIGR01075; uvrD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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US DOE Joint Genome Institute;
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ID OBEZTI HUMAN PRELIMINARY;
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AC QBEZTI;
DI-JUN-2001, integrated into
DT 01-JUN-2001, sequence version
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Query Match
Best Local Similarity 72....
Best Local Similarity 72....
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237 PIAKVRIITPLI 248
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QBTP38 METAC PRELIMINARY; PRT;
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                                                       Name=srsx-30; ORFNames=C51E3.5; Caenorhabditis elegans.
21-FEB-2006, entry version 31. Hypothetical protein srsx-30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cation efflux system protein.
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Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T., Hammon N., Israni S., Pitluck S., Di Bartolo G., Chain P., Schmutz J., Larimer F., Land M., Lykidis A., Richardson P.;

"Complete sequence of Thermobifida fusca YX.";
Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Streptosporangineae, Nocardiopsaceae, Thermobifida.
NCBI_TaxID=269800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.4%; Score 39; DB 2; Length 141; 53.3%; Pred. No. 50; 1. Indels 1:ve 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53.4%; Score 39; DB 2; Length 140; 64.3%; Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE. That X.-B., Zhu F., Liu X.-S., Li Z Yu W.-Q., Sun B.-Z., Chai Y.-B., Zhu F., Liu X-B., Yan W., Yang H., Zhao Z.-L.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 AA; 14666 MW; CC24A2B46964BA77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF274958; AAK07533.1; -; mRNA.
SEQUENCE 140 AA; 16335 MW; 68CCA7520ED6CE51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996, integrated into UniProtKB/TrEMBL. 01-MAR-2005, sequence version 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.75.32 THEFY PRELIMINARY; PRT; 141 AA. 047.823.
13-SEP-2005, integrated into UniprotKB/TrEMBL. 13-SEP-2005, sequence version 1.
07-FEB-2006, entry version 4.
Putative ATP(GTP binding protein. OctoredLocusNames=Tfu 0697; Thermobifida fusca (strain XX).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; CP000088; AAZ54735.1; -; Genomic_DNA.
GO; GO:0006950; P:response to stress; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||| |||::|
124 PVSKALAATPITLDA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 PVSKMRMATPLLMQA 15
              07-FEB-2006, entry version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 PVSKMRMATPLLMQ 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVSVFRLATQLLHQ 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 64.3
nes 9; Conservative
                                                               Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome. SEQUENCE 141 AA;
                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q18767_CAEEL
Q18767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 34
Q18767 CAE
ID Q1876
AC Q1876
DT 01-NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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RESULT RE

g

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CSTRAIN=C12A / ARCC 35395 / DSM 2834.

RX GARAN=C12A / ARCC 35395 / DSM 2834.

RX Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,

A Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,

RA Allen N., McWann P., McKernan N., Talamas J., Tirrell A., Ye W.,

RA Allen R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,

Radderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,

Radderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,

Radderich R., Ingram-Smith C., Mutchopadhyay B., Reeve J.N., Smith K.,

Radderich W., Juwayam L.A., White O., White R.H., de Macario E.C.,

Rerry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.T.,

Retry J.G., Jarren B.,

Recalf W.W., Birren B.,

Radderich W.W., Birren B.,

Radderich W.W., Birren B.,

Radderich W.W., Entren B.,

Radderich W.W., Elwen 
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                                                                                                                                                                                                                                                                                                                                                                       MEDIJINE-99069613; PubMed-9851916; DOI=10.1126/science.282.5396.2012;
The C. elegans sequencing consortium;
"Genome sequence of the nematode C. elegans: a platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        investigating biology.";
Science 282:2012-2018(1998).
-!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMEL, Z78410; CAB01637.2; -; Genomic_DNA.

PIR, T20133; T20133.

Brasmbl, T51E3.5; Caenorhabditis elegans.

WormBase; WBGenen00008251; C51E3.5.

WormPep; C51E3.5; CE37815.

G0; G0:0016021; C:integral to membrane; IEA.

G0; G0:001584; F:rhodopsin-like receptor activity; IEA.

G0; G0:000186; P:G-portein coupled receptor protein signalin. Interpro; IPR000276; GPCR Rhodpsn.

PROSITE; PS50262; GPROFEIN RECEP_F1_2; 1.

Complete protecome; Hypothetical protein.

SEQUENCE 304 AA; 34320 MW; 28DF98B71CCE198D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
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Methanosarcīna acetivorans.
Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
Archanosarcinaceae; Methanosarcina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.4%; Score 39; DB 2; I 57.1%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
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Gaps

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Indels

1;

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STRAIN=RIB 40;

RA PubMed=16372010; DOI=10.1038/nature04300;

RA Machida M., Asai K., Sano M., Tanaka T., Kumagai T., Terai G.,

Rusumoto K., Arima T., Akita O., Kashiwagi Y., Abe K., Gomi K.,

Horiuchi H., Kitamoto K., Kobayashi T., Takeuchi M., Denning D.W.,

Galagan J.B., Nierman W.C., Yu J., Archer D.B., Bennett J.W.,

Bhatnagar D., Cleveland T.E., Fedorova N.D., Gotoh O., Horikawa H.,

Hosoyama A., Ichinomiya M., Igarashi R., Iwashita K., Juvvadi P.R.,

Kato M., Kato Y., Kin T., Kokubun A., Maeda H., Maeyama N.,

Kato M., Kato Y., Kin T., Kokubun A., Maeda H., Maeyama N.,

Kato M., Kato Y., Kin T., Kokubun A., Maeda H., Hata S., Paulsen I.,

Sakamoto K., Sawano T., Takahashi M., Takase K., Terabayashi Y.,

Wortman J.R., Yamada O., Yamagata Y., Anazawa H., Hata Y., Koide Y.,

Kuhara S., Ogasawara N., Kikuchi H.,

Kuhara S., Ogasawara N., Kikuchi H.,

Nature 438:1157-1161(2005).
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Distributed under the Creative Commons Attribution-NoDerivs License
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes;
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
Mashreghi-Mohammadi M.;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AP007169; BAE63971.1; -; Genomic DNA.
SEQUENCE 469 AA; 52120 MW; CC1BB0E8A6C9930D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.4%; Score 39; DB 2; I
66.7%; Pred. No. 1.8e+02;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                 07-DEC-2004, integrated into UniProtKB/TrEMBL.
07-DEC-2004, sequence version 1.
07-FBB-2006, entry version 11.
Name=FAF1; ORFNames=RP5-850015.2-003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  490 AA.
   Mismatches
                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QSVTA2_HUMAN PRELIMINARY; PRT;
QSVTA2;
5
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                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 PVSKMRMATPLLMQA 15
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les 10; Conservative
7; Conservative
                                                                                                                     378 PVSKLKIRTP 387
                                                            1 PVSKMRMATP 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aspergillus oryzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=5062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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QZU394 ASPOR
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Matches
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                                                                                                                                                                                                                     RESULT 37
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                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53.4%; Score 39; DB 2; Length 411; 53.8%; Pred. No. 1.6e+02; ive 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.4%; Score 39; DB 2; Length 464; 70.0%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         411 AA; 45126 MW; 64652A3A73BEEB94 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C3F730400AF6EC4F CRC64;
                                                                                                                                                                                                                                                                    GO; GO:0016020; C:membrane; IEA...
GO; GO:0008324; F:cation transporter activity; IEA.
GO; GO:0006812; P:cation transport; IEA.
InterPro; IPR002524; Cation efflux.
InterPro; IPR003731; FeMo-Co_biosynth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, AL603746, CAH72115.1; -; Genomic_DNA.

EMBL, AC118557; CAH72115.1; JOINED; Genomic_DNA.

EMBL, AL049637; CAH72115.1; JOINED; Genomic_DNA.

EMBL, AL049637; CAI23012.1; -; Genomic_DNA.

EMBL, AC118557; CAI23012.1; JOINED; Genomic_DNA.

EMBL, CAI8557; CAI23012.1; JOINED; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-DEC-2004, integrated into UniProtKB/TrEMBL. 07-DEC-2004, sequence version 1. 07-FBB-2006, entry version 11. Fas KTHRSFE) associated factor 1. Name=FARI, ORFNAMES=RPS-850015.2-002; Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       464 AA.
                                                                                                                                                  EMBL; AE010299; AAM05485.1; -; Genomic_DNA
HSSP; Q9X2D6; 1013.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMR; OSVTA1; 375-433.
Ensembl; ENSG00000185104; Homo sapiens.
                                                                                                                                                                                                        GenomeReviews; AE010299 GR; MA2085.
BioCyc; MACE188937:MA2085-MONOMER; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01545; Cation efflux; 1. Pfam; PF02579; Nitro FeMo-Co; 1. TIGRFAMB; TIGR01297; CDF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53654 MW;
Genome Res. 12:532-542(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QSVTA1 HUMAN PRELIMINARY;
QSVTA1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :| |::| |:||
291 ISVMKIAVPVLMO 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VSKMRMATPLLMQ 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 53.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR006577; UAS.
InterPro; IPR001012; UBX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00789; UBX; 1.
SMART; SM00594; UAS; 1.
SMART; SM00166; UBX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mashreghi-Mohammadi M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UBX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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Matches

RESULT 36

셤 8

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Gaps

7

3; Indels

Length 469;

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Complete proteome. SEQUENCE 524 AA;
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                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4952;
                                                                                                                                                                                                                                                QGCSN2_YARLI
ID QGCSN2_YARLI
AC QGCSN2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Capsicum annuum (Bell pepper).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
asterids, lamiids, Solanales, Solanaceae, Capsicum.
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0
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Pred. No. 1.9e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kim K.-W., Lee S.-W.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the cytochrome P450 family.
                     to the EMBL/GenBank/DDBJ databases.
                                                                 to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                    490 AA; 55998 MW; 99CC7ED351A0C251 CRC64;
                                                                                                                        EMBL; AL603746; CAH72114.1; -; Genomic_DNA.
EMBL; AC091610; CAH72114.1; JOINED; GENOMic_DNA.
EMBL; AC191857; CAH72114.1; JOINED; GENOMic_DNA.
EMBL; AL049637; CAH72114.1; JOINED; GENOMIC_DNA.
EMBL; AL049677; CAH72114.1; JOINED; GENOMIC_DNA.
                                                                                                                                                                                                                            Genomic_DNA.
                                                                                                                                                                                                        Genomic_DNA
Genomic_DNA
                                                                                                                                                                                                                                                   CAH70190.1; JOINED; Genomic_DNA
                                                                                                                                                                                                                                                               CAH70190.1; JOINED; Genomic_DNA. CAH70190.1; JOINED; Genomic_DNA. CAH70190.1; JOINED; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                AL049637; CA123010.1; -; Genomic_DNA.
AC091610; CA123010.1; JOINED; Genomic_
AC118557; CA123010.1; JOINED; Genomic_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF212318; AAG43824.1; -; mRNA.
GO; GO:0020037; F:heme binding; IEA.
GO; GO:0005506; F:iron ion binding; IEA.
GO; GO:0046872; F:metal ion binding; IEA.
                                                                                                                                                                                                                                                                                                             Ensembl; ENSG0000185104; Homo sapiens
                                                                                                                                                                                                                  CAI23010.1; JOINED;
CAI23010.1; JOINED;
                                                                                                                                                                                                                                                                CAH70190.1; JOINED;
CAH70190.1; JOINED;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001, sequence version 1. 07-FEB-2006, entry version 20. Cinnamic acid 4-hydroxylase.
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InterPro; IPR001012; UBX.
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412 PVSKLRIRTP 421
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SMART; SM00166; UBX; 1.
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                                                                                                                                                                                                                                                                                                                                            Pfam; PF00789; UBX; 1.
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Best Local Similarity
7; Conserve
                        Submitted (MAY-2005)
                                                                  Submitted (MAY-2005)
                                                                                                                                                                                                                                                                                                  SMR; Q5VTA2; 409-490
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  NUCLEOTIDE SEQUENCE
                                             NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=C4H;
              Moore M.;
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EMBL;
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EMBL;
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EMBL;
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CSTRAIN=CLIB 122 / E 150;

RX PubMed=15225592; DOI=10.1038/nature02579;

RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,

RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,

RA Lafontaine I., Manck C., Neuveglise C., Talla E.,

RA Lafontaine I., Balcherich J.-M., Beyle E., Blaykasten C.,

RA Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,

RA Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,

RA Boisrame A., Hongel R., Fairhead C., Ferry-Dumazet H., Groppi A.,

RA Rerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,

RA Kerrest A., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,

RA Swennen D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,

Rouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,

R Genome evolution in yeasts.";

L Nature 430:35-44(2004).
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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-AUG-2004, sequence version 1.
Or-FBB-2006, entry version 12.
Similar to tr|[004472 Saccharomyces cerevisiae YMR115w.
OrderedLocusNames=YALI0E166219;
OrderedLocusNames=YALI0E166219;
OrderedLocusNames=YALI0E166219;
Barrowia lipolytica (Candida lipolytica).
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
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                                                                                                                                                                                                                                                                                                                                                                            Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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                                                                                                                        PANTHER; PTHR19383; Cytochrome_P450; 1.
Pfam; PF00067; p450; 1.
PRINTS; PR00463; EP4501.
PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME P450; UNKNOWN 1.
Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductas SEQUENCE 505 AA; 58020 MW; 38E61FCCE249FE0F CRC64;
GO; GO:0004497; F:monooxygenase activity; IEA. GO; GO:0006118; P:electron transport; IEA. InterPro; IPR001128; Cytochrome_P450. InterPro; IPR002401; EP4501.
                                                                                                                                                                                                                                                                                                                                                                         53.4%; Score 39; DB 2; 70.0%; Pred. No. 2e+02; tive 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY; PRT;
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Best Local Similarity 70...
7; Conservative
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Title: Perfect score: Sequence:

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protein

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Scoring table:

Minimum DB Maximum DB

Database

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ADD02808
ADD041159
ABERS4516
ABC08161
AAG135185
ABG0135185
ABG08167
ABG15501
AAG135185
ABG135185
ABG135134
ABG1351363
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                                             7; Search time 89.924 Seconds (without alignments) 61.014 Million cell updates/sec
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Adv98917 ID
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Abb65718 ID
Abb06573 M
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Abb69213 BS
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Abb71564 D1
Aaco1050 P1
Abb71564 D1
      GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                     2589679
                                                                                                                                     Total number of hits satisfying chosen parameters
                                                                                                                        2589679 seqs, 457216429 residues
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AD129007
AD129007
AD02575
AD062214
AER30018
ADR98917
ADR98917
ADR987142
ABB67142
ABB67142
ABB67143
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                                protein search, using sw model
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ABB 69217
ADX 78446
ADX 96203
AAE 05813
ABB 71564
AAO 20499
AAO 20699
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Gapop 10.0 , Gapext 0.5
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geneseqp1990s:*
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geneseqp2003as:*
geneseqp2003bs:*
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Maximum Match 100%
Listing first 100
                                                                                                                                                    seq length: 0
seq length: 200000000
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Match
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Add02808 SCD28 mol Add02808 SCD28 mol Add02895 Synthetic u Abb2895 Synthetic u Abb2895 Synthetic Add02895 Synthetic Abg15501 Novel hum Add02586 Novel hum Add00192 Human TAT Aea00192 Human TAT Aea00192 Human TAT Aea00192 Human TAT Aea00192 Human TAT Aea00193 Human SEC Abb53173 Breast an Abb53173 Breast an Abb53013 Breast an Abb53013 Breast an Abb53013 Human Sch Abb53013 Human Sch Add04966 Antipsori Add058600 Drosophil Add058600 Drosophil Abb858000 Drosophil Abb858000 Drosophil Add64824 Human Src Adb14148 Human Src Adb6800 Drosophil Add64824 Human pro Add64824 Human pro Add64824 Human pro Add6630 Brosophil Adm40047 Bacterial Adm0036 Brosophil Adm40044 Bacterial Adm5044 Bacterial Adm5044 Bacterial Adm5044 Bacterial Adm5044 Bacterial Adm5044 Bacterial Adm5044 Bacter

Human pro Drosophil

Drosophil Drosophil

Abb65450 1 Abb71561 1 Abb70499 1 Abp54340 1

2210 2210 2210 2310 2310 2310 2310 2310

Score

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Drosophil Drosophi Mouse POS Murine PO POSH prot Mouse POS

Aaw00137 1 Abb71577 1 Abu64278 1 Adh73564 1 Adr89697 1 Ads34245 1

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MHC class II compound; MHC class II component; MHC class II alpha chain; MHC class II beeta chain; peptide binding groove; spaceholder molecule; effector component; immune response; immune disorder; virucide; antibacterial; antiparasitic; cytostatic; immunosuppressive; gene therapy; viral infections; bacterial infection; parasitic infection;
POS
POS
POS
                                                                                                                                                                                                                                                                                                                                                                                                                 New MHC class II compound, useful for preparing a composition for treating immune disorders e.g. viral infections, bacterial infections, parasitic infections, neoplastic disease, autoimmunity or toxicity.
         House
Mouse
                           Mouse
Adu73761 N
Adu68997 N
Adw87412 N
Adz66429 N
                                                                                                                                                            Human MHC class II compound spaceholder molecule SEQ ID NO:2.
                                                                                                                                                                                                                            neoplastic disease; autoimmunity; toxicity; human.
                                                        ALIGNMENTS
ADU73761
ADU68997
ADW87412
ADZ66429
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; SEQ ID NO 2; 92pp; English
                                                                                                                                                                                                                                                                                                                                                             (DAND ) DANA FARBER CANCER INST INC.
                                                                                                      ADI29006 standard; peptide; 12 AA
                                                                                                                                                                                                                                                                                                                                  12-JUL-2002; 2002US-0395494P.
22-JUL-2002; 2002US-0397893P.
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                                                                                                                                                                                                                                                                                                                                                                               Wucherpfenning KW, Seth N;
 8 8 6 6
                                                                                                                                            (first entry)
 892
892
892
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 80.0
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                                                                                                                                                                                                                                                        Synthetic.
 0444
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The present invention describes an isolated WHC class II compound (I)

comprising: (a) an WHC class II component comprising at least a portion

of an WHC class II alpha chain and at least a portion of an WHC class II beta

beta chain, such that the WHC class II alpha chain and WHC class II beta

chain form a peptide binding groove; (b) a spaceholder molecule; and (c)

an effector component, where the effector component is linked to the MHC class II component. Also described: (1) a pharmaceutical composition

comprising the MHC class II molecule and a carrier; (2) a method of producing an MHC class II compound; (3) a method of directly identifying an antigen-specific T cell; (4) a method of tregulating an immune disorder in a subject; and (5) a method of regulating an immune disorder in a subject; and (7) a method of treating an immune disorder avivo in a subject; and (7) a method of treating an immune disorder avivo in a subject; and (7) a method of treating an immune disorder avivo in a subject; and (7) a method of treating an immune disorder avivo in a subject; (1) has criticies, and can be used in gene therapy. The MHC class II compound (1) can be used for preparing a composition for treating immune

contricties, and can be used in gene therapy. The MHC class II compound infections, parasitic infections, neoplastic disease, autoimmunity or traiting immune control infections, parasitic an MHC class II compound from the present invention.
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Sequence 13 AA;

Sequence 12 AA;

The present invention describes an isolated WHC class II compound (1)

Comprising: (a) an WHC class II component comprising at least a portion

of an MHC class II alpha chain and at least a portion of an WHC class II beta

Co beta chain, such that the WHC class II alpha chain and WHC class II beta

CC clain form a peptide binding groove, (b) a spaceholder molecule; and (c)

an effector component, where the effector component is linked to the MHC

CC class II component, Also described: (1) a pharmaceutical composition

CC class II component, Also described: (2) a method of producing an MHC class II compound; (3) a method of directly identifying

CC class II component, Also described: (1) a method of treating an immune response

CC in a subject; (5) a method of treating an immune disorder in a subject; and

(7) a method of treating an immune response ex vivo in a subject; and

(7) a method of treating an immune disorder ex vivo in a subject; and

(7) a method of treating an immune disorder ex vivo in a subject; and

(7) a method of treating an immune disorder ex vivo in a subject; and

(7) a method of treating an immune disorder ex vivo in a subject;

(1) can be used for preparing a composition for treating immune

CC disorders, e.g., viral infections, bacterial infections, parasitic

CI class II compound from the present invention.

CC an MHC class II compound from the present invention. ö MHC class II compound, MHC class II component, MHC class II alpha chain; MHC class II beta chain; peptide binding groove; spaceholder molecule; effector component, immune response; immune disorder; virucide; antibacterial; antiparasitic; cytostatic; immunosuppressive; gene therapy; viral infections; bacterial infection; parasitic infection; neoplastic disease; autoimmunity; toxicity; human. New MHC class II compound, useful for preparing a composition for treating immune disorders e.g. viral infections, bacterial infections, parasitic infections, neoplastic disease, autoimmunity or toxicity. Gaps ö Human MHC class II compound spaceholder molecule SEQ ID NO:3. DB 8; Length 12; 0; Indels 0.23; Mismatches Score 50; Pred. No. ( Claim 11; SEQ ID NO 3; 92pp; English. (DAND ) DANA FARBER CANCER INST INC. ADI29007 standard; peptide; 13 AA. . 0 100.0%; 11-JUL-2003; 2003WO-US021767. 12-JUL-2002; 2002US-0395494P. 22-JUL-2002; 2002US-0397893P. Seth N; 15-APR-2004 (first entry Query Match Best Local Similarity 100. ....hes 12; Conservative 1 AAMAAAAAAMA WPI; 2004-122876/12 Wucherpfenning KW, WO2004007528-A2. sapiens. 22-JAN-2004 Synthetic ADI29007; Ното RESULT 2 ADI29007 원 ð

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09-AUG-2002; 209-AUG-2002; 217-DEC-2002; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New transgenic plant comprising a recombinant polynucleotide of any one of more than 500 nucleotide sequences, useful in bioinformatic search
                                                                                                                                                                                                                                                                                                                                                                              glyphosphate folerance; hormone sensitivity; disease resistance; sugar sensing; flowering; flower structure; stem bifurcation; branching pattern; apical dominance; trichome; stem morphology; root thair; seed development; cell proliferation; cell differentiation; premature senescence; necrosis; plant size; leaf morphology; seed morphology; seed anothology; seed blochemistry; root anthocyanin; plant anthocyanin; light response; shade avoidance; bioinformatic; transcription factor; gene; de.
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Keddie J, Broun PE;
                                                        Gaps
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0
                    8; Length 13;
                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                   transgenic; plant; enhanced tolerance to abiotic stress;
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Reuber TL,
                  Score 44; DB 8
Pred. No. 1.9;
0; Mismatches
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                                                                                                                                                                                                                  ADI42025 standard; protein; 233
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                  88.0%;
91.7%;
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12
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HEARD J E.
HAAKE V.
CREELMAN R A.
RATCLIFFE O.
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REUBER T L.
KEDDIE J.
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PILGRIM M L.
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PINEDA O.
YU G.
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Pilgrim ML,
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(CREE/)
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(HEAR/)
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(REUB/)
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(DUBE/)
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AD142025
AD2625
AD262
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altered flower structure, change in stem bifurcations, altered branching pattern, reduced apical dominance, reduced trichome density; lack of trichomes reduced actopic trichome development; altered trichome development; increase in trichome number; altered stem morphology; increased root growth; increased root hairs; altered seed development; altered call proliferation or call differentiation; rapid development; premature senescence; increased necrosis; increase in seedling or plant size; decreased plant size; leaf morphology; seed morphology; seed biochemistry; increase in root anthocyanins; increase in plant anthocyanins, or alteration in light response or shade avoidance. The transgenic plant, polymucleotides and polypeptides are useful in bioinformatic search methods. This is the amino acid sequence of a plant transcription factor, and an orthologue of Arabiodopsis thaliana transcription factors isolated in the invention, that can be used in the creation of a transgenic plant with altered traits.
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0
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Pred. No. 33;
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21-JAN-2000; 2000US-00489376.
22-MAR-2000; 2000US-00505720.
22-MAR-2000; 2000US-00533029.
22-MAR-2000; 2000US-00533030.
22-MAR-2000; 2000US-00533030.
22-MAR-2000; 2000US-0053392.
22-MAR-2000; 2000US-0053392.
22-MAR-2000; 2000US-0053392.
16-NOV-2000; 2000WS-00533948.
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17-APR-2001; 2001US-00837444.
30-JAN-2002; 2002US-00958131.
14-JUN-2002; 2002US-00171468.
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2002US-00225068
2002US-0434166P
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91.7%;
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Best Local Similarity 91...,
Best 11; Conservative
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25-FEB-2003; 2003US-00374780.
       ZHANG J.
FROMM M E.
HEARD J E.
RIECHMANN J L.
                                       JIANG C.
SAMAHA R S.
PILGRIM M L.
                                                     CREELMAN R A.
                                                            RATCLIFFE O. KUMIMOTO R.
                                                                   SHERMAN B K.
                                                                                            WPI; 2004-225755/21.
                           PINEDA O. REUBER T L. KEDDIE J S.
                    ADAM L J.
BROUN P E.
                                                         DUBELL A N.
                                                                          Zhang J, Frc
Pineda O, Re
Pilgrim ML,
Sherman BK;
                                          (JIAN/)
                                                 (PILG/)
(CREE/)
                                                        (DUBE/)
(RATC/)
(KUMI/)
                                                                   (SHER/)
                           (PINE/)
(REUB/)
                                   (KEDD/)
       ZHAN/)
                         BROU/)
                     (ADAM/)
             HEAR/
                  RIEC/
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nmm ME, Heard JE, Riechmann JL, Adam LJ, Broun PE; suber TL, Keddie JS, Yu G, Jiang C, Samaha RS; Creelman RA, Dubell AN, Ratcliffe O, Kumimoto R; Fromm ME, Hea

transgenic plant, useful in developing phenotypes with altered or improved characteristics or traits.

Claim 1; SEQ ID NO 989; 213pp; English

the invention relates to a transgent plant compliable and inclinated in transfer of the complementary sequence comprising a polymerlectide, that initiates transgering a sequence encoding a polymerlectide, that initiates transgering to a transgering and plant, an expression cassette (comprising as Abo01588 (Alco included are using a transgering plant to grow a progeny plant, an expression cassette (comprising a recombinant polymerlectide described above), a host cell comprising the expression cassette, producing a medified plant having a modified trait, identifying a factor that is modulated by or interacts with a polypoptide encoded by the polymuclectide sequence and identifying at least one downstream polymuclectide sequence and identifying at least one downstream companies encoded by the polymuclectide sequence and identifying a plant that has an altered the polymuclectide sequence and identifying a plant that has an altered transgeric plant is useful for producing a plant that has an altered transgeric plant is useful for producing a plant that has an altered transgeric plant is useful for producing a plant that has an altered transgeric plant is useful for producing a plant that has an altered transgeric plant is useful for producing a plant that has an altered transgeric plant is useful for producing a plant that has an altered transgeric plant is useful for producing a plant that has an altered transgeric plant is useful for producing a plant that has an altered transgeric plant is useful for producing a plant that has an altered to complix, to decrease to semistivity to bascisic stid an altered usecptibility to because to potassium the plants of t The invention relates to a transgenic plant comprises a recombinant

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        content, an alteration of leaf glucosinolate content, change in seed biochemistry, an increase in seed oil content, decrease in seed fatty acid content, decrease in seed fatty acid content, increase in seed fatty acid content, increase in seed protein content, decrease in seed protein content, alteration in seed prenyl lipid content, increase in seed prenyl lipid content, increase in seed pretain in seed prenyl lipid content, increase in seed protein secondary metabolism, increase in root anthocyanins, increase in plant anthocyanins, and alteration in light response or shade avoidance. The present sequence represents an orthologue of a thalecress transcription factor isolated from Rice.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant; transcription factor; transgenic plant; abiotic stress tolerance; osmotic stress tolerance; cold tolerance; heat tolerance; low nitrogen tolerance; low phosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to novel plant transcription factor proteins (1) and nucleotide sequences (II) (ADO61534-AD063778). The sequences can be used to produce transgenic plants, which overexpress (II), where the transgenic plant has an altered trait as compared to a non-transgenic plant or wild-type plant. The transgenic plant comprises an altered trait selected from increased tolerance to abiotic stress, increased tolerance to obld; increased clerance to common in cold, increased tolerance to cold, increased tolerance to cold, increased tolerance to heat, increased germination in heat, increased tolerance to heat, increased increased tolerance to low nitrogen conditions, increased tolerance to low nitrogen conditions, increased tolerance to low phosphate conditions, increased tolerance to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.
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Pred. No. 33;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                       88.0%;
91.7%;
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Matches 11, Conservative
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                                                                                                                                                                                                                                Sequence 233 AA;
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Claim 1; SEQ ID NO 2218; 612pp; English.

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increased tolerance to multiple fungal pathogens, increased resistance to glyphosate, increased sensitivity to ABA, reduced sensitivity to ABA, increased sensitivity to ABA, reduced sensitivity to ABA, concreased sensitivity to ABA, reduced sensitivity to ABA, altered sensitivity to ABA, reduced sensitivity to ABA, to sugars, altered carbon/nitrogen sensing, early flowering, latered flower structure, loss of flower determinacy, reduced fertility, altered structure, altered branching pattern, altered stem morphology, altered density, altered branching pattern, apical dominance, altered trichome density, altered stade and altered seed trichome structure, altered seed stade avoidance, altered seed development, altered seed shade avoidance, altered seed development, altered seed seed call proliferation, altered cell differentiation, altered senseconce, abnormal embryo development, altered phase change, caltered senseconce, abnormal embryo development, altered phase change, green leaves, change in leaf shape, increased leaf size and mass, light green leaves, cloration, altered seed shape, large, altered seed coloration, altered seed shape, large, altered seed shape, large, altered seed seed coloration, altered seed shape, large, altered seed coloration, altered seed shape, large.
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                                                                                                                                                                                                                                                                                                                                                                                                                            seed, increased leaf wax, increased leaf fatty acids, altered seed oil content, altered seed protein content, altered seedprenyl content, altered leaf prenyl lipid content, increased anthocyanin levels, and decreased anthocyanin levels. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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disease and particularly Erysiphe, Fusarium and Botrytis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44; DB 8; Length 233; Pred. No. 33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lead_CeresClone681222 protein homolog SEQ ID NO:2218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AEF30018 standard; protein; 233 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-2004; 2004US-0583621P.
30-JUN-2004; 2004US-0584800P.
30-JUN-2004; 2004US-0584829P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.0%;
91.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alexandrov N, Brover V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plant growth regulation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2006-090599/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2006004955-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-2006
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The phenotypes and characteristics, comprising a molecule modification that phenotypes and characteristics, comprising a molecule encodes an amino acid sequence exhibiting at least 8% sequence in the cortholog alignments of Figure 1, a muclaic acid, which is a complement of cartholog alignments of Figure 1, a muclaic acid, which is a complement of cartholog alignments of Figure 1, a muclaic acid capable of the that the reverse muclocitide sequence has a sequence order which is the reverse of the muclocitide sequence order of (a) but a muclaic acid capable of is the reverse of the muclocitide sequence order of (a) but a muclaic acid capable of the property of the muclaic acid duplex at a temperature of 40-48 degrees C below the melting capable of causing transforming a regulatory sequence construct (comprising a first muclaic acid having a regulatory sequence construct (comprising first muclaic acid duplex and/or translation in a plant, operably linked to a second muclaic acid duplex. Also included are a vector construct, an isolated polypeptide comprising an amino acid muclaic acid maleuted. A nost cell comprising the vector construct, an isolated polypeptide comprising an amino acid muclaic acid muclaic acid into a host cell, transforming a host cell, detecting a muclaic acid into a host cell, transforming an isolated muclaic acid into a host cell, transforming an isolated muclaic acid maleured. A plant generated from the plant cell introducing an isolated acid maleure, a plant generated from the plant cell or seed, a plant plant cell, plant material or seed, a plant promoter so that the comprising the muclaic acid maleured. A plant material or seed, a plant part with the nuclaic acid maleured cell or seed, a plant part with the nuclaic acid maleured cell, intended acid muclaic acid maleured. A plant with the nuclaic acid maleured cell or a wild type plant), improving plant compressed to a wild type plant), improving plant promoter so that the component is ecopolately and progenitor plant exhibits faster rate 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                       invention relates to an isolated nucleic acid molecule modifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic, gene therapy, vaccine, lung, diagnosis, cancer; non-cancerous lung disease, lung tissue, antagonist, gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.0%; Score 44; DB 10; Length 233; 91.7%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lung specific gene splice variant encoded protein #89.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADR98917 standard; protein; 278 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transgenic animal; splice variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-DEC-2003; 2003WO-US038896.
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The invention describes a recombinant DNA construct comprising a polymucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at the invention are also useful in physical arrays of molecules and as of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme compositions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, increased resistance to plant disease, for increasing the rate of homologous recombination in plants, for increasing the rate of homologous recombination in plants, for introgen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert polymeptide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for improving yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 44, DB 8, Length 646;
Pred. No. 92;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Zhou Y, Kovalic DK, Screen SE, Tabaska JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster polypeptide SEQ ID NO 28218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 65028; 15pp; English.
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05-NOV-2001; 2001US-00985678.
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                                                                                              28-APR-2003; 2003US-00425114
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                                                                                                                                                                                                                                     ZHOU Y.
KOVALIC D K.
SCREEN S E.
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-180133/17.
                                                                                                                                                                                                                                                                                                                    TABASKA J E.
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US2004034888-A1
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                                                                                                                                                                                                                     LIU J.
                                                                                                                                                                                                                                                                                                                                                CAO Y.
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                                             19-FEB-2004
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                                                                                                                                                                                                                                                                                                                    (TABA/)
(CAOY/)
                                                                                                                                                                                                                   (LIUJ/)
                                                                                                                                                                                                                                                                   (KOVA/)
(SCRE/)
                                                                                                                                                                                                                                            (ZHOU/)
                                                                                                                                                                                                                                                                                                                                                                                              Liu J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        molecule (I) comprising any of 113 fully defined nucleotide sequences given in the specification, their encoded protein sequences, sequences given in the specification, their encoded protein sequences, sequences at least 60% identity to the nucleotide sequences. The methods and compositions of the present invention are useful for identifying.

C compositions of the present invention are useful for identifying L cancerous diseases of the lung. They are also used for identifying lung tissue, monitoring and identifying and/or designing antagonists of the polypeptide of the invention, gene therapy, production of transgenic polypeptide of the invention, gene therapy, production of transgenic animals and production of engineered lung tissue for treatment and research. Lung specific genes (LSGs) were identified by a systematic analysis of gene expression data in the LIFESEO Gold database using the data mining software package candidate lead automatic search program (CLASP). Genes were grouped into gene bins where each bin is a cluster of sequences grouped together where they share a common contig.

CC percentage level in the targeted tissue versus all the other tissues. The expression levels from cancer patients were compared with the expression cumour tissues from cancer patients were compared with the expression cumour tissues from cancer patients were compared with the expression compared with tumour or disease. This sequence represents a protein of the invention.
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                                                                                                                                                                                                                                                                                             New isolated human lung specific nucleic acid molecule, useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous diseases of the lung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a new isolated lung specific nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plant full length insert polypeptide seqid 65028.
                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 202; 542pp; English
                                                                                                                                                                        Liu S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADY09213 standard; protein; 646 AA.
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                                                                                                                                                                        Sun X,
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                      06-DEC-2002; 2002US-0431307P.
06-DEC-2002; 2002US-0431510P.
06-DEC-2002; 2002US-0431516P.
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                                                                                                                                                                        Macina RA, Turner LR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity '
                                                                                                                     (DIAD-) DIADEXUS INC
                                                                                                                                                                                                                        WPI: 2004-635553/61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 278 AA;
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Gaps

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Drosophila melanogaster.

WO200171042-A2

Unidentified

ADY09213;

RESULT 8

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y 1000 or more and cell-cell

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Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease, diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                         capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                  insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes substantially purified human proteins
                                                                                                                                      invention relates to an isolated nucleic acid detection reagent
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                 isolated nucleic acid detection reagent for detecting 1000 as from Drosophila and for elucidating cell signaling and ce
                                                                                             Disclosure, SEQ ID NO 19356; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                       Score 42; DB 4; Length 2857;
Pred. No. 7.9e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hyperproliferative disorders and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 13122; 1037pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human ORFX protein sequence SEQ ID NO:13122.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                     84.0%;
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29-AUG-2000; 2000US-0228716P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Conservative
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              nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-106308/14.
                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                   Sequence 2857 AA;
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                                                         interactions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP06570;
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                                    genes
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                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequence (ABD1840-ABL16175) and the encoded proteins (ABB37737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 28218; 21pp + Sequence Listing; English
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Pred. No. 1e+02;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myers EW;
                                                                                                                                                                                                   Myers EW;
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                                                     23-MAR-2001; 2001WO-US009231
                                                                                           23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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11-JUL-2000; 2000US-00614150
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83.3%;
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10; Conservative
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                                                                                                                                                                                                 Adams M,
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N-PSDB; ABL08291.
                                                                                                                                                                                                                                          WPI; 2001-656860/75
                                                                                                                                                         (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                               N-PSDB; ABL11245
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pharmaceutical
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                                                                                       23-MAR-2000;
              .27-SEP-2001.
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Best Local 9
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Matches

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23-JUN-1999;
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16-JUL-1999;
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 Treferred to as open reading frame, ORFX, where X is 1.11491 lese lable 1 in the specification). ABN15752 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder. ORFX polynucleotide syndrome associated with ORFX-associated disorder. ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, Keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hyperthroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune disorders, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also bone degenerating burns, incisions, ulcers, for treating sate opporosis, bone degeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage. NB The sequence data for this patent did not form mpart of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
where X is 1-11491 (see Table
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   referred to as open reading frame, ORFX,
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99US-0123180P.
99US-0123548P.
99US-0126264P.
99US-012678SP.
99US-012678SP.
99US-012678SP.
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99US-0130449P.
99US-0130510P.
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nes 10; Conservative
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11 AALAAAAAAAA 22
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                                                                                                                                                                                                                                                                                          Sequence 129 AA;
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05-MAR-1999;
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09-MAR-1999
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29-MAR-1999
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99US-0142920P.
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99US-0143542P.
99US-0143624P.
        990S-0132485P
990S-0132487P
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990S-0134218P
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990S-013421P
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990S-0134370P
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99US-0144325P.
99US-0144331P.
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99US-0144333P.
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99US-0140354P.
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99US-0142154P.
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99US-0132484P
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990S-0145088P

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990S-0145192P

990S-0145214P

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99US-0160741P
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04-AUG-1999;
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06-AUG-1999;
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09-AUG-1999;
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26-AUG-1999;
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20-SEP-1999;
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18-AUG-1999
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                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        plant; transgenic plant; crop improvement; abiotic stress tolerance; plant growth regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid molecule modifying plant phenotypes and characteristics and the polypeptide it encodes, useful for making transgenic plants with improved characteristics.
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                                                                                                                                                                                                                             Length 156;
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                                                                                                                                                                                                                              DB 3;
62;
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                                                                                                                                                                                                                               Score 41;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                  AEF30016 standard; protein; 243 AA.
        990S-0160768P-
990S-0160710P-
990S-0160814P-
990S-0160981P-
990S-0160981P-
990S-0161404P-
990S-0161406P-
990S-0161406P-
990S-0161406P-
990S-0161406P-
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99US-0161993P.
99US-0162142P.
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30-JUN-2004; 2004US-0584800P.
30-JUN-2004; 2004US-0584829P.
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99US-0161920P
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99US-0160767P
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AAMAAAAAALVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CERE-) CERES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Triticum aestivum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2006004955-A2
                                21-OCT-1999;
22-OCT-1999;
22-OCT-1999;
22-OCT-1999;
25-OCT-1999;
25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
           21-OCT-1999;
21-OCT-1999;
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Matches
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ID AEF3
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hybridizing (a-c), under conditions that permit formation of a nucleic acid duplex at a temperature of 40-48 degrees C below the melting temperature of the nucleic acid duplex. Also included are a vector construct (comprising a first nucleic acid having a regulatory sequence capable of causing transcription and/or translation in a plant, operably incled to a second nucleic acid having the sequence of the isolated nucleic acid molecule that is flanked by exogeneus sequence, a host cell comprising the vector construct, an isolated polypeptide comprising a maino acid sequence exhibiting at least 85% sequence identity to those cited above, introducing an isolated nucleic acid into a host cell, transforming a host cell, detecting a nucleic acid into a host cell, transforming a host cell, a plant generated from the plant comprising the nucleic acid molecule, a plant generated from the plant cucleic acid molecule (where the plant material or seed) comprising the nucleic acid molecule (where the plant material or seed) comprising the nucleic acid molecule (where the plant with the nucleic acid sequence, and a transgenic plant having a gene construct (comprising the nucleic compared to a wild type plant), improving plant promoter so that the component specially overexpressed in the transgenic plant exhibits faster rate of growth, greater fresh of dry weight of maturation, greater fruit or seed yield, higher tolerance to low phosphate concentration, or higher tolerance to low prospine or plant, or higher tolerance to low prospine or plant, or higher tolerance to low plant or plant, or higher plant promoter so plant promoter and plant or plant o pH, higher tolerance to low phosphate concentration, or higher tolerance to low mitrogen concentration than a progenitor plant, which does not contain the progenitor construct, when the transgenic plant and progenitor plant are cultivated under identical environmental conditions, where the component is any one of the polypeptides cited above. The nucleic acid molecules are useful for producing transgenic plants with improved characteristics. The present sequence is an ortholog of a protein encoded by a plant nucleic acid (cDNA) of the invention. osteopathic; vulnerary; cytostatic; gene therapy; diagnosis; forensics; gene mapping; mutation identification; biodiversity; chromosome marker; immune response; myenloid cell disorder; lymphoid cell disorder; bone cartilage; tendon; ligament; nerve tissue growth; wound healing; burns; incision; ulcer; cancer. Gaps ö 82.0%; Score 41; DB 10; Length 243; 83.3%; Pred. No. 96; 1; Indels 1; Mismatches ADI60138 standard; protein; 276 AA. 18-SEP-2001; 2001US-0323349P. 16-SEP-2002; 2002US-00323349. 18-SEP-2002; 2002WO-US029636. (first entry) Secreted polypeptide #22. 10; Conservative 1 AAMAAAAAAMA 12 SAAAAAAAAAA 29 Best Local Similarity Sequence 243 AA; WO2003025142-A2. Homo sapiens 15-APR-2004 27-MAR-2003 ADI60138; Query Match Matches 유 ò

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The invention relates to novel isolated polynucleotides or a sequence encoding a polypeptide with biological activity, where the polynucleotide with biological activity, where the polynucleotide to the polynucleotide under stringent hybridization conditions or has greater than 99% sequence identity with the polynucleotide. The polynucleotides and polypeptides are useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic also disorders and other traits, to assess biodiversity, as nutritional sources or supplements. The polynucleotides may also be used as molecular weight markers, chromosome markers or map related gene positions, or as an antigen to rasise anti-DNA antibodies or elicit immune response. The polypeptides are useful for raising antibodies, as markers for tissues in which the corresponding polypeptide is expressed, for re-engineering damaged or diseased tissues, for treating myeloid or lymphoid cell calsoners, in bone cartilage, tendon, ligament and/or nerve tissue growth car regeneration, in wound healing, in tissue repair and replacement, in healing of burns, incisions and ulcers, and in treating cancer. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                            New polynucleotides and secreted proteins, useful for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve tissue growth or regeneration, in wound healing, and in tissue repair and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila, developmental biology, cell signalling, insecticide,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence corresponds to a protein sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41; DB 7; Length 270, Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
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                                                                                                                                                     Claim 20; SEQ ID NO 173; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB69217 standard; protein; 328 AA.
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Conservative
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5 AALSAAAAAALA 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-656860/75.
              WPI; 2003-354601/33.
N-PSDB; ADI60483.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 276 AA;
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                                                                                                                          replacement
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Wang J;

Goodrich RW, Ren F, Zhang J, Zhao QA, thrman T, Weng G, Zhou P, Drmanac RT;

Asundi V, Goodrich Xue AJ, Wehrman T,

Tang YT, Ghosh M,

(HYSE-) HYSEQ INC

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The invention describes a recombinant DNA construct comprising a valiable in electronic form from the US patent office at available in electronic form from the US patent office at ftp. seqdata.uspto.gov/sequence.html?Doc1D:2004034888. The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme commotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert polypeptide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; hat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistence; alactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Revised record issued on 23-MAR-2006 : Corrected organism line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 8; Length 333
Pred. No. 1.3e+02;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant full length insert polypeptide seqid 58867.
Claim 1; SEQ ID NO 47812; 15pp; English.
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05-NOV-2001; 2001US-00985678.
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157 SAMAAAAAAAA 168
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les 10; Conservative
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ZHOU Y.
KOVALIC D K.
SCREEN S E.
TABASKA J E.
CAO Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 333 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                             invention.
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(ZHOU/)
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                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL1840-ABL16175, and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for improving yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oll; protein yield; protein yield;
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                                       Disclosure; SEQ ID NO 34443; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                               82.0%; Score 41; DB 4; Length 328; 100.0%; Pred. No. 1.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                            100.0%; Preu. ...
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Best Local Similarity 100.
Matches 10; Conservative
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CAO Y.
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                                                                                                                                                                                                                                                                                                                     Sequence 328 AA;
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interactions
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21-APR-2005
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Gaps

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Cao Y;

Liu J,

(LIUJ/) (ZHON/)

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The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant colerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for increasing the rate of homologous recombination in plants, for imprevaing yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert in the polymetric content. This is the amino acid sequence of a plant full length insert in the recombinant DNA construct of the
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                            recombinant DNA construct, useful for improving plant tolerance to 1, heat, drought, herbicides, extreme osmotic conditions, pathogens or is, for conferring increased resistance to plant disease, or for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; small cell lung cancer; therapy; hCAAP; nucleic acid; NA; melanoma; cancer; colon; breast; head; neck; transitional cancer; leimyosarcoma; synovial sarcoma; cytostatic; SOX3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human small cell lung cancer associated protein, SOX3.
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/note= "DNA-binding HMG domain"
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                                                                                                                       Claim 1; SEQ ID NO 58867; 15pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE05813 standard; protein; 443 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LUDW-) LUDWIG INST CANCER RES. (SLOK ) SLOAN KETTERING INST CA (CORR ) CORNELL RES FOUND INC.
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Matches 10; Conservative
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WPI; 2004-180133/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 429 AA;
                                                                                    improving yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200153349-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE05813;
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                                                                      pests,
                                                    cold,
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                                                                                                                                   The invention relates to nucleic acids and encoded polypeptides which are cancer associated antigens expressed in patients afflicted with small cell lung cancer. The molecules provided by the invention can be used in the diagnosis, monitoring, research or treatment of conditions characterised by the expression of one or more cancer associated antigens. The polypeptide is used to treat a disorder characterised by expression of an expression of an abnormal amount of a protein encoded by a nucleic acid (NA) Group I molecule. The disorders are small and non-small cell lung cancer, melanoma, colon, breast, head and neck, or transitional cancer, leimyosarcoma or synovial sarcoma. The present sequence is human SOX3 protein, encoded by a small cell lung cancer associated gene designated as NY-SCLC-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is
                                       Isolated polypeptide, used to treat or prognose a disorder characterized by expression of a hCAAP e.g. cancer, is encoded by an isolated nucleic acid comprising an NA Group 3 or 4 molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                       Length 443;
                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster polypeptide SEQ ID NO 41484.
                                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB 4; I
Pred. No. 1.7e+02;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Li PWD, Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB71564 standard; protein; 524 AA.
                                                                                                            Disclosure; Fig 1; 152pp; English.
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 83.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AAMAAAAAAAMA 12
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N-PSDB; ABL15667.
2001-457597/49.
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WPI; 2001-457597/
N-PSDB; AAD11118
                                                                                                                                                                                                                                                                                                                                                                          Sequence 443 AA;
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Matches
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ABB71564
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protein of the APP related human homologue hCP41313
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                                                                                                                                                                                                                                                                                                                                                                                                           Neuroprotective; nootropic; transgenic fly; Alzheimer's disease; Abeta; amyloid precursor protein; tissue-specific expression control; human APP; APP pathway modulator; gene therapy.
useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL0176-ABL30511), expressed DNA sequences (ABL0176-ABL30511), expressed DNA sequences (ABL0176-ABL30511), expressed DNA sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New transgenic fly, containing DNA encoding an Abeta portion of human APP, useful for identifying agents which modulate the APP pathway and which can be used to treat Alzheimer's disease.
                                                                                                                                                                                Gaps
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                                                                                                                                                     Length 524;
                                                                                                                                       Score 41; DB 4; Length car. Pred. No. 2.1e+02;
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                                                                                                                                                                               1; Mismatches
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(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 25; Page 90-91; 129pp; English
                                                                                                                                                                                                                                                                                                    AAO20499 standard; protein; 593 AA.
                                                                                                                                                  82.0%;
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14-JUN-2001; 2001US-0298309P.
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                                                                                                                                    Query Match
Best Local Similarity 83.55
Fines 10; Conservative
                                                                                                                                                                                                                                   163 AAQAAAAAAA 174
                                                                                                                                                                                                        1 AAMAAAAAAMA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dengler UJ,
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                                                                                                                          Sequence 524 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                              AA020499;
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                                                                                                                                                                                                                                                                           RESULT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neuroprotective; nootropic; transgenic fly; Alzheimer's disease; Abeta; amyloid precursor protein; tissue-specific expression control; human APP; APP pathway modulator; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New transgenic fly, containing DNA encoding an Abeta portion of human APP, useful for identifying agents which modulate the APP pathway and which can be used to treat Alzheimer's disease.
                                                                                                            Gaps
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                                                    Length 593
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                                                                                                            0; Indels
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75.0%; Pred. No. 2.5e+02;
ive 3; Mismatches 0.
                                                    Score 41; DB 5; Pred. No. 2.3e+02;
                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 25; Page 92-93; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                     AAO20500 standard; protein; 645 AA.
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                                                    82.0%;
75.0%;
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Best Local Similarity 75.0%
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Best Local Similarity 75.v.
For 9, Conservative
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508 SSMASAAAAAMA 519
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N-PSDB; AAK99394.
Sequence 593 AA;
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                                                                                                                                                                                                                                                                                                                RESULT 21
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RESULT 27

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed control in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is custful for generating antibodies against it, detecting or quantitating a custful for generating antibodies against it, detecting or quantitating a cupplement. (II) and its binding partners are useful in medical imaging of states expressing (II). (I) and (II) are useful for treating disorders of states expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein esquences have applications in collypeptide and polynucleotide sequences have applications in cresponsible for genefic disorders or other trails to assess biodiversity and to produce other types of data and products dependent on DNA and cannon acid sequences of the invention. Note: The sequence data for this amino acid sequences of the invention. Note: The sequence data for this caterial format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                              Human, chromosome mapping, gene mapping, gene therapy, forensic;
food supplement, medical imaging, diagnostic, genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 4; Length 791;
Pred. No. 3.1e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; SEQ ID NO 53910; 103pp; English.
                                                                                                        Novel human diagnostic protein #23542.
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23-AUG-2000; 2000US-00649167.
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                                                             (first entry)
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Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    biodiversity.
                                                                                                                                                                                                                             Homo sapiens.
                                                             18-FEB-2002
                                                                                                                                                                                                                                                                                                                     11-OCT-2001.
                   ABG23551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to novel abiotic stress responsive polynucleotides and polypeptides. Also disclosed are vectors, expression cassettes, host cells, and plants containing such polynucleotides. Also disclosed are methods for using the polynucleotides and polypeptides to alter the responsiveness of a plant to abiotic stress. The invention is useful in agriculture. The nucleic acid is useful for determining whether a test plant has been exposed to an abiotic stress condition. It is also useful for selecting an agent that alters abiotic stress regulated for selecting an abiotic stress polynucleotide expression in a plant cell, and to identify a homolog or ortholog to an abiotic stress responsive polynucleotide. The nucleic acid molecule and the polypeptide encoded by it are useful in altering the responsiveness of a plant to an abiotic stress, such as cold stress, salt stress, osmotic stress ray of their combinations. The present sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New stress-responsive nucleic acid, useful for altering the responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold stress, salt stress or osmotic stress.
                                                                                                                                                                                                                                                                                                                                                                  abiotic stress tolerance; transgenic plant; plant; cereal; agriculture.
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                                                                                                                                                                                                                                                                                                                     Rice abiotic stress responsive polypeptide SEQ ID NO:5945.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goff SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glazebrook J,
), Zhu T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              claim 1; SEQ ID NO 5945; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cooper B, G]
N, Ricke D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SYGN ) SYNGENTA PARTICIPATIONS AG
                                                                                                                                                                                  ABM87699 standard; protein; 648 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JUN-2001; 2001US-0300112P.
24-AUG-2001; 2001US-0314662P.
26-SEP-2001; 2001US-0325277P.
21-NOV-2001; 2001US-0332132P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 83.3%;
Marches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUN-2002; 2002WO-US019668
                                                                                                                                                                                                                                                                            (first entry)
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558 SSMASAAAAAA 569
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Moughamer T, Provart N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AAMAAAAAAMA 12
                          1 AAMAAAAAAMA 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003008540-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa
                                                                                                                                                                                                                                                                               02-JUN-2005
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Gaps

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ADD02808;

ABG23551 standard; protein; 791 AA.

RESULT 23 ABG23551 ID ABG

ઠે g Peptide useful for coded probe useful in biomolecule analysis.

(first entry)

29-JUL-2004

ADO43159;

ADO43159 standard; peptide; 30 AA.

Nano-barcode; scanning probe microscopy; probe

/note= "C-terminal amide"

WO2004038037-A2

06-MAY-2004

Modified-site

Synthetic

22-SEP-2003; 2003WO-US029726 20-SEP-2002; 2002US-00251152 19-SEP-2003; 2003US-00667004

Su X, Yamakawa M;

Chan S,

(ITLC ) INTEL CORP

WPI; 2004-399960/37.

Location/Qualifiers

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AD043159
                                                                      The present invention describes a superantigen binding site within the CD28 molecule that specifically and directly binds to a superantigen. Also described: (1) a method for treating a superantigen-related disorder in a mammalian subject; (2) a method of inhibiting pyrogenic exotoxin-mediated activation of Th1-1ymphocytes and protecting against toxic shock induced by a pyrogenic exotoxin or by a mixture of pyrogenic exotoxins, in a subject; (3) a method of eliciting protective immunity against toxic shock induced by a pyrogenic exotoxin in a subject; (4) a substance that inhibits the binding of a superantigen to a superantigen binding site in CD28; (5) a pharmaceutical composition for treating or preventing superantigen-related disorders comprising the substance that inhibits the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preparing a pharmaceutical composition for treating superantigen-related disorders caused by Staphylococcus aureus or Streptococcus pyogenes. The present sequence represents an sCD28 molecule related peptide motif, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                preparing a pharmaceutical composition for treating superantigen-related disorders caused by Staphylococcus aureus or Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        direct interaction between CD28 molecule and the pyrogenic exotoxin, which leads to antagonising of toxin-mediated activation of Thi lymphocytes; (6) an isolated and purified peptide having an amino acid sequence homologous to an amino acid sequence comprised within a superantigen binding site within the CD28 molecule, (7) a method of screening for a test substance which specifically binds to the CD28 molecule and is capable of antagonising pyrogenic exotoxin-mediated activation of Thi lymphocytes and optionally of eliciting protective immunity against toxic shock induced by a pyrogenic exotoxin or by a mixture of at least two pyrogenic exotoxins; and (8) a method of preparing a therapeutic composition for treating a superantigen-related disorder in a mammalian subject. The substance and pharmaceutical composition have antibacterial activities, and can be used in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New superantigen binding site within the CD28 molecule, useful for
                                                                                                                  superantigen binding site; CD28; superantigen; antibacterial; gene therapy; superantigen-related disorder; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapy. The substance, peptide or CD28 molecule can be used
                                                                 SCD28 molecule related motif peptide SEQ ID NO:7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CO HEBREW UNIV JERUSALEM.
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                                                                                                                                                                                                                                                                                                                                                                      2003WO-IL000278
                                                                                                                                                                                                                                                                                                                                                                                                                        04-APR-2002; 2002IL-00148993
                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arad G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-804296/75.
                                                                                                                                                                                                                                                                    WO2003084995-A2.
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                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                      03-APR-2003;
               01-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaempfer R,
                                                                                                                                                                                                                                                                                                                     16-OCT-2003
                                                                                                                                                                                           Synthetic
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The present sequence is that of a peptide of potential use for production of a coded probe useful in the method of the invention. The sequence was obtained by solid-phase peptide synthesis, and is pradicted to be an alpha helix. The invention provides methods, apparatus and compositions for the detection, identification and/or sequencing of biomolecules, such as nucleic acids or proteins. Coded probes comprising a probe molecule attached to one or more nano-barcodes are allowed to bind to target molecule and coded probes are allowed to bind to target complex cound coded probes are allowed to bind to target to probe microscopy (SPW). The nano-barcodes may be any molecule or complex that is distinguishable by SPW, such as carbon nanotubes, fullarenes, submariner metallic barcodes, nanoparticle or quantum dots. The methods allow the sequencing of long mucleic acid sequences in a single sequencing run, high sefficiency in terms of operator time, and sensitive and accurate detection and/or identification of nucleic acids with low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
Detecting, identifying and sequencing of biomolecules using controlled alignment of nano-barcodes encoding specific information for scanning probe microscopy, useful in the fields of molecular biology.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2;
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0; Mismatches
                                                                                                                                      Example 3; SEQ ID NO 1; 63pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and accurate detection and/or ident
incidence of false positive results
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AEB28995 standard; peptide; 30 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83.3%;
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Gaps

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Indels

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DB 7; Length 16;

Score 40; DB 7 Pred. No. 9.1; 0; Mismatches

80.0%;

Similarity

Query Match Best Local S Matches

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RESULT 25

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method for determining a nucleotide sequence of a nucleic acid. The method comprises: (a) providing one or more coded oligonucleotide probes, each coded oligonucleotide probes comprising an oligonucleotide associated with at least one nanocode comprising a detectable non-encoding feature; (b) contacting a target nucleotide acid with the one or more coded oligonucleotide probes; and (c) identifying coded oligonucleotide probes that bind to the target nucleotide acid using scanning probe microscopy (SPM) to detect the nanocode and the detectable non-encoding feature. Nanocodes of the invention in certain aspects include detectable features beyond the arrangement of tags that concode information about the barcoded object. The tags that encode information about the barcoded object. The detecting the tags that encode information about the barcoded object. The concode information about the barcoded object. The detectable features include structures of a nanocode or associated with a nanocode, referred to as detectable feature tags, for error.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  checking/error correction, encryption and data reduction/compression. The present sequence represents a synthetic peptide which connects four buckeyballs on graphite in an example from the present invention, where the example is about the synthesis and SPM scanning of a nanocode.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying target nucleic acid sequence, by contacting target nucleic acid with coded oligonucleotide probes, and identifying probes binding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human prostate/colon/lung/breast cancer-related protein 1442, SEQ:1499.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; cancer; tumour; prostate cancer; colon cancer; lung cancer;
                                                                    nucleic acid determination; scanning probe microscopy; nanocode.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        target nucleic acid using scanning probe microscopy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; SEQ ID NO 1; 29pp; English.
                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADN13984 standard; protein; 92 AA.
                                Synthetic peptide SEQ ID NO:1.
                                                                                                                                                                        /note= "-CONH2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.0%;
                                                                                                                                                                                                                                                                                31-DEC-2003; 2003US-00750515.
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08-SEP-2005 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                     Berlin A;
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2005-511772/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                 (ITLC ) INTEL CORP.
                                                                                                                                                                                                            US2005147981-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 30 AA;
                                                                                                                                                        Modified-site
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                                                                                                                                                                                                                                              07-JUL-2005
                                                                                                      Synthetic
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the invention transce to inverse cause converse.

The invention transce to inverse cause converse.

The invention also relates to these cDNA sequences proteins (ADN13970). The invention also relates to vectors and host cells comprising a nucleic acid of the invention; a method for the recombinant production of a protein of the invention; a method for the recombinant confined a protein of the invention; a method for the recombinant confined acid sequence of the invention; a method for detecting a cancerous cell by PCR or probe hybridisation; inhibiting at least concernus cell by PCR or probe hybridisation; inhibiting at cancerous phenotype (particularly aberrant proliferation) of a cell; a method of identifying an agent that modulates the biological activity of a gene or product differentially expressed in a cancerous cell; a method of control cell; and a method of treating a cancer or product differentially expressed in a cancerous cell; ompared with a normal cell; and a method of treating a cancer patient using the agent of product differentially expressed and polypeptides can be used to diagnose, controlling or prognose, treat or prevent cancers such as prostate, colon, lung or prognose, treat or prevent cancers such as prostate, colon, lung or prognose, treat or prevent cancers such as prostate, colon, lung or cancer. The nucleic acids can also be used for gene mapping, tissue concerned and for this patent did not form part of the printed specifically claimed cancer-related protein of the invention. Note: The specifically chaimed in the print of the printed forms and or prevent of the printed forms and propertion of the printed forms of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                profiling, as diagnostic reagents, and for gene mapping or tissue typing or e.g. prostate, colon, or breast cancer.
breast cancer; drug screening; diagnosis; prognosis; prevention;
gene mapping; tissue typing; tissue profiling; cytostatic; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention relates to nucleic acids (ADN12486-ADN13970) isolated
                                                                                                                                                                                                                                                                                                                                                                                                                        Garcia PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                          Sakamoto D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome derived single exon protein #4601.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                        Kassam A, Zhang G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 18; SEQ ID NO 1499; 190pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABO58367 standard; protein; 109 AA.
                                                                                                                                                                                                                                            16-MAY-2003; 2003WO-US015465.
                                                                                                                                                                                                                                                                                            17-MAY-2002; 2002US-0381533P.
04-FEB-2003; 2003US-0445222P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.08;
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Best Local Similarity 90.9
Matches 10, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                          Scott EM, Lamson G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2004-376173/35.
                                                                                                                                                                                                                                                                                                                                                                          (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ADN13927
                                                                                                                                      WO2004039943-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 92 AA;
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                                                                                     Homo sapiens
                                                                                                                                                                                           13-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AB058367
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RESULT 29
ABG15501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acids sequences ("Illy defined in the specification. The probe is a single exon probe that bybridises under high stringency conditions to a nucleic acid molecule expression (comprising a plurality of single exon nucleic acid molecule expression (comprising a plurality of single exon nucleic acid gene expression (comprising a plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon addressably isolatable or amplifiable from the plurality), a single exon addressably isolatable or amplifiable from the plurality), a single exon addressably isolatable or amplifiable from the plurality), a single exon addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a vector comprising the single exon probe cited above, where each of the above- mentioned amino acid of any of the above- mentioned amino acid sequences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing human gene expression data by subscription, and a computer-readable exorped each record including data on the expression of a single exon probe expression analysis. The probes may be used as tools for surveying the above. The probes are used a tools for surveying a cited above. The probes are used in identifying and characterising gross a leterative splicing events, in priming the synthesis of nucleic acids, or in constructing genome-decived single exon microarrays. In addition, the probes are used in identifying and characterising grantler genomic alterations, in priming 
                                                                                                                                                                                                                                                                                                                                                                                                                         New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               segdata.uspto.gov/seguence.html?DocID=20030194704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 45; SEQ ID NO 32001; 80pp; English.
                                                                                                                                                                                                                                                                                                                                      Penn SG, Rank DR, Hanzel DK;
                                                                                                                                                      03-APR-2002; 2002US-00029386.
                                                                                                                                                                                                  03-APR-2002; 2002US-00029386
                                                                                                                                                                                                                                           (PENN/) PENN S G.
(RANK/) RANK D R.
(HANZ/) HANZEL D K.
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-119264/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 surveying tissues.
                                                              US2003194704-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 109 AA;
                       Homo sapiens.
                                                                                                            16-OCT-2003
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ö Gaps ; 0 DB 8; Length 109; 1; Indels Pred. No. 61; 1, Mismatches Score 40; DB Pred. No. 61; 80.08; 83.3%; Query Match
Best Local Similarity 83.3
Matches 10; Conservative 1 AAMAAAAAAMA 12 ð

36 AAVAAAAAAA 47

RESULT 30 AAG35185

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain caction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed contains an expressed sequence tags for identifying expressed containing the charapy techniques to reserve normal cutivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) and (II) are useful for treating disorders involving abberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in capponsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and to produce other types of data and products dependent on DNA and amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                       Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID NO 45860; 103pp; English.
                                                                                                                Novel human diagnostic protein #15492.
ABG15501 standard; protein; 112 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang YT;
                                                                                                                                                                                                                                                                                                                                     30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                          31-MAR-2000; 2000US-00540217, 23-AUG-2000; 2000US-00649167,
                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-639362/73.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAS79688.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 112 AA;
                                                                                                                                                                                                                                                     WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          biodiversity.
                                                                                                                                                                                                                    Homo sapiens.
                                                                           18-FEB-2002
                                                                                                                                                                                                                                                                                              11-OCT-2001.
                                      ABG15501;
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990S-0139461P.
990S-0139462P.
990S-0139763P.
990S-0139763P.
990S-0140333P.
990S-0140333P.
990S-0140331P.
990S-014287P.
990S-014287P.
990S-014287P.
990S-014287P.
990S-014287P.
990S-0144332P.
990S-014508P.
990S-014508P.
990S-014508P.
990S-014508P.
990S-0145192P.
990S-0145192P.
990S-014518P.
990S-014518P.
990S-0145318P.
990S-0145318P.
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990S-014743P

990S-014813P

990S-0148319P

990S-0148664P

990S-0148664P

990S-0149368P

990S-0149175P

990S-014972P

990S-014972P

990S-014972P
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99US-0147260P.
99US-0147303P.
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10-AUG-1999)
11-AUG-1999)
12-AUG-1999)
13-AUG-1999)
13-AUG-1999)
16-AUG-1999)
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28-JUL-1999;
02-AUG-1999;
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20-AUG-1999;
23-AUG-1999;
18 - JUN - 1999;
22 - JUN - 1999;
23 - JUN - 1999;
                                                           23 - JUN - 1999;
24 - JUN - 1999;
28 - JUN - 1999;
29 - JUN - 1999;
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05-AUG-1999;
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                                                                                                                                                                                                                                                                                      22-JUL-1999
  Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                             Zea mays protein fragment SEQ ID NO: 42946.
   AAG35185 standard; protein; 126 AA
                                                                                                                                                  9905-0121825P.
9905-0123180P.
9905-0125788P.
9905-0126784P.
9905-0126784P.
9905-0128724P.
9905-0128724P.
9905-0130077P.
9905-0130077P.
9905-0130077P.
9905-0131449P.
9905-0131449P.
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9905-0131449P.
9905-01314487P.
9905-01314219P.
9905-01314219P.
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9905-01314219P.
9905-01314219P.
9905-0131421P.
9905-0131452P.
9905-0131452P.
9905-0131452P.
9905-0131452P.
9905-0131452P.
                                                                                                                                     25-FEB-2000; 2000EP-00301439
                               18-OCT-2000 (first entry)
                                                                                         Zea mays subsp. mays
                                                                                                                                                  25-FBB-1999;
05-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
06-APR-1999;
19-APR-1999;
21-APR-1999;
21-APR-1999;
21-APR-1999;
30-APR-1999;
30-APR-1999;
06-MAY-1999;
06-MAY-1999;
06-MAY-1999;
06-MAY-1999;
11-MAY-1999;
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18-MAY-1999;
19-MAY-1999;
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25-MAY-1999;
27-MAY-1999;
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01-JUN-1999;
03-JUN-1999;
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14-MAY-1999
                                                                                                                       06-SEP-2000
                 AAG35185;
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capable of detecting 1000 or more genes from brosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-ABB7072). The sequence data for this patent did not form part of the from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic; antipsoriatic; antiinflammatory; gene therapy; Nanodisc; proliferative disorder; inflammatory disorder; immune disorder; metabolic disorder; bone disorder; CNS disorder; cancer; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent
                               Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 35520; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Length 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB
Pred. No. 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                            Li PWD, Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human polypeptide segid 1053.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADU02586 standard; protein; 191 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-APR-2004; 2004WO-US012047.
                                                                                                                                                  23-MAR-2001; 2001WO-US009231
                                                                                                                                                                          23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ulcerative colitis; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97 AAAAAAAAAAA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 83.3
Matches 10; Conservative
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                                                                       Drosophila melanogaster
                                                                                                                                                                                                                                            Adams M,
                                                                                                                                                                                                                                                                     WPI; 2001-656860/75.
                                                                                                                                                                                                                 (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 158 AA;
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                                                                                              WO200171042-A2
                                             pharmaceutical
                                                                                                                                                                                                                                                                                                                                      interactions.
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                                                                                                                        27-SEP-2001.
                                                                                                                                                                                                                                            Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADU02586;
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No.
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9905-0159638P.
9905-0169584P.
9905-0160767P.
9905-0160768P.
9905-0160814P.
9905-0160814P.
9905-0160815P.
9905-0160815P.
                99US-0149930P.
99US-015066P.
99US-0151065P.
99US-0151066P.
99US-0151080P.
99US-0151303P.
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990'S-0153070P.
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99US-0158029P.
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990S-0159295P.
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990S-0159339P.
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99US-0162142P.
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ses 10; Conservative
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-OCT-1999;
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-OCT-1999;
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1D ABB6
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AC ABB6
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Sequence 191 AA;

2003US-0463708P. 2003US-0463732P. 2003US-0467199P.

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New first nucleic acid molecule comprising a polynucleotide sequence given in the specification, useful in preparing a composition for diagnosing or treating e.g., cancer, psoriasis or ulcerative colitis.
                                                                                                                                                                             Claim 14; SEQ ID NO 1053; 291pp; English.
                                                                                                 (FIVE-) FIVE PRIME THERAPEUTICS INC.
                  02-MAY-2003; 2003US-0467230P.

19-MAY-2003; 2003US-0471306P.

19-MAY-2003; 2003US-0471336P.

08-JUL-2003; 2003US-0485224P.

08-JUL-2003; 2003US-0486446P.

14-JUL-2003; 2003US-0486480P.

08-AUG-2003; 2003US-0486480P.

08-AUG-2003; 2003US-0493573P.
                                                                                   08-SEP-2003; 2003US-0505059P
                                                                                                                            WPI; 2004-775861/76.
                                                                                                              Hestir K,
                                                                                                                                   N-PSDB; ADU01854.
18-APR-2003;
18-APR-2003;
02-MAY-2003;
02-MAY-2003;
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The invention relates a recombinant DNA construct comprising a CC polymucleotide having any of 5544 mucleotide sequences (CDNAs SEQ ID NO: 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences (1-5544) and encoding a polypeptide with any of 5544 amino acid sequences (SEQ ID NO: 5545-11088). The CDNAs and proteins are from corn, soybean, Arabidopsis, wheat and rape but the specification does not indicate which sequences is derived from which organism. Also included is a method of producting a plant having an improved property, comprising transforming a plant with a recombinant DNA construct comprising a promoter region tunctional in a plant cell operably joined to a polynucleotide encoding a CC plant. The property is selected from improving plant cold tolerance, for plant. The property is selected from improving plant cold toleranse, for pathway, for improving plant tolerance, for galactomannan production, for production of plant growth regulators, for improving plant tolerance to plant disease, for galactomannan production, for improving plant tolerance to herbicides, for increasing the rate of improving plant tolerance to extreme osmotic conditions, for improving plant tolerance to extreme osmotic conditions, for improving plant tolerance to extreme osmotic conditions, for improving plant tolerance to pathogens or pests, for yield improvement by modification of conditioning seed oil yield improvement by modification of modifying seed protein yield and/or content, for yell improvement by modification of carbohydrate, nitrogen or phosphorus use and/or uptake and for yield improvement by providing improved plant growth and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant DNA constructs useful in the field of biochemistry and genetics, and in particular for producing transgenic plants with improved biological characteristics.
                                                                                                                                                                                                                                                                                                                                                                                                      Plant; transgenic; cold tolerance; growth rate; drought tolerance; disease resistance; galactomannan production; plant growth regulator; heat tolerance; herbicide tolerance; lignin production tolerance; extreme osmotic condition tolerance; pathogens resistance; pest resistance;
                                                Gaps
                                                .
0
    Length 191;
                                           1; Indels
      Score 40; DB 8; 1
Pred. No. 1.1e+02;
                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; SEQ ID NO 7771; 14pp; English.
                                                                                                                                                                                                                                             ADT57694 standard; protein; 227 AA.
                                                                                                                                                                                                                                                                                                                                                                     Plant polypeptide, SEQ ID 7771.
    80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-APR-2003; 2003US-00424599.
28-APR-2003; 2003US-00425115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-DEC-2003; 2003US-00739930
                                                                                                                                                                                                                                                                                                                            13-JAN-2005 (first entry)
                                                    Conservative
                                                                                         1 AAMAAAAAAM 11
                                                                                                                                  20 AAAAAAAAA 30
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Query Match
Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                    RESULT 33
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Williams LT;

Chu K, Masuoka L,

The invention describes a new first nucleic acid molecule comprising a polymucleotide sequence given in the specification. Also described are: an animal injected with the nucleic acid molecule; a second nucleic acid molecule; a second nucleic acid molecule and animal injected with the nucleic acid molecule and settingence comprising a second polymucleotide sequence that is at least abour 70 80, 90 or 95% homologous to the first nucleic acid molecule and a tringency conditions; a vector comprising the nucleic acid molecule; a promoter that drives the expression of the mucleic acid molecule; a promoter that drives the expression of the mucleic acid molecule; and one composition comprising the nucleic acid molecule; and one crop composition comprising the polypeptide and a carrier or before cell; a substantially purified polypeptide; and nucleic acid molecule; weetor or host cell; a substantially purified polypeptide; and minal injected with the polypeptide and a carrier or buffer; a cell animal injected with the polypeptide or polypeptide or transfected cells cransfected with the polypeptide molecule and a carrier or buffer; acid molecule; vector or host cell; a substantially purified polypeptide; or comprising the polypeptide molecule; worthersising a series of simultaneously-symthesised Nanodises coll transfected with the polypuppid the molecule or transfected with the polypeptide molecule or from the polypeptide or transfected with the proposed processor of the molecial activity; a disquestic composition comprising the presence of the nucleic acid molecule or in endinger and for symthesising and the presence of the nucleic acid molecule or modulating the antendry specifically recognising, binding to or modulating the bacteriophage; a non-human animal injected with the antibody composition; a host cell that secretes the antibody is displayed on the bacteriophage; a non-human animal, and one or more cells desired with the antibody composition; a molecule and disease, disorder, syndecules and carriers; gene thera invention. us-10-617-568-2.rag

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Sequence 231 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-APR-2004
                                                                             Century K;
                                                                                                                                                                                                                                                                                                                                                                                                                      homologue.
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(FROM/)
  (HAAK/)
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development under at least one stress condition. The polynucleotide may also encode a plant transcription factor. The methods and compositions of the present invention are useful in the field of blochemistry and genetics, in particular for producing transgenic plants with improved blological characteristics such as increased yield, improved nitrogen flow, increasing plant tolerance to cold or heat, improving plant tolerance to extreme osmotic and drought conditions, and improving plant tolerance to plant pests or pathogens. They can also be used in physical arrays of molecules, plant breeding markers, computer-based storage and analysis systems. The present sequence is one of the 5544 plant protein sequences of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in sequence clearronic format directly from USPTO at
                                                                                                                                                                                     Gaps
                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                  Plant, C-repeat/DRE binding factor; CBF; transgenic; biomass; cold inducible promoter; environmental stress; cold tolerance; cell injury; growth inhibition; drought; high salt condition.
                                                                                                                                                                 Score 40; DB 8; Length 227; Pred. No. 1.3e+02;
                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                Corn C-repeat/DRE binding factor (CBF) G3441.
                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                        ADH75874 standard; protein; 231 AA.
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98US-00018235.
98US-00198119.
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98US-00017816.
98US-00018227.
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2001US-00773990
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ZARKA D.
JIANG C.
ZHANG J.
                                                                                                                                              Sequence 227 AA;
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15-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-NOV-1999;
                                                                                                                                                                                                                                                                                                              15-APR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-NOV-1998;
28-JAN-1999;
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(STOC/)
(JAGL/)
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(ZHAN/)
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(ZARK/)
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The invention relates to a transgenic plant having an altered trait as compared to a wild type or untransformed plant. The trait is altered, i.e. increasing or decreasing levels of at least one cell protectant in cells of the transgenic plant to rattered, i.e. increasing or decreasing levels of biomass, where the transgenic plant is transformed with a cells of blomass, where the transgenic plant is transformed with a crecombinant polymucleotide comprising an AP2 domain. Also included are a cold inducible promoter comprising an AP2 domain. Also control of the Rabls or Dreb2a promoters, a method of inducible promoter comprising an AP2 domain. Also controlly the levels of a cell protectant in a cell, a method for inducitying the levels of a cell protectant in a plant cell, a method for controlly the tolerance of a plant cell to an environmental stress, a method of altering the biomass of a method of sof altering the biomass of a plant. The improved environmental stress is selected from a decrease in content of a plant is or cells injury, plant sequence to cold temperatures, survival of a plant after exposure to freezing temperatures, cextent of a plant after exposure to drought conditions, cextent of a plant after exposure to drought conditions, cextent of a plant after exposure to drought conditions, cextent of a plant after exposure to drought conditions, cextent of a plant after exposure to drought conditions, cextent of a plant after exposure to drought conditions, cextent of a plant after exposure to high salt conditions; and which has survival of a cell after exposure to high salt conditions; and which has an increased tolerance to an environmental stress, e.g. drought, cold, the plant after the present sequence represents a plant CBF or handled or high salt. The present sequence represents a plant CBF or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New transgenic plants comprising C-repeat/DRE binding factor, useful in producing phenotypes with increased tolerance to an environmental stress. e.g. drought, cold, freezing or high salt.
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                                                                                                                                                                                                                                               Jaglo K, Gilmour SJ, Zarka D;
Riechmann JL, Sherman BK, Fromm M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 20; SEQ ID NO 314; 223pp; English.
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                                                                                                                                                                                                                                               Thomashow M, Stockinger EJ,
Jiang C, Zhang J, Haake V,
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RIECHMANN J L.
SHERMAN B K.
FROMM M.
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                                                                                                                                                       (CENT/) CENTURY K.
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The invention describes a transgenic plant comprising a recombinant polymucleotide of any one of more than 500 nucleotide sequences fully defined in the specification or its complement. The method of the invention can be used to produced a plant having altered traits such as invention can be used to produced a plant having altered traits such as: enhanced tolerance to abiotic stress; glyphosphate tolerance, hormone sensitivity; disease resistance; sugar sensing; early or late flowering; altered flower structure, change in stem biturcations, altered branching pattern, reduced apical dominance, reduced trichome density; lack of trichomes; reduced ectopic trichome development; altered stem morphology; increased root growth; increased root hairs; altered stem morphology; increased root growth; increased root hairs; altered seed development; premature senescence; increased necrosis; increase in seedling or plant; premature senescence; increased morphology; seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 biochemistry; increase in root anthocyanins; increase in plant anthocyanins, or alteration in light response or shade avoidance. The transgenic plant, polymucleotides and polymeptides are useful in bioinformatic search methods. This is the amino acid sequence of a plant transcription factor, and an orthologue of Arabiodopsis thaliana transcription factors isolated in the invention, that can be used in the creation of a transgenic plant with altered traits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New transgenic plant comprising a recombinant polynucleotide of any one of more than 500 nucleotide sequences, useful in bioinformatic search
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haake V;
Keddie J, Broun PE;
plant anthocyanin; light response; shade avoidance; bioinformatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heard JE, F
Reuber TL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jiang C, Heard
Adam LJ, Reube
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 1245; 435pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sherman BK, Riechmann JL, Jiang C
Creelman RA, Ratcliffe O, Adam LJ
Pilgrim ML, Dubell AN, Pineda O,
                  transcription factor; gene; ds.
                                                                                                                                               25-FEB-2003; 2003US-00374780.
                                                                                                                                                                                 18-APR-2001; 2001US-00837944
                                                                                                                                                                                                                                                JIANG C.
HEARD J E.
HAAKE V.
CREELMAN R A.
                                                                                                                                                                                                                  SHERMAN B K.
RIECHMANN J L.
                                                                                                                                                                                                                                                                                                                RATCLIFFE O. ADAM L J. REUBER T L. KEDDIE J.
                                                                                                                                                                                                                                                                                                                                                                                 BROUN P E.
PILGRIM M L.
DUBELL A N.
PINEDA O.
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                                                                                  US2004019927-A1.
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                                                    Zea mays
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(ADAM/)
(REUB/)
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(PINE/)
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                                                                                                                                                                                                                                                                                   (HAAK/)
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                                                                                                                                                                                                                                                    JIAN/
                                                                                                                                                                                                                                                                   HEAR/
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The invention describes a method of producing a transformed plant comprises transforming a target plant with the first polynucleotide, which is a member of the CBF clade of transcription factors, and is mutagenized to produce a second or a third polynucleotide, where the second or third polypeptide has an amino acid sequence different than the first polypeptide, and identifying a transformed plant comprising the second polynucleotide or the third polynucleotide. Also described are: a transgenic plant produced by the method above; a seed produced by the transgenic plant, where the seed comprises the second or third

Producing transformed plant, by transforming a target plant with a first polynucleotide, which is a member of the CBF clade of transcription factors, and which is mutagenized, and identifying a transformed plant.

Example 9; SEQ ID NO 178; 225pp; English.

Canella D;

Cook DD,

Gilmour SJ,

Thomashow M,

WPI; 2006-010542/01. N-PSDB; AEE27924.

19-MAY-2005; 2005WO-US017583. 21-MAY-2004; 2004US-0573443P (UNMS ) UNIV MICHIGAN STATE

WO2005112608-A2.

Zea mays.

01-DEC-2005

transformation; transgenic plant; plant; abiotic stress tolerance; transcription factor; CBF.

CBF clade transcription factor G3441 SEQ ID NO 178.

(first entry)

09-FEB-2006

AEE27925;

AEE27925 standard; protein; 231 AA.

RESULT 36

AEE27925

polymucleotide; and a transgenic plant comprising a recombinant, overexpressed mutated polymucleotide that encodes a mutant member of the cupe class class of transcription factor polypeptides, where the transgenic plant exhibits fewer or reduced adverse morphological or developmental effects than a plant that overexpresses a wild-type form of the mutated plynucleotide. The method is useful for producing a transformed plant having increased abiotic stress tolerance, as compared to wild type or control plants. This is the amino acid sequence of a CBF clade

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Pred. No. 1.3e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                         AEE27977 standard; protein; 231 AA.
                                                                                                                                                                                    80.0%;
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Best Local Similarity 90.>
                                                                                                                                                                                                        170 AAAAAAAAAA 180
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                                                                                                                                                                      transcription factor
                                                                                                                                                                             Sequence 231 AA;
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Score 40; DB 8; Length 231; Pred. No. 1.3e+02; 0; Mismatches 1; Indels

80.08;

Query Match Best Local Similarity

0; Mismatches

10; Conservative

Matches

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Gaps

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03-JUL-2003.
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                                                                                                                                                                                                                                                                                                                                            The invention describes a method of producing a transformed plant comprises transforming a target plant with the first polynucleotide, which is a member of the Cadee of transcription factors, and iss mutagenized to produce a second or a third polynucleotide, where the second or third polypeptide, and identifying a transformed plant comprising the first polypeptide, and identifying a transformed plant comprising the second polynucleotide or the third polynucleotide. Also described are: a transgenic plant produced by the method above; a seed produced by the transgenic plant, where the seed comprises the second or third overexpressed mutated polynucleotide that encodes a mutant member of the CBF clade of transcription factor polypeptides, where the transgenic
                                                                                                                                                                                                                                                                        Producing transformed plant, by transforming a target plant with a first polynucleotide, which is a member of the CBF clade of transcription factors, and which is mutagenized, and identifying a transformed plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plant exhibits fewer or reduced adverse morphological or developmental effects than a plant that overexpresses a wild-type form of the mutated polymucleotide. The method is useful for producing a transformed plant having increased abiotic stress tolerance, as compared to wild type or control plants. This is the amino acid sequence of a CBF clade transcription factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      novel gene; novel protein; tissue marker; molecular weight marker; chromosome marker; genetic disorder.
                                             transformation; transgenic plant; plant; abiotic stress tolerance; transcription factor; CBF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel protein (useful for identifying genetic disorders) #161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40; DB 10; Length 231;
Pred. No. 1.3e+02;
); Mismatches 1; Indels
                                                                                                                                                                                                                            Thomashow M, Gilmour SJ, Cook DD, Canella D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                       CBF clade transcription factor G3441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADE08006 standard; protein; 232 AA.
                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 3; 225pp; English
                                                                                                                                                      19-MAY-2005; 2005WO-US017583.
                                                                                                                                                                           21-MAY-2004; 2004US-0573443P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.98;
                                                                                                                                                                                                    (UNMS ) UNIV MICHIGAN STATE
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 AAAAAAAAAM 180
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                                                                                                                                                                                                                                                   WPI; 2006-010542/01.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 231 AA;
                                                                                                      WO2005112608-A2.
                                                                                Unidentified.
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                                                                                                                              01-DEC-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADE08006;
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anticonvulsant; cerebroprotective, vasotropic, gene therapy; gene mapping; forensic; mutation identification; biodiversity; cancer; gene mapping; forensic; mutation identification; biodiversity; cancer; autoimmune disorder; multiple sclerosis; rheumatoid arthritis; myasthenia gravis; tissue growth; tissue regeneration; tissue repair; tissue replacement; burn; incision; ulcer; osteoporosis; osteoarthritis; bone degenerative disorder; periodontal disease; nervous system disease; neuropathy; mechanical disorder; tranmatic disorder; nerve injury; Alzheimer's disease; Parkinson's disease; Huntington's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed, as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence represents a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhao QA, Wang J;
anac RT, Wang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antirheumatic; antiarthritic; muscular; osteopathic; vulnerary; antiulcer; antiinflammatory; CNS; nootropic; antiparkinsonian;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang J, Zhao UA,
ou P, Drmanac RT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40; DB 7; Length 232; Pred. No. 1.3e+02; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            Ren F, Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang YT, Asundi V, Goodrich RW, Ren F,
Ghosh M, Xue AJ, Wehrman T, Weng G, Zh
Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID NO 1072; 1177pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human polypeptide seg id 161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADU40376 standard; protein; 232 AA.
                                                           10-DEC-2001; 2001US-0339739P.

11-DEC-2001; 2001US-0339453P.

14-MAR-2002; 2002US-036591P.

14-MAR-2002; 2002US-0365384P.

12-APR-2002; 2002US-0372381P.

12-APR-2002; 2002US-037261SP.

22-APR-2002; 2002US-0012858.

24-APR-2002; 2002US-0012858.
10-DEC-2002; 2002WO-US039555
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                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ADE07095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 232 AA;
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Sequence 232 AA;

us-10-617-568-2.rag

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The invention describes an isolated polynucleotide comprising a nucleotide sequence selected from 124 nucleotide sequences (SEQ ID NO: 1-
124), or a polynuclectide enroding a polypeptide with biological
cativity, where the polynucleotide hybridises to the nucleotide sequence
under stringent hybridisation conditions or has greater than 99% sequence
cuder stringent hybridisation conditions or has greater than 99% sequence
cuder stringent hybridisation conditions or has greater than 99% sequence
conditions in therapeutic, diagnostic (as expressed sequence
tags for identifying expressed genes) and research methods such as gene
mapping, forensics, identification of mutations responsible for genetic
disorders or other traits, to assess biodiversity, and to produce many
cother types of data and products dependent on DNA and amino acid
disorders or other traits, to assess biodiversity, and to produce many
cother types of data and products dependent on DNA and amino acid
sequences. The polynucleotide or the polypeptide is useful in methods for
conserving and/or treating disorders involving aberrant protein
control many anyloid or lymphoid cell disorders and for treating
and myasthenia gravis, in bone, cartilage, tendon, ligament and/or nerve
control many are placement, and in healing of burns, incisions and utsers,
control disease. The composition is useful in assays for
crepair and replacement, and in healing of burns, incisions and utsers,
controliferation and differentiation of various hematopoietic lines, assays
con periodontal disease.

Con periodontal mervens evertem disease and neurons of various neural cells
and neripharal nervous system diseases and neurons and neural disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue, particularly diseases such as peripheral neuropathy and localised neuropathies, Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy'-Drager syndrome, as well as stroke. This sequence represents a novel polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide, useful in therapeutic (i.e. for treating e.g., cancer, neurodegenerative disorders), diagnostic (as expressed sequence tags for identifying expressed genes) and research methods
amyotrophic lateral sclerosis; Shy-Drager syndrome; stroke; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10; SEQ ID NO 161; 138pp; English.
                                                                                                                                                                                                                                                                                            25-JAN-2001; 2001WO-US002623.
05-FEB-2001; 2001WO-US003800.
26-FEB-2001; 2001WO-US004927.
05-MAR-2001; 2001WO-US004941.
                                                                                                                                                                                                                                                                                                                                                                                                        18-APR-2001; 2001WO-US008656.
11-DEC-2001; 2001US-0339453P.
                                                                                                                                                                                                                                                                                                                                                                                 2001WO-US008631
2001WO-US008656
                                                                                                                                                                      22-APR-2002; 2002US-00128558
                                                                                                                                                                                                             2000US-00488725
2000US-00491404
                                                                                                                                                                                                                                                        2000US-00552317
                                                                                                                                                                                                                                                                                2000WO-US035017
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DRMANAC R T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TANG Y T.
WANG Z.
WENG G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ADU40252
                                                                                    JS2004219521-A1
                                               Homo sapiens.
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                                                                                                                             04-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TANG/)
(WANG/)
(WENG/)
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(DRMA/)
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Drmanac RT;

Boyle BJ,

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The invention describes a method of treating a mammal having a tumor of glial origin comprising cells that express a type A or B glial tumor antigen comprises contacting the cells with a composition of: a first binding agent comprising a first antibody, oligopeptide or organic molecule that binds to a type A or B glial tumor antigen; and a second binding agent comprising a second antibody, oligopeptide or organic molecule that binds to a type B or A glial tumor antigen. Also described is a method of determining the presence of a type A or B glial tumor in a mammal. The method is useful in treating a mammal at unor of glial origin comprising cells that express a type A or B glial tumor of glial origin comprising cells that express a type A or B glial tumor antigen. This sequence represents a human tumor-associated antigenic target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treating a mammal having a tumor of glial origin comprising cells that express a type A or B glial tumor antigen by contacting the cells with a composition comprising first and second binding agents.
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                                    Gaps
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   Length 232;
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                                    Indels
                                                                                                                                                                                                                                                                                  Tumor-associated antigenic target polypeptide TAT285.
                                                                                                                                                                                                                                                                                                                   cytostatic, diagnosis, therapy; tumor;
tumor-associated antigenic target polypeptide; TAT.
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Score 40; DB 9; I
Pred. No. 1.3e+02;
); Mismatches 1;
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                                                                                                                                                                                      ADV70174 standard; protein; 236 AA
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27-FEB-2004; 2004US-0548299P.
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      80.08;
                     90.98;
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                                        Conservative
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                                                                      1 AAMAAAAAAM 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC.
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N-PSDB; ADV70078.
                  Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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          Query Match
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Job time : 92.924 secs

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